The biology and molecular ecology of *Oreixenica* and related southeast Australian Satyrinae

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The biology and molecular ecology of *Oreixenica* and related southeast Australian Satyrinae

by

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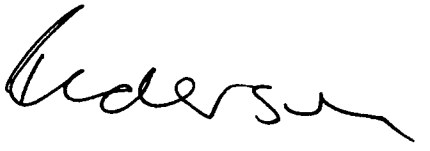

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Abstract

In the Australian region, the family Nymphalidae contributes one fifth of the butterfly fauna, with the endemic species and genera all belonging to the subfamily Satyrinae, which is most diverse in the south eastern part of the continent. Here, extensive geographical variation has developed in the phenotype of many satyrines. This is best illustrated in the genus *Oreixenica,* which is endemic to the cooler parts of southeast Australia.

This thesis comprehensively examines the relationships of a cross section of five genera and fourteen species from this group. New morphological data from the eggs and genitalia of these taxa are provided and used to test existing hypotheses of relationships. On this basis, it can be shown that the southeast Australian Satyrinae conform to a monophyletic group.

Further evidence was sought from molecular data. Sequence data from three genes: the mitochondrial Cytochrome Oxidase Subunit 1 gene (CO1), the nuclear Elongation Factor 1α (EF-1α) protein-coding gene, and the nuclear *Wingless* gene, were utilised to construct a phylogeny of twelve satyrine species plus two nymphalid outgroup genera. Phylogenetic trees derived from all data sets recovered very similar, well-supported relationships. The major findings from these analyses are: the temperate zone southeast Australian Satyrinae are indeed a monophyletic group based upon molecular evidence; the *Heteronympha* clade is sister to the *Oreixenica* clade; *O. latialis* from the Australian Alps is the sister species to the Tasmanian endemic *O. ptunarra*; *H. cordace* is derived from the ancestor of *H. penelope* and *H. merope*; and, *G. klugii* is placed basally within the group. Estimated ages of divergence for the taxa are presented and these are related to the broad evolutionary history of the expansion of native grasslands in southern Australia.

Whilst these results have implications for the conservation management of Australian Satyrinae, particular attention is focussed on the threatened Tasmanian *O. ptunarra*, which has a fragmented and restricted distribution. Since European settlement a considerable reduction and modification of *O. ptunarra* habitat has occurred, particularly throughout the Midlands, a major agricultural region. The genetic relationships between sampled populations suggest that *O. ptunarra* does broadly interact within the traditional subspecies ranges, and some populations are becoming increasingly genetically isolated particularly in the Midlands and eastern regions of Tasmania. This detail is presently overlooked in current management plans and conservation efforts which are opportunistic in their approach to butterfly protection.

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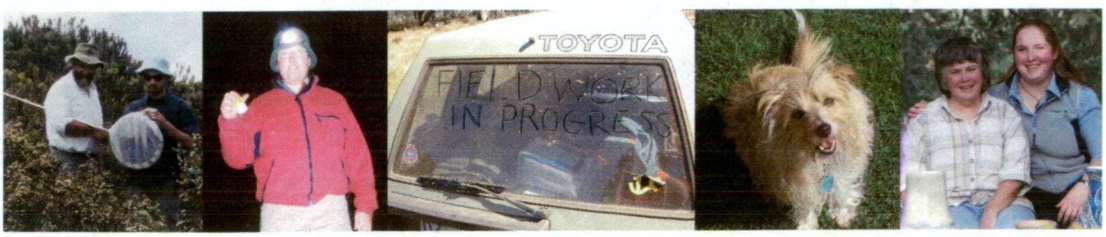

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Chapter 1

General Introduction

1 CONTEXT OF RESEARCH

1.1 *Background*

Butterflies and other grassland species are disappearing due to human activity. In Tasmania less than 3% of the pre European extent of native grassland still exists (Reid *et al.* 1999). Much of the grassland remaining is on south facing, rocky hill slopes, that were left because the land was too poor to plough and cultivate. This marginal habitat is now all that remains of Tasmania's native tussock grassland which is one of the most threatened natural habitats (Kirkpatrick 1991). Consequently invertebrates that depend on these grasslands are threatened with decline.

The butterfly subfamily Satyrinae depends on grasses as foodplant for their larvae (Ackery 1988). Prior to European settlement, the Midlands of Tasmania was a mosaic of grasslands, woodlands and open forest, but over 90% of this habitat has now been converted to improved pasture (Fensham & Kirkpatrick 1989). Many Tasmanian butterfly species, which rely on these grasslands and grassy woodlands, are therefore prone to local extinction. Much remains to be learnt about the butterflies of Tasmania, in particular: how they interact with their environment; how they react to disturbances; what factors control their population sizes; their evolutionary relationships; and their patterns of movement.

Globally lepidopteran conservation has had a chequered history since Pyle (1967) first raised the issue. In Australia, lepidopteran conservation has only very recently started to appear on scientific and political agendas, as part of a growing concern over the future of the Australian environment and biota, but has not yet developed to encompass the broad public and scientific concern it engenders in much of the northern hemisphere (New 1990(92); Sands 1999; New & Sands 2004).

Butterflies are recognised as important flagship taxa for invertebrate conservation (New *et al.* 1995; New & Sands 2004); single-species butterfly management has become well established where knowledge and expertise on habitat management and butterfly

ecology are relatively advanced in the northern hemisphere (Pullin 1994; New *et al.* 1995). However, despite the advances in butterfly conservation management globally over recent decades, many species remain poorly understood (New *et al.* 1995), particularly in the Australasian region, where there is not a bank of conservation experience equivalent to that available for parts of the northern hemisphere (New 1990(92); New *et al.* 1995; New 1999; New & Sands 2002a, 2002b; Sands & New 2002; New 2007).

Oreixenica ptunarra, which is currently listed as vulnerable under the Tasmanian *Threatened Species Protection Act 1995* (Parliament of Tasmania 1995) and indeed the genus *Oreixenica* in general, is a case in point. The phylogeny and biology of *Oreixenica* is not clear. To date, there is little available published data relating to this question. In order to advance the effective conservation of *O. ptunarra* it is vital that the species be better understood.

Unfortunately lepidopteran conservation is littered with examples of conservation efforts which have failed due to a lack of understanding the biology of the species in question or its habitat requirements. In many butterfly species adults may have particular needs with regard to topography for mating, nectar sources for food, and larval foodplant for oviposition. Caterpillars may need certain foodplants, sometimes in specific growth stages or combinations thereof, or in the case of many Lycaenidae may need to cohabit with particular ant species (New *et al.* 1995). These various complementary resource suites determine the suitability of a habitat and need to be understood if conservation measures are to be successful. A classic example is the attempt in Britain to conserve the Large Blue - *Maculinea arion* (Lycaenidae) by fencing grassland habitat, to exclude grazing stock. These actions ultimately lead to the extinction of the butterfly, as the biology of the species was not understood and the relationship between the butterfly and attendant ants was overlooked. Fencing to exclude grazing resulted in the vegetation growing too tall, thereby changing the microclimate for the attendant ants (Thomas 1980). It is therefore vital that conservation efforts are based on a sound ecological understanding.

Two main themes recur in butterfly conservation; the first concerns conservation of butterflies *per se*, the second concerns the use of butterflies to indicate community or

habitat 'health' (New 1997b). Both of these themes prevail in relation to the conservation of *Oreixenica* (Neyland 1992, 1993; Bell 1998; Anderson 2001b; New & Sands 2003).

By using butterflies as targets and tools for fostering interest in conservation, many other coexisting and co-dependent organisms (such as food plants and natural enemies) may also be safeguarded effectively (New *et al.* 1995). The relatively precise and restricted environmental requirements of particular butterflies means that these species can have considerable value as 'indicator taxa' – groups which can shortcut total community documentation by furnishing information which indicates the broader effects of environmental change or reflects a particular suite of ecological conditions (New 1997b). Few butterflies in Australia are regarded as umbrella species (New 1990(92)). Some species of *Oreixenica* are potentially strong candidates as umbrella species as they are restricted to alpine herbfield/grassland communities, and they are abundant over limited altitudinal ranges. Any pronounced diminution in abundance of the species may reflect wider-reaching effects on these communities (New 1997a). If *Oreixenica* species are going to be promoted as umbrella taxa it is even more important that we fully understand the biology and phylogenetics of the genus.

1.2 *Taxonomy and Phylogenetic Relationships of the Nymphalidae*

The large butterfly family Nymphalidae was first described by Rafinesque in 1815. Since then the systematic relationships among its many different taxa has been the subject of much dispute and are still fairly poorly understood; most subfamilies are only vaguely defined or supported by few characters (Freitas & Brown 2004).

Müller (1886) first proposed a number of subordinate lineages within Nymphalidae, and provided a foundation for the widely accepted infra-familial classification. Many of Müller's characters were based on early stages (Freitas & Brown 2004). Most European literature in the nineteenth century elevated the "browns" to family rank, as Satyridae, due to their distinctive phenotype. The first higher classification of the Satyridae (Herrich-Schäffer 1844) defined all but one of the currently accepted satyrid subfamilies. More recently Clark (1947; 1949) subdivided the Satyridae into five subfamilies; unfortunately he gave no definitive reasons for his classification. Following a critique of this work, Ehrlich (1958) attempted a coherent classification of all butterfly groups, using a large character set based on early stages and adults. On this evidence he argued a case for downgrading Satyrinae to a subfamily of Nymphalidae (Ehrlich 1958). Ehrlich and Ehrlich (1967) then went on to present a phenetic taxonomy for butterflies. Unfortunately, phenetic taxonomies do not always give convincing insights into evolutionary relationships between the taxa, since they are biased by features, which may be homoplasious (Farris 1979; Sokal 1985; Michael 1990). In contrast, phylogenetic taxonomies based on cladistic approaches, which produce taxonomies based on monophyletic groups generally better reflect evolutionary relationship among taxa (deQueiroz & Good 1997; King & Stansfield 1997; Lincoln *et al.* 1998; Nogrady 1998).

Miller's (1968) higher classification and phylogeny of the Satyridae was arguably the most influential classification of Satyridae in the latter half of the twentieth century. Miller employed an orthogenetic criterion to develop his phylogeny, apportioning genera to subfamilies, tribes and in some cases, to subtribes. Miller (1968) following Clark (1947; 1949) considered the "browns" to have family rank as Satyridae. Two decades later, Ackery and Vane-Wright (1984) and Ackery (1988) attempted to define the main groups within the superfamily Papilionoidea producing quite conservative results, especially for the subfamilies of Nymphalidae. Unfortunately neither

contribution sought to define the relationships within the different subfamilies of Nymphalidae (Freitas & Brown 2004).

The nymhalid classification of Harvey (1991) became popular in the final decade of the twentieth century. Harvey's classification, partly based on the larval characters of Müller (1886), listed genera for each group, although the relationships within and among the subgroups were still not fully resolved. Drawing heavily on Miller (1968) Harvey's classification treated Satyrinae as only a subfamily of Nymphalidae, and similarly down-ranked many of Miller's subordinate taxa. Harvey's classification was widely accepted until recent molecular data and more thorough cladistic analysis contributed new insights leading to several changes. The review of de Jong *et al.* (1996) summarised progress in Nymphalidae systematics until then, however, it was general in scope and did not focus on the subdivisions of the family.

In the last decade, the application of new molecular data and phylogenetic methods has assisted in resolving the relationships within Nymphalidae at a higher level. Brower (2000) using the *wingless* gene and Wahlberg *et al.* (2003b), using the *Cytochrome Oxidase Subunit 1* (CO1), *Elongate Factor 1α* (EF-1α) and *Wingless* gene fragments, showed that many of the traditional subgroups in Nymphalidae are indeed monophyletic (Freitas & Brown 2004). The comprehensive review of Freitas & Brown (2004), supported by the work of Brower (2000), Wahlberg *et al.* (2003b), and Wahlberg *et al.* (2005b), provided a well supported higher level phylogeny of Nymphalidae and showed that satyrine butterflies form a clade within the family Nymphalidae. However, at subdivisions below family, there are many unresolved relationships. The work of Viloria (1998; 2003) and Murray & Prowell (2005) seeks to resolve the other major lineages within the Satyrinae.

In recent years *The Nymphalidae Systematics Group* headed by Niklas Wahlberg, has made several significant contributions to understanding the phylogenetic relationships of taxa in the family, using mainly molecular methods (Wahlberg 2008a). The study by Peña *et al.* (2006) provides the most comprehensive higher level phylogeny of the Satyrinae to date. In regard to the subtribe Hypocystina, the genera placed in the Hypocystina by Peña *et al.* (2006) corresponded with Miller's (1968) taxa, but not with Viloria (2003).

Within the Australian butterfly literature, nomenclature has been conservative. All major works (e.g. Waterhouse & Lyell 1914; Common & Waterhouse 1981; Braby 2000) starting with the first detailed book on the Australian butterflies Waterhouse & Lyell (1914), have apportioned genera on the basis of well-established families and subfamilies only. Waterhouse & Lyell (1914) provided detailed descriptions of adults and keys for identification, including a scheme of classification and systematic index. In 1972 Common & Waterhouse published the landmark *Butterflies of Australia* revised as Common & Waterhouse (1981). *Butterflies of Australia: their identification, biology and distribution* (Braby 2000) is the current culmination of the monographic literature on Australian butterflies. Braby (2000) aimed to provide a manual for identification and a comprehensive, authoritative and up-to-date summary of the Australian fauna.

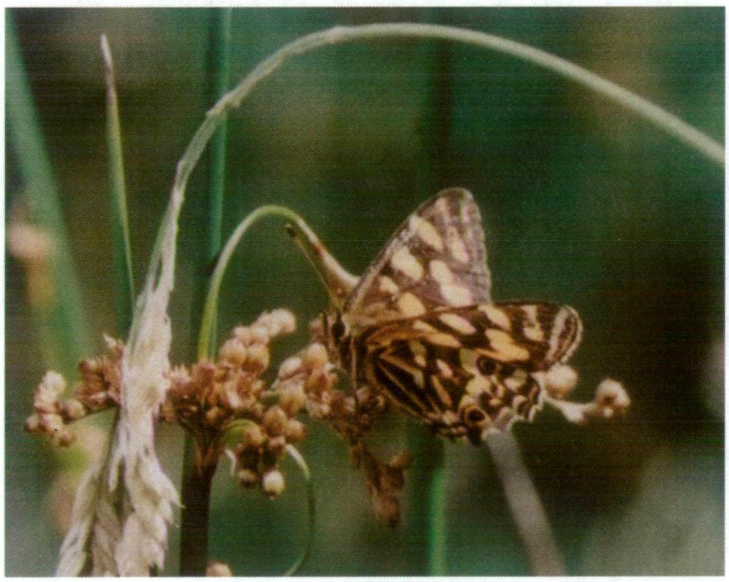


Plate 1 *O. kershawi* male, Lake Mountain Victoria

1.3 *Australian Satyrinae*

In the Australian subregion, the Nymphalidae comprise one fifth of the butterfly fauna, with the endemic species and genera all belonging to the sub-family Satyrinae (Braby 2000). In southeast Australia, Satyrinae are represented by the tribe Hypocystini (Miller 1968). One current school of thought is that this group may be Gondwanan in origin (Braby 2000; Peña *et al.* 2006), however Miller (1968) suggested that Australian Hypocystina were derived from the Indo-Malayan region and recent work by de Jong (2003) casts further doubt on a Gondwanan origin.

Michael Braby has been the most prolific recent author contributing to our understanding of Australian Satyrine. Much of his Australian work has focused on tropical and sub-tropical region (Braby & Jones 1994; Braby 1995a, 1995b, 1995d; Braby & Jones 1995; Braby 1996, 2002) and species and genera endemic to this region particularly *Tisiphone* and *Mycalesis* (Braby 1993, 1994a, 1995c). Braby's work in southern Australia has focused mainly on *Geitoneura* (Braby & New 1988a, 1988b, 1999). Other authors who have studied Australian Satyrine include: Edwards (1973) and Pearse & Murrary (1981; 1982) who focused on *Heteronympha*; Neyland (1993), McQuillan & Ek (1997) and Anderson & McQuillan (2003) who studied aspects of *Oreixenica ptunarra* biology; and finally studies by Lucas (1969) on *Tisiphone abeona*, Wood (1988) on *Hypocysta* genus and Johnson *et al* (1995) on the early stages of *Orsotriaena medus* and *Melanitis constantia.*

My work will substantially contribute to filling the gap in our understanding of the temperate zone southeast Australian Satyrinae fauna. Whist this work focuses on endemic Australian genera and species it will significantly contribute to the global understanding of the origins and morphological and molecular relationships of the Satyrinae.

1.4 *Spec ies used in this research*

Seven genera of temperate zone southeast Australian Nymphalidae were used in my research: *Argynnina* (Butler 1867), *Geitoneura* (Butler 1867), *Heteronympha* (Wallengren 1858), *Nesoxenica* (Waterhouse & Lyell 1914), and *Oreixenica* (Waterhouse & Lyell 1914) as representatives of the subfamily Satyrinae ('in group'), and two genera *Junonia* (Hübner 1819) and *Vanessa* (Fabricius 1807) subfamily Nymphalinae were included as 'out groups'. *Junonia* and *Vanessa* are the only Nymphalinae that occur in southeast Australia (Braby 2000).

The choice of species within each genus was based on local abundance and to represent the diversity within the genera. In total fourteen different species were used in my research: *O. ptunarra, O. latialis, O. lathoniella, O. orichora, O. correae, O. kershawi, N. leprea, A. hobartia, H. cordace, H. penelope, H. merope, G. klugii, V. kershawi,* and *J. villida.* Three of these species and one genus are endemic to Tasmania.

For the genera discussed within my study, I have followed a family and subfamily arrangement as accepted by modern Australian authors, and underpinned by the following classification (Wahlberg 2008b):

Family: **Nymphalidae** (Rafinesque 1815)
- subfamily: **Satyrinae** (Boisduval 1833)
  - tribe: **Satyrini** (Boisduval 1833)
    - subtribe: **Hypocystina** (Miller 1968)
      - genus: ***Argynnina*** (Butler 1867)
      - ***Geitoneura*** (Butler 1867)
      - ***Heteronympha*** (Wallengren 1858)
      - ***Nesoxenica*** (Waterhouse & Lyell 1914)
      - ***Oreixenica*** (Waterhouse & Lyell 1914)
        - species: ***A. hobartia*** (Butler 1867)
        - ***G. klugii*** (Guérin-Méneville 1830 [1830-32])
        - ***H. cordace*** (Geyer 1832 [1827-1837])
        - ***H. merope*** (Fabricius 1775)
        - ***H. penelope*** (Waterhouse 1937)
        - ***N. leprea*** (Hewitson 1864 [1863-1878])

O. correae (Olliff 1890)

O. kershawi (Miskin 1876)

O. lathoniella (Westwood 1851 [1850-1852])

O. latialis, (Waterhouse & Lyell 1914)

O. orichora (Lucas 1892)

O. ptunarra (Couchman 1953)

subfamily: **Nymphalinae** (Rafinesque 1815)

tribe: **Nymphalini** (Rafinesque 1815)

genus: ***Vanessa*** (Fabricius 1807)

species: ***V. kershawi*** (McCoy 1868)

tribe: **Junoniini** (Reuter 1896)

genus: ***Junonia*** (Hübner 1819)

species: ***J. villida*** (Godart 1819)

Plate 2 *O. ptunarra* male, sunning on dandelion Liawenee Moor 2001

1.5 *Currently recognised Apomorphies*

The following characteristics are often cited as synapomorphies, however there are numerous exceptions, and many of these traits are not unique.

1.5.1 Character(s) that define Nymphalidae

The Nymphalidae are characterised by the tri-carinate antenna and the elongate chaetosemata being parallel to the eye margin (Nielsen & Common 1991).

The following character state combination has been used to define the Nymphalidae: small to large; most antennal segments are relatively close together at the base; in the forewing the radial vein has five branches, some of which are stalked, and there is one anal vein; in the hindwing the humeral vein is usually present but sometimes is vestigial or absent, there are two anal veins, and the tornus is usually rounded, rarely tailed; legs reduced in size, pressed against the thorax and not used for walking; male forelegs lack pretarsus, the fore tarsus is often reduced to a single elongated segment and may be clubbed or brush-like without an apical claw; female forelegs usually have five segments and is clawed apically (Nielsen & Common 1991; Braby 2000; Freitas & Brown 2004).

Egg: variable in shape, taller than diameter, with vertical and horizontal ribs, or nearly spherical and sometimes nearly smooth. Larva with long, paired filaments, branching spines, or with fine, secondary setae and bifid anal segment or horned head; crochets multiordinal. Pupa suspended by cremaster or, rarely, loose on ground beneath debris (Nielsen & Common 1991).

1.5.2 Character(s) that define Satyrinae

No unique and universal characters, have been found to distinguish the Satyrinae from other Nymphalidae (de Jong *et al.* 1996; Ackery *et al.* 1998; Braby 2000).

The following character state combination has been used to define the Satyrinae: adults are usually orange and black, with eye-spots; at least one vein of the forewing is swollen basally (except in *Melanitis*); vein 3A is generally not free basally; the cells of

both wings are usually closed by tubular veins; and the precostal cell is absent except in *Elymnias* (Ackery 1984; Nielsen & Common 1991; Braby 2000).

The antenna is always scaled, at least near the base, with the club varying from narrow in *Melanitis*, to broad, rounded and flat in *Oreixenica*. The male frequently has a patch of sex-scales on the forewing, and sometimes has tufts of hairs or patches of sex-scales, on the hindwing. The valvae of the male genitalia are simplified and dentate (Braby 2000; Peña *et al.* 2006).

The larvae feed on grasses or sedges; the posterior abdominal segment is always forked and often a pair of horns are present on the head (Nielsen & Common 1991; Braby 2000).

1.5.3 Character(s) that define Satyrini

Midtibia with a long dorsal spine at the distal end (Miller 1968);
Third segment of palpus less than one-fourth the length of the second (Miller 1968).

1.5.4 Character(s) that define Hypocystina

The less miniaturised forelegs in both sexes serves to distinguish the hypocystines from all other Satyrinae (Miller 1968).

1.5.5 Character(s) that define Oreixenica

The following character state combination has been used to define the genus *Oreixenica*: veins of forewing swollen at base; eyes smooth; vein 10 from subcosta close to end of cell (Waterhouse & Lyell 1914).

2 RESEARCH APPROACH / STRUCTURE OF STUDY

Through the use of field based research, laboratory examination and molecular phylogenetics this project will examine the relationships within the southeast temperate zone Australian Satyrinae. A particular focus of this study is the endemic Tasmanian species *Oreixenica ptunarra.*

2.1 *Ai ms*

The aims of this research project are to:

1. Increase the pool of knowledge and understanding of the genus *Oreixenica*, and the relationship of *Oreixenica* to other temperate zone southeast Australian Satyrinae.
2. Characterise the adult morphology of five genera, and twelve species of temperate zone southeast Australian Satyrinae;and two genera, and two species of Nymphalidae.
3. Comprehensively describe the eggs of the temperate zone southeast Australian Satyrinae.
4. Describe and document the larva and pupa of *O. ptunarra.*
5. Contribute to understanding the species *O. ptunarra*, and the relationship of *O. ptunarra* to its relatives.
6. Investigate the genetic diversity of *O. ptunarra* populations which will contribute towards conservation management strategies for *O. ptunarra.*

To achieve these ends, this research has been conducted as a series of studies each focusing on specific research questions, linked by the common theme of furthering understanding of the genus *Oreixenica,* in particular the species *O. ptunarra.*

The thesis is presented in five main chapters bound by introductory and concluding chapters. Chapter 2, *Adult Morphology* and Chapter 3 *Immature stages of Oreixenica with notes on associated temperate zone southeast Australian Satyrinae* comprehensively describes all the life stages of *Oreixenica* and other related taxa. This is the first time that the morphology of the temperate zone southeast Australian Satyrinae has been described in detail.

Chapter 4, *molecular relationship of temperate zone southeast Australian Satyrinae* presents a phylogeny for the group based on molecular data. Chapter 5, *propositions for understanding the phylogeny and evolutionary history of temperate zone southeast Australian Satyrinae*, draws together information from the first three chapters.

Chapter 6, *population management of Oreixenica ptunarra* presents a population genetic analysis, and a brief discussion of land management practices in, and surrounding *O. ptunarra* populations which will help to inform proposed conservation strategies.

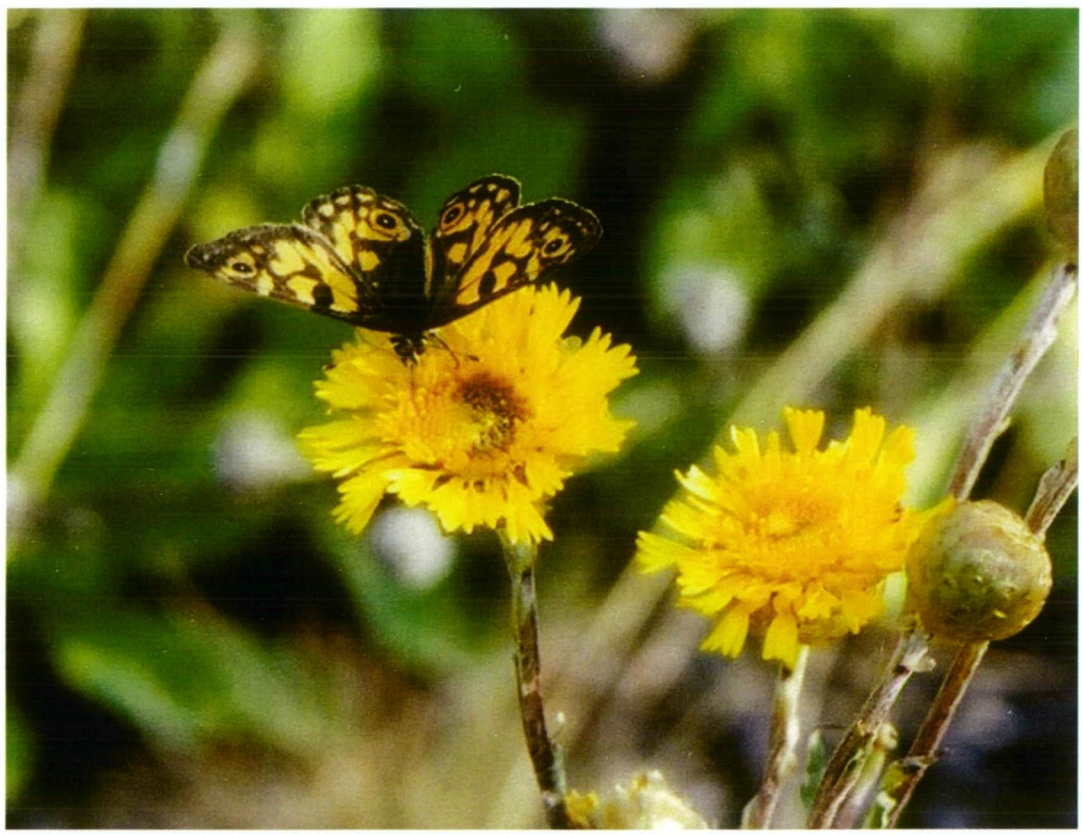


Plate 3 *O. latialis,* Lake Catania, Mt Buffalo Victoria

Chapter 2

Adult Morphology

1 INTRODUCTION

The large butterfly family Nymphalidae was first proposed by Rafinesque in 1815. Since then, the systematic relationships among its many taxa have been the subject of much dispute (Harvey 1991; Wahlberg *et al.* 2003b; Freitas & Brown 2004; Wahlberg *et al.* 2005b; Peña *et al.* 2006; Wahlberg 2008a), and are still fairly poorly understood; most subfamilies are only vaguely defined or supported by few characters (Freitas & Brown 2004). In the Australian region, the Nymphalidae comprises one fifth of the butterfly fauna, with the endemic species and genera all belonging to the sub-family Satyrinae (Braby 2000). In southeast Australia, Satyrinae are represented exclusively by the tribe Hypocystini (Miller 1968). Of particular interest is the extensive geographical variation that has developed in the phenotype of southern members of this subfamily, especially in Tasmania, where a number of species have western and eastern subspecies described (Waterhouse & Lyell 1914; Couchman 1953, 1956; Couchman & Couchman 1978).

In this chapter, focusing on adult morphology, I characterise and re-describe all five of the temperate zone southeast Australian satyrine genera and a cross-section of twelve species: *Oreixenica ptunarra, O. latialis, O. lathoniella, O. orichora, O. correae, O. kershawi, Nesoxenica leprea, Argynnina hobartia, Heteronympha cordace, H. penelope, H. merope,* and *Geitoneura klugii*. Three of these species and one genus are endemic to Tasmania. I also describe two species from the subfamily Nymphalinae, (*Junonia villida* and *Vanessa kershawi*) as they are under-described and are used as out groups in the phylogeny based on molecular data presented in chapter 4.

A particular aim of this chapter is to characterise in detail the morphology of the genus *Oreixenica* including its genitalia. From the information presented in this and subsequent chapters, the placement of the genus *Oreixenica* in the broader satyrine fauna can be determined.

The phylogeny of *Oreixenica* in particular and Satyrinae in general, remains poorly understood. This is mainly due to a lack of research; only a small number of published

descriptions of Nymphalidae genitalia are available and even fewer descriptions of Satyrinae genitalia have been published. No descriptions of both the male and female genitalia of temperate zone Satyrinae species from the Australian faunal region are available.

It is generally accepted that combining morphological and molecular data is one of the most robust methods to develop phylogenies (Nice & Shapiro 1999; Baker & Gatesy 2002; Wahlberg & Nylin 2003; Freitas & Brown 2004; Nazari *et al.* 2007). Within an evolutionary context morphological information helps relate form and function to evolution. It also provides collaborative evidence for the molecular phylogeny.

I present physical descriptions of the taxa, with emphasis on the genitalia of the species, which have not been comprehensively studied in any previous research. The superficial adult morphology of these species, such as wing pattern, venation and colour has been covered in previous publications e.g. Common & Waterhouse (1981) and Braby (2000), therefore are only briefly summarised herein.

The comparative study of genitalia, the origin of which dates back to the1850's, has been established as a standard method for morphology-based taxonomy in the Lepidoptera (Scoble 1995; Knolke *et al.* 2005). Recently Mutanen (2006) highlighted the importance of not using genitalia in isolation as genital structures show intra-specific variation, and in closely related species may show structural overlap. However, several studies have shown that the genitalia of Nymphalidae are generally of such sufficient complexity that a character set, developed through close examination of both male and female genitalia, should provide support to relationships obtained by other means (including molecular data) to provide a resolved phylogeny (Warren 1944; Dos Passos & Grey 1945; Warren *et al.* 1946; Warren 1955; Goulson 1993; Grund & Hunt 2000; Wakeham-Dawson *et al.* 2003; Simonsen 2005; 2006a; 2006b; 2006c; 2006).

2 MATERIALS AND METHODS

2.1 *Terminology*

Terminology used to describe the wings follows Common & Waterhouse (1981) (Figure 2.1). Terminology used to describe features of the genitalia is drawn from Sibatani *et al.* (1954), Klots (1970), Scoble (1995) and Simonsen (2006a). Male genitalic structures are illustrated in Figure 2.5 and Figure 2.6. Female genitalic structures are illustrated in Figure 2.2, Figure 2.3 and Figure 2.4.

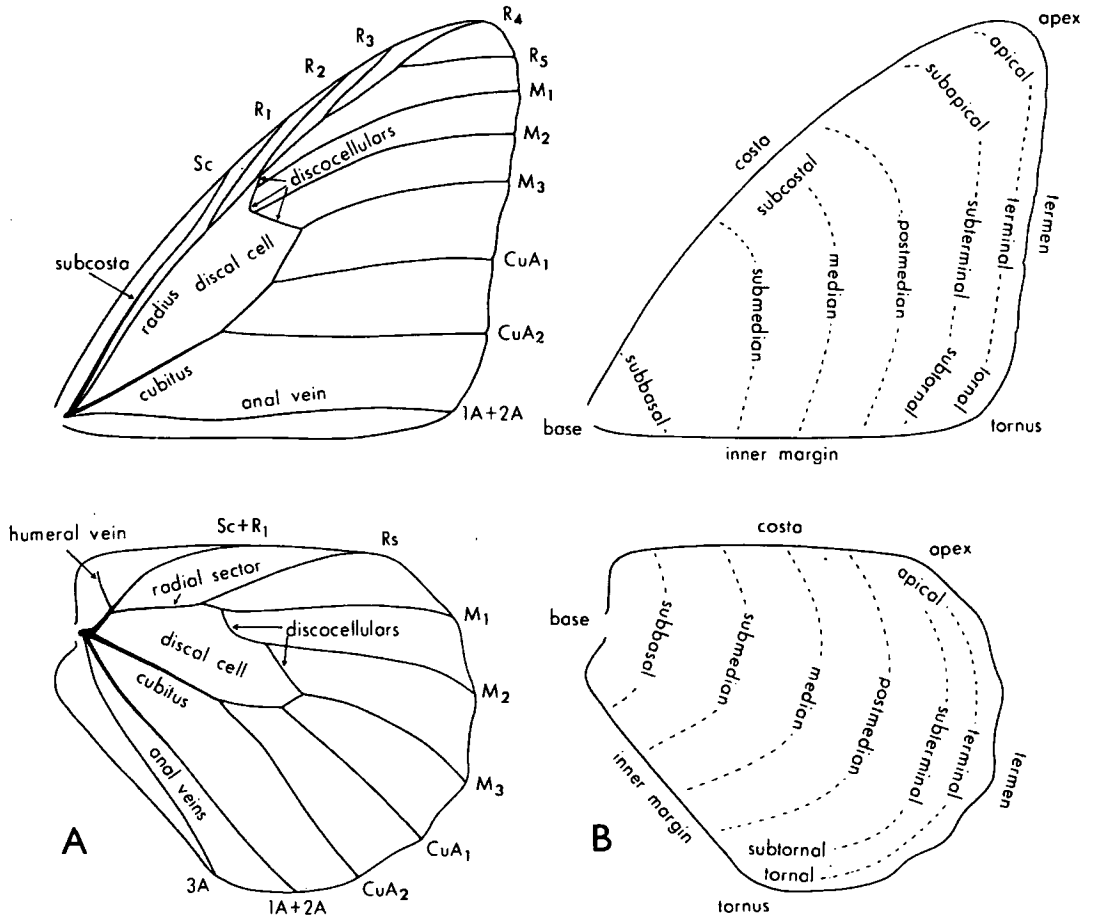


Figure 2.1 Structure of wings of adult butterflies: A venation and B areas (after Common & Waterhouse 1981; Braby 2000)

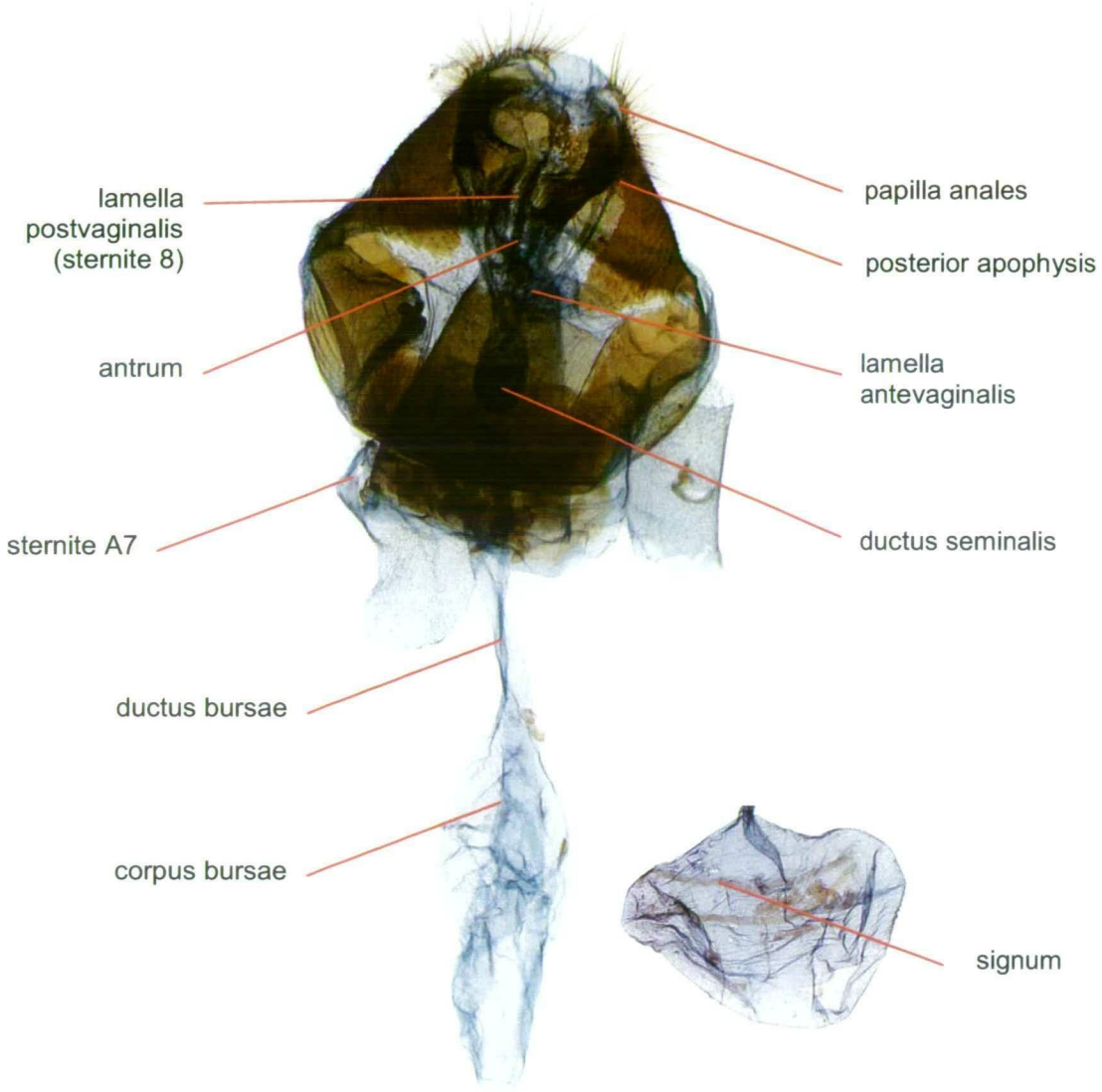


Figure 2.2 Labelled photograph of the female genitalia of *O correae*, ventral view

Figure 2.3 Labelled photograph of the corpus bursae of *H merope* detailing signum

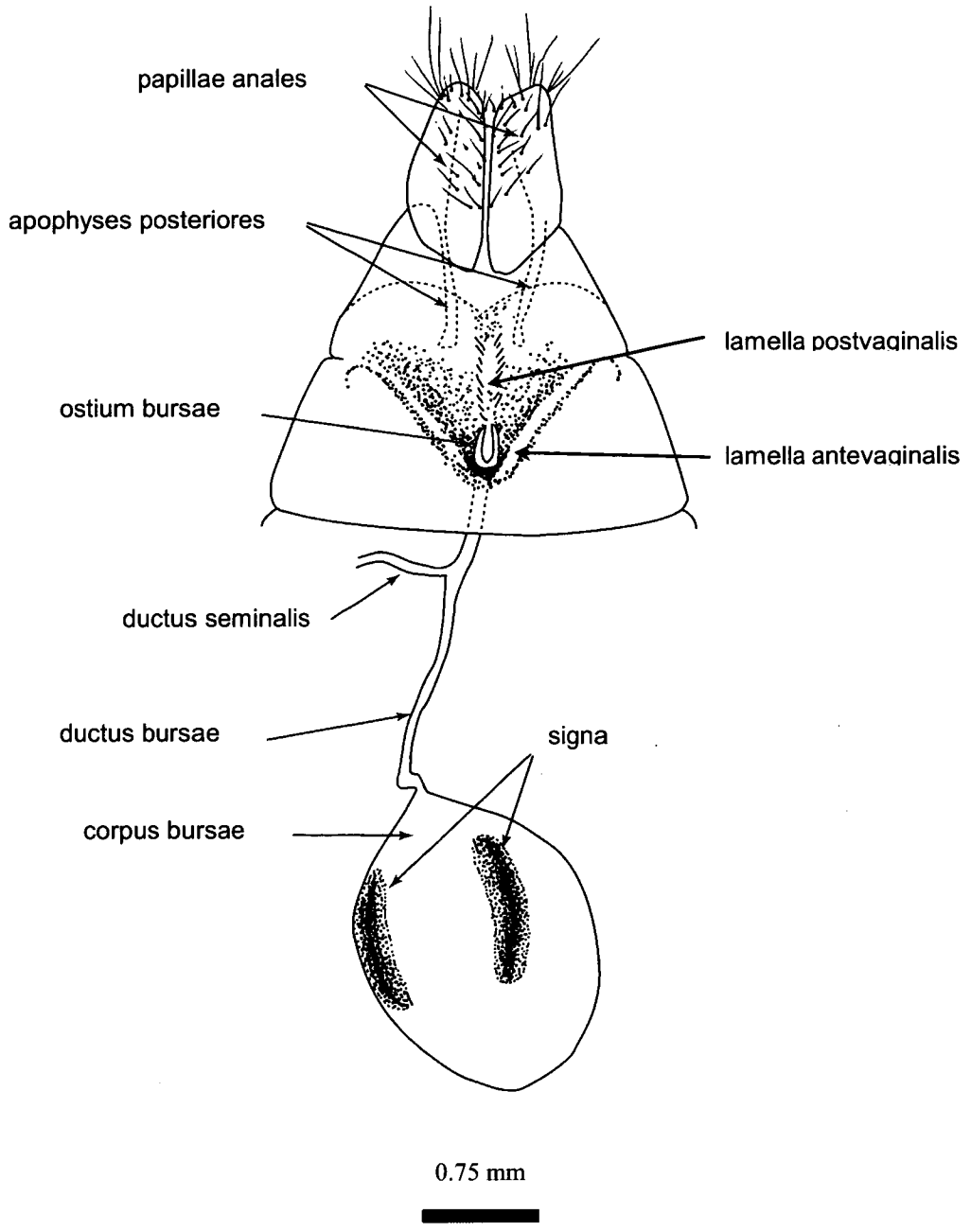


Figure 2.4 Structure of the female genitalia of *V kershawi*, ventral view
(after Common & Waterhouse 1981; after Braby 2000)

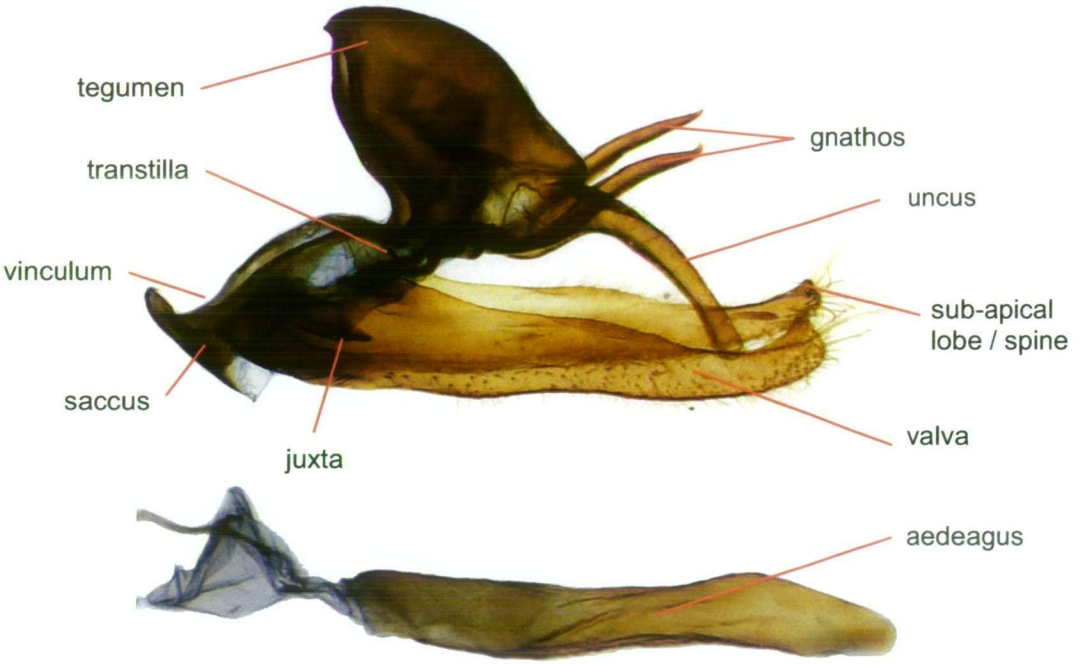


Figure 2.5 Labelled photograph of the male genitalia of *O correae*

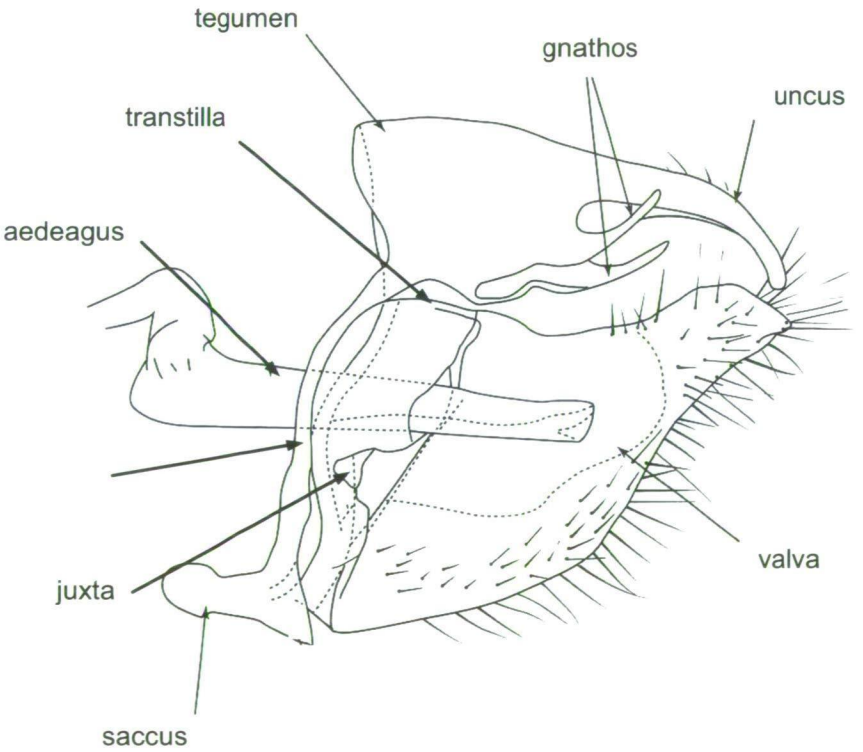


Figure 2.6 Structure of the male genitalia of *A cyrila*,
lateral view with right valva removed
(after Common & Waterhouse 1981; after Braby 2000)

2.2 *Taxa*

The genitalia of fifteen species (*O. ptunarra, O. latialis, O. lathoniella, O. orichora, O. correae, O. kershawi, N. leprea, A. hobartia, H. cordace, H. penelope, H. merope, G. klugii, G. acanthi, V. kershawi* and *J. villida*) from seven genera (*Argynnina, Geitoneura, Heteronympha, Nesoxenica*, and *Oreixenica, Junonia* and *Vanessa*) representing a cross-section of the temperate zone southeast Australian Nymphalidae was studied (Appendix 1). Species were chosen based on the availability of specimens, and to mirror those studied for immature characters and molecular taxonomy, to facilitate comparison between the morphological and molecular analyses.

2.3 *Preparation of Genitalia for Examination and Description*

Adult specimens were dissected for genitalia examination using standard techniques (Knolke *et al.* 2005). Appendix 1 details the provenance of specimens dissected for examination and description. Body parts were digested by boiling in a saturated solution of sodium hydroxide for approximately five minutes or until the body parts were softened. Digested parts were stained with 1% Chlorazol Black in 70% ethanol, then stored in 80% ethanol. Body scales were removed with a brush and fine forceps before being mounted onto microscope slides in Euparal. The genitalia were photographed using a Leica MZ16 microscope with a motorised stage and Nikon MQA21010 digital camera control unit DS-L2 with a Nikon MQA141010 digital camera head DS-Fi1. The software used to montage the images is an adapted version of *CombineZ* (Hadley 2008) by Dr Steve Shattuck CSIRO Entomology to enable automated "Z-stacking". Most images were then enhanced to maximise contrast and clarity using Adobe Photoshop CS.

3 RESULTS

3.1 *Oreixenica* Waterhouse & Lyell

The genus *Oreixenica* (Waterhouse & Lyell 1914) is endemic to Australia and comprises six distinctive 'alpine brown' species: *O. ptunarra* (Couchman 1953), *O. latialis,* (Waterhouse & Lyell 1914), *O. lathoniella* (Westwood 1851 [1850-1852]), *O. orichora* (Lucas 1892), *O. correae* (Olliff 1890); and *O. kershawi* (Miskin 1876) (Figure 2.7). The recognition of subspecies within the various *Oreixenica* in Tasmania is the subject of ongoing debate and research. Following the work of McQuillan and Ek (1997) and Berry (1997) the Tasmanian subspecies of *O. ptunarra* and *O. lathoniella* are not recognised in this work. Where appropriate, individuals will be referred to in the context of locality.

McQuillan and Ek (1997), Berry (1997) and Anderson & McQuillan (2000) have demonstrated that most variation in phenotypic characters of wing pattern and size observed in *O. ptunarra* and *O. lathoniella* is due to longitudinal clines. McQuillan and Ek (1997) observed a modest amount of variation in the male genitalia between various *O. ptunarra* populations, but did not study female genitalic variation.

3.1.1 Habitat

Oreixenica is prevalent in the montane grasslands and grassy woodlands of New South Wales, Victoria and Tasmania. In mainland Australia, species occur mainly at high altitudes in alpine and subalpine grassland habitat. In Tasmania the genus extends from sea level to high alpine grassland. *Oreixenica* can be locally abundant, with several of the species occurring sympatrically. Various species in the genus show pronounced differences in the seasonal timing of adult emergence, preferred habitat, altitudinal extent and larval food plants. Larvae feed on a few genera of native tussock grasses especially *Poa* species (Common & Waterhouse 1981; Braby 2000).

3.1.2 Habitus

Oreixenica are small weak flying butterflies, with silver-white patterning on ventral wing surface (Common & Waterhouse 1981). Forewings are narrow, usually with hindwings rounded and a hairy basal area (Braby 2000). Antenna is about half the length of the costa of the forewing with a broad club (Common & Waterhouse 1981); eye smooth. In the forewing, main veins are strongly swollen at base and the discocellular vein is sharply bent; in the hindwing, the cell is more than half the length of the wing, and the male usually lacks sex scales (Braby 2000).

3.1.3 Male genitalia

Uncus long, simple, parallel sided; truncated, rounded apically. Gnathos simple, lateral arms not joined medially, narrow, sinuous, acute apically. Tegumen tall, rounded hood-like. Valvae simple, markedly to gradually tapering, or relatively uniformly board. Vinculum relatively short; transtilla well sclerotised; juxta small, rounded, well sclerotised; saccus curved dorsally, apex rounded; aedeagus long to relatively short, straight to sinuous, stout to slender, apex rounded; cornuti absent from vesica.

3.1.4 Female genitalia

Ovipositor short, broad; papillae anales well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, extremely short to long, apophyses anteriores, absent; lamella postvaginalis (sternite 8) membranous, deeply rugose, adorned with minute spicules; lamella antevaginalis a median, moderately large to large, well sclerotised, subrectangular to rhomboidal, transverse plate; sternite 7 sclerotised; antrum not distinct, membranous, funnel shaped; colliculum not well defined; ductus bursae, membranous, moderately long to long, moderately slender to relatively broad; corpus bursae, moderate size, elongated, ovoid or 'boot' shaped, membranous; signum absent.

3.1.5 Remarks

Oreixenica genitalia are fairly homogenous so that the different species are not easily differentiated on this basis.

Male genitalia display some variation in the aedeagus but more significantly in the shape of valva. In particular differences occur in the width, degree of tapering, the presence or absence of a dorsal subapical lobe and if present, the shape and size of the lobe and the presence or absence of spines towards the apex of the valva.

Female genitalia display variation in the length of the posterior apophyses, the size and shape of the lamella antevaginalis, and the shape of the ductus bursae and corpus bursae.

3.1.6 Diagnosis

Two characteristics are unique to *Oreixenica*: signa is absent from the corpus bursae and in the forewing vein 10 from subcostal are close to end of cell with discocellular vein sharply bent. The following character state combination can be used to define *Oreixenica* from other southeast Australian Satyrinae: antenna with a broad club; eyes smooth (*Heteronympha*, *Geitoneura*, have a narrow club; *Argynnina* and *Nesoxenica* have hairy eyes).

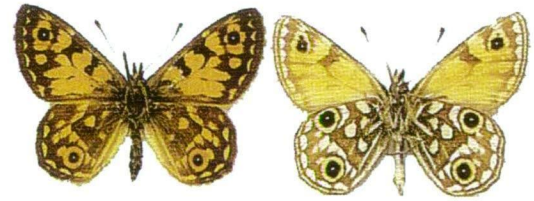
O. ptunarra male

O. ptunarra female

O. latialis

O. lathoniella

O. kershawi



O. orichora

O. correae male

O. correae female

25mm

Figure 2.7 Habitus of *Oreixenica* species.

3.2 *O. ptunarra* Couchman

3.2.1 Habitat

O. ptunarra is restricted to grassy open-woodland and tussock grassland in open plains and poorly drained areas in Tasmania. The establishment of improved pasture and expansion of cropping into the original *Poa* grassland over the last 200 years, has caused *O. ptunarra* to contract to a very restricted and patchy habitat range (Common & Waterhouse 1981; Neyland 1992; 1993; Bell 1998; Braby 2000).

3.2.2 Habitus

Wingspan: ♂ ♀ 28 mm.
Males - dorsal side brownish-black with pale orange-yellow markings and spots; forewing with a white centred black eyespot ringed with orange, and a narrow orange-yellow band of spots; hindwing with a basal spot, and prominent white-centred black eyespot ringed with orange. Ventral side base colour dull reddish-brown suffused with grey; forewing similar to dorsal side but markings paler, (Figure 2.7, Figure 2.8) (Couchman & Couchman 1978; Common & Waterhouse 1981; McQuillan 1994; Braby 2000).

Females - forewing brownish-black, with extensive orange markings, short cream band of four spots, beyond which is a prominent white centred black eyespot ringed with darker orange, and a narrow cream band of spots, sometimes followed by a dark orange band. Ventral side base colour dull reddish-brown suffused with grey markings on forewing with extensive pale orange (Figure 2.7, Figure 2.9).

O. ptunarra displays extensive sexual dimorphism in phenotype (Figure 2.8, Figure 2.9). Females display extensive orange colouration, whereas the males are predominantly dark brown (Couchman & Couchman 1978; Common & Waterhouse 1981; McQuillan 1994; Braby 2000).

McQuillan and Ek (1997) recognised two main subspecies on the basis of male phenotype: one with its populations restricted to the Southern Midlands region and the adjacent parts of the Central Plateau and Eastern Tiers; the second subspecies is restricted to the Northwest Plains around Surrey Hills. These subspecies have not been formally described or recognised.

3.2.3 Male genitalia

Uncus long, simple, parallel sided, truncated, rounded apically; gnathos simple, lateral arms not joined medially, narrow, sinuous, acute apically; tegumen tall, rounded, hood-like; valvae simple, long, narrow, tapering apically, rounded distally; apex of valva expanded, rounded, curved dorsally, small dorsal sub apical lobe present, long setae on ventral margin; vinculum relatively short; transtilla well sclerotised; juxta small, rounded, well sclerotised; saccus curved dorsally, apex rounded (Figure 2.18); aedeagus (Figure 2.24) long, sinuous, stout, apex rounded; cornuti absent from vesica.

3.2.4 Female genitalia

Ovipositor short, broad; papillae anales well-sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, moderately long, slender, anteriores, absent; lamella postvaginalis (sternite 8) membranous, deeply invaginated, rugose, adorned with minute spicules; lamella antevaginalis median, large, well sclerotised, rhomboidal, transverse plate; sternite 7 sclerotised; antrum non distinct, membranous, funnel shaped; colliculum not well defined; ductus bursae, membranous, moderately long, moderately slender; corpus bursae, moderate size, ovoid, membranous; signum absent (Figure 2.30).

3.2.5 Remarks

O. ptunarra, was one of the last members of the Australian satyrine fauna to be discovered (Edwards *et al.* 2001). Tasmania's *Threatened Species Protection Act* lists *O. ptunarra* as vulnerable. Its national conservation status is also ranked as vulnerable (Sands & New 2002).

Midlands populations of *O. ptunarra* can be distinguished from northwest populations on the basis of male phenotypic characteristics. Northwest males are consistently darker and smaller than Midlands *O. ptunarra* (Anderson 2001b). No obvious genitalic difference exists between subspecies (McQuillan & Ek 1997).

3.2.6 Diagnosis

Male *O. ptunarra* can be distinguished from *O. latialis* by the pale orange-yellow, rather than orange markings and spots on the dorsal side of the wings (Braby 2000).

In male *O. ptunarra, O. latialis* and *O. lathoniella* the valva tapers markedly, whereas in *O. orichora, O. correae* and *O. kershawi* the valva is relatively uniformly broad, gradually tapering. In male *O. ptunarra* there is a small dorsal sub apical lobe on the valva which is flattened and not spinose, in *O. latialis* the valva is spinose, and in *O. lathoniella* the dorsal sub-apical lobe is not well defined. The aedeagus in *O. ptunarra* is long, sinuous, stout with a rounded apex.

In the female the posterior apophyses are relatively long, similar to *O. lathoniella.* In other *Oreixenica* species the posterior apophyses are very short. In *O. ptunarra* the lamella antevaginalis is a median, large, well sclerotised, rhomboidal transverse plate, in *O. lathoniella* the lamella antevaginalis is a large, well sclerotised, subrectangular plate, with a medially indented posterior margin.

3.3 *O. latialis* Waterhouse & Lyell

3.3.1 Habitat

O. latialis is restricted to the tablelands and mountains of southeast mainland Australia. It flies in alpine grassland and sedgeland, such as frost hollows below the tree line and occasionally on the edges of woodland dominated by *Eucalyptus pauciflora.*

The subspecies *O. l. theddora* (Figure 2.10 Figure 2.11) is found only on the Mount Buffalo Plateau above 1230m, in an isolated habitat separated from all other alpine areas in Victoria (Common & Waterhouse 1981; Braby 2000).

3.3.2 Habitus

Wingspan: ♂ ♀ 29 mm.
Male - dorsal side: brown-black, with orange markings; forewing with a prominent white-centred black eyespot ringed with orange; hindwing with basal spot, band of spots, and prominent white-centred black eyespot ringed with orange. Ventral side: forewing similar to dorsal side, base colour paler, orange markings larger and paler, with series of white spots; hindwing reddish-brown suffused with yellow, three large pale yellow basal spots, a series of silvery-white spots, and prominent white-centred black eyespot, each bordered proximally by distinct silvery-white crescent shaped band (Figure 2.7, Figure 2.10, Figure 2.11) (Waterhouse & Lyell 1914; Couchman 1953; Common & Waterhouse 1981; Braby 2000).

Female similar to male; wings more rounded, orange markings on dorsal side of forewing slightly paler near costa and suffused with cream; ventral side paler (Figure 2.7) (Common & Waterhouse 1981; Braby 2000).

3.3.3 Male genitalia

Uncus long, simple, parallel sided, truncated, rounded apically; gnathos simple, lateral arms not joined medially, lateral arms narrow, sinuous, acute apically; tegumen tall, rounded, hoodlike; valvae simple, long, narrow, tapering apically, rounded distally, expanded into dorsal, spinose, sub-apical lobe, long setae on ventral margin; vinculum relatively short; transtilla well sclerotised; juxta small, rounded, well sclerotised; saccus, curved dorsally, tapering, apex rounded (Figure 2.19); aedeagus (Figure 2.25) long, slender, slightly sinuate, apex rounded; cornuti absent from vesica.

3.3.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, extremely short, anteriores, absent; lamella postvaginalis (sternite 8) membranous, deeply invaginated, rugose, adorned with minute spicules; lamella antevaginalis median, large, well sclerotised, rhomboidal, transverse plate; sternite 7 sclerotised; antrum non distinct, membranous, funnel shaped; colliculum not well defined; ductus bursae membranous, moderately long, moderately slender; corpus bursae, moderate size, rounded, membranous, not well differentiated from ductus; signum absent (Figure 2.31).

3.3.5 Remarks

Many populations are reproductively isolated from one another because of the discontinuous nature of the mountainous terrain (Braby 2000). Adults often fly with *O. lathoniella*, but tend to favour more open areas (Common & Waterhouse 1981).

O. l. theddora is listed as having a lower risk (near threatened) national conservation status (Sands & New 2002).

3.3.6 Diagnosis

O. latialis males are distinguished from *O. lathoniella* by their smaller size and narrower forewing with the tornus distinctly rounded (Braby 2000).

In male *O. latialis* the valva tapers markedly, expanding into a rounded dorsal sub-apical lobe, with long setae on the ventral margin. The aedeagus is long, slender and slightly sinuate.

The genitalia of female *O. latialis* are not easily distinguished from other *Oreixenica*. In *O. latialis* the apophyses posteriores are extremely short compared to *O. ptunarra* moderately long. Ductus bursae moderately long, moderately slender, in *O. orichora* it's relatively broad. The corpus bursae rounded where as in *O. correae* elongated and *O. kershawi* which is 'boot' shaped.

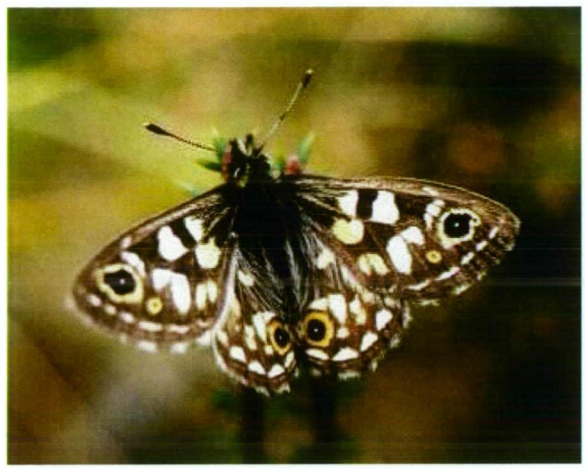


Figure 2.8 *O ptunarra* male, Lake Augusta, Tasmania

Figure 2.9 *O ptunarra* female, Tunbridge Tiers, Tasmania

Figure 2.10 *O latialis theddora*, Lake Catania, Mt Buffalo Victoria.

Figure 2.11 *O latialis theddora*, Lake Catania, Mt Buffalo Victoria.

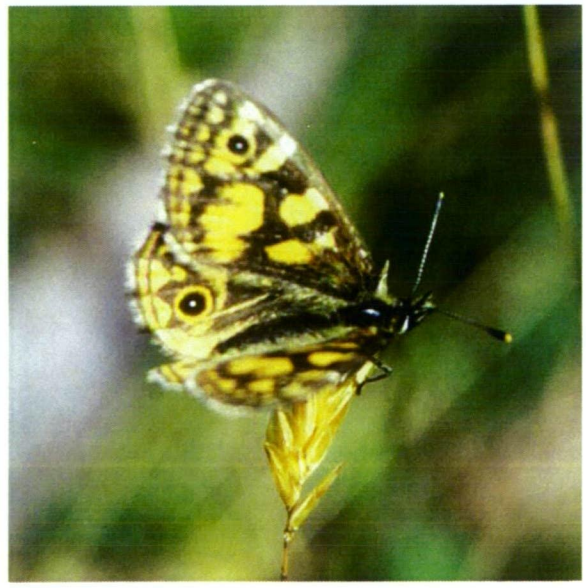


Figure 2.12 *O lathoniella* male, Tunbridge Tiers, Tasmania.

3.4 *O. lathoniella* Westwood

3.4.1 Habitat

O. lathoniella is the most widespread and abundant *Oreixenica,* flying in the tablelands and mountains of New South Wales and the Australian Capital Territory, and in the mountains and coastal area of Victoria and Tasmania. *O. lathoniella* flies in tall open eucalypt forest, subalpine woodland and alpine woodland with a predominantly grassy understory, mainly in cooler higher rainfall areas in the mountains and tablelands (Common & Waterhouse 1981; Braby 2000).

3.4.2 Habitus

Wingspan: ♂ ♀ 29 mm.
Male - dorsal side: black, with extensive orange-yellow markings and spots; forewing with a black spot extending and usually joining to a broad black band, white-centred black eyespot, and other spots; hindwing with angular basal spots, a postmedian band, a white centred black eyespot, and a series of spots. Ventral side: forewing similar to dorsal side but base colour duller and paler, a series of spots becoming silvery-white towards apex, and an orange-yellow band; hindwing base colour dull reddish-brown suffused with orange-yellow, three or four silvery-white basal spots, a prominent white-centred black eyespot, white-centred spots, and an orange yellow terminal band (Figure 2.7, Figure 2.12) (Common & Waterhouse 1981; Braby 2000).

Female - wings slightly broader than male, with termen more rounded, hindwing is larger relative to forewing, and abdomen is shorter and broader (Figure 2.7) (Common & Waterhouse 1981; Braby 2000).

3.4.3 Male genitalia

Uncus long, simple, parallel sided, truncated, rounded apically; gnathos simple, lateral arms not joined medially, narrow, sinuous, acute apically; tegumen tall, rounded, hoodlike; valvae simple, long, narrow, tapering apically, rounded distally, apex not expanded but rather elongated, curved dorsally, spinose apically; vinculum relatively short; transtilla moderately well sclerotised; juxta small, rounded, well sclerotised; saccus curved dorsally, apex rounded (Figure 2.20); aedeagus (Figure 2.26) long, slender, slightly sinuate, apex rounded; cornuti absent from vesica.

3.4.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, relatively long, slender, anteriores, absent; lamella postvaginalis (sternite 8), membranous, deeply invaginated, rugose, adorned with minute spicules; lamella antevaginalis large, well sclerotised, subrectangular plate, with medially indented posterior margin; sternite 7 sclerotised; antrum membranous, funnel shaped; colliculum not well defined; ductus bursae, membranous, moderately long, moderately slender; corpus bursae, moderate size, rounded, membranous; signum absent (Figure 2.32).

3.4.5 Diagnosis

O. lathoniella can be distinguished from most other *Oreixenica* species by the extensive bright silvery-white markings on the ventral side.

Male *O. lathoniella* is notable because of the spinose elongated apex of the valva, and the absence of a dorsal sub apical lobe, which is present in *O. ptunarra, O. latialis, O. orichora,* and *O. correae.* The aedeagus is long slender and slightly sinuate, different to *O. ptunarra* which is long, sinuous and stout, *O. orichora* which is relatively short, straight and stout, and *O. kershawi* which is stout.

Female *O. lathoniella* is distinguished from other *Oreixenica,* in particular *O. ptunarra,* by the relatively long apophyses posteriores. Additionally the lamella antevaginalis is characterised by the medially indented posterior margin, absent in all other *Oreixenica.*

3.5 *O. orichora* Lucas

3.5.1 Habitat

O. orichora is restricted to the higher mountains of the Australian Capital Territory, southeast New South Wales, eastern Victoria and central Tasmania, at altitudes above 1200m, reaching up to1800 m at Mt Gingera (ACT), and Mt Buller (VIC), and 2100 m on Mt Kosciuszko (NSW). In Tasmania, *O. orichora* inhabits the high rainfall areas of the central plateau at altitudes between 760 and 1500 m. *O. orichora* occurs abundantly in subalpine and alpine open grasslands, extending into woodlands (Common & Waterhouse 1981; Braby 2000).

3.5.2 Habitus

Wingspan: ♂ 30 mm; ♀ 31 mm.
Male - dorsal side: brown-black, with orange markings and spots; forewing with a white centred black eyespot; ventral side forewing similar to dorsal side but base colour paler, orange areas duller and more extensive, eyespot without obvious ring and a narrow white band of spots; hindwing base colour grey-brown weakly suffused with pale yellow (Figure 2.7, Figure 2.13) (Common & Waterhouse 1981; Braby 2000).

Female is similar but slightly larger; brownish-orange markings on dorsal side often paler, and less extensive (Figure 2.7) (Common & Waterhouse 1981; Braby 2000).

3.5.3 Male genitalia

Uncus long, simple, parallel sided, relatively broad basally, truncated, tapering slightly, rounded apically; gnathos simple, lateral arms not joined medially, narrow, sinuous, acute apically; tegumen tall, rounded; valvae simple, long, narrow, gradually tapering apically, rounded distally, very small dorsal sub apical lobe present, not spinose; vinculum relatively short; transtilla well sclerotised; juxta small, rounded, well sclerotised; saccus curved dorsally, tapering, apex rounded (Figure 2.21); aedeagus (Figure 2.27) relatively short, straight, stout, apex rounded; cornuti absent from vesica.

3.5.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, short, anteriores, absent; lamella postvaginalis (sternite 8) membranous, deeply invaginated, rugose, adorned with minute spicules; lamella antevaginalis median, moderately large, relatively narrow, well sclerotised, rhomboidal, transverse plate; sternite 7 sclerotised; antrum not distinct, membranous, funnel shaped; colliculum not well defined; ductus seminalis inserted medially dorsally; ductus bursae, membranous, relatively broad; corpus bursae, membranous, moderate size, rounded; signum absent (Figure 2.33).

3.5.5 Diagnosis

O. orichora can be distinguished by the dull white basal, postmedian and subterminal spots on the ventral side of the hindwing. The subapical eyespot on the ventral side of the forewing is never ringed with dark orange as in other *Oreixenica* (Braby 2000).

The genitalia of male *O. orichora* are defined by the valva being relatively uniformly broad, with a very small dorsal spineless sub-apical lobe present. The aedeagus is relatively short, straight, and stout.

The genitalia of female *O. orichora* are characterised by the relatively broad ductus bursae and the relatively narrow lamella antevaginalis.

3.6 *O. correae* Olliff

3.6.1 Habitat

O. correae is restricted to the southeast highlands of mainland Australia at altitudes above 1200 m, usually most abundant above 1500 m extending to 1800 m at Mt Gingera in the Australian Capital Territory. *O. correae* occurs predominantly in alpine and subalpine eucalypt woodlands, from the Brindabella Range (ACT) through southeast New South Wales and into Victoria, favouring the denser shady vegetation, rather than open grasslands. *O. correae* is absent from Tasmania. The adults venture into the open areas to take advantage of flowers (Kitching *et al.* 1978; Braby 2000).

3.6.2 Habitus

Wingspan: ♂ ♀ 33 mm.
Male - dorsal side: black, with rich brownish-orange spots and markings; forewing with a single or double white-centre black eyespot, a series of small spots towards apex; hindwing with a white-centred black eyespot, and a series of small spots. Ventral side: base colour dull brownish-orange; forewing similar to dorsal side with black markings more restricted and heavily suffused with brownish-orange; hindwing with an obscure pale orange band, followed by white-centred black eyespots (Figure 2.7, Figure 2.14, Figure 2.15) (Common & Waterhouse 1981; Braby 2000).

O. correae display marked sexual dimorphism.
Female - dorsal side: forewing termen more rounded than male; spots pale with prominent subterminal black and pale brownish-orange spots and markings. Ventral side: subterminal spots and markings near costa pale yellow; hindwing grey-brown, suffused with orange markings and spots; basal spots pale yellow, conspicuous silver-white postmedian band and subterminal spots (Figure 2.7) (Common & Waterhouse 1981; Braby 2000).

3.6.3 Male genitalia

Uncus long, simple, parallel sided, truncated, rounded apically; gnathos simple, lateral arms not joined medially, narrow, sinuous, acute apically; tegumen tall; valvae simple, gradually tapering apically, rounded distally, apex slightly expanded into small rounded, dorsal subapical lobes, spinose, spines very small; vinculum relatively short; transtilla

well sclerotised; juxta small, rounded, well sclerotised; saccus curved dorsally, tapering, apex rounded (Figure 2.22); aedeagus (Figure 2.28) long, slender, slightly sinuate, apex rounded; cornuti absent from vesica.

3.6.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, extremely short, anteriores, absent; lamella postvaginalis (sternite 8) membranous, deeply rugose, adorned with minute spicules; lamella antevaginalis median, moderately large, well sclerotised, rhomboidal, transverse plate; sternite 7 sclerotised; antrum not distinct, membranous, funnel shaped, colliculum not well defined; ductus bursae membranous, long, moderately slender; corpus bursae, membranous, moderate size, elongated, apex rounded, well differentiated from ductus; signum absent (Figure 2.34).

3.6.5 Diagnosis

O. correae is distinguished from other *Oreixenica* species by wing colour and pattern. *O. correae* along with *O. ptunarra* is sexually dimorphic. Female *O. correae* have conspicuous silvery-white bands and spots which are far less extensive than in *O. orichora* and *O. lathoniella*. In male *O. correae* the silvery-white bands and spots are replaced with orange.

Male *O. correae* genitalia are distinguished by the uniformly tapering valva with a relatively small rounded dorsal subapical, spinose lobe. The aedeagus is long, slender and slightly sinuate.

The female genitalia are distinguished by the extremely short apophyses posteriories; the shortest in all *Oreixenica*. The corpus bursae is of moderate size and elongated, and is well differentiated from the ductus bursae.

3.7 *O. kershawi* Miskin

3.7.1 Habitat

O. kershawi occurs in open eucalypt woodland and tall open forest in montane areas of New South Wales, the Australian Capital Territory and Victoria, preferring cool, wet areas with a lush understorey of ferns and grasses; range also extends into subalpine woodland up to 1300 m and down to near sea level.

3.7.2 Habitus

Wingspan: ♂ 33 mm; ♀ 34 mm.
Dorsal side: black with brownish-orange spots; forewing with a small obscure black eyespot; hindwing with a white-centred black eyespot. Ventral side: forewing similar to dorsal side but with narrow silvery-white bands; hindwings base colour red-brown, spots and markings similar to dorsal side but larger and silvery-white, a larger white-centred black eyespot and smaller white-centred black eyespots, each ringed with orange (Figure 2.7, Figure 2.16 Figure 2.17) (Common & Waterhouse 1981; Braby 2000).

The male is similar to the female but is distinguished by the presence of a broad dull black oblique patch of sex scales on the dorsal side of the forewing (Braby 2000).

3.7.3 Male genitalia

Uncus long, simple, parallel sided, truncated, rounded apically; gnathos simple, lateral arms not joined medially, narrow, sinuous, acute apically; tegumen tall; valvae simple, gradually tapering apically, rounded distally, dorsal sub apical lobe with spinose apex; vinculum relatively short; transtilla well sclerotised; juxta small, rounded, well sclerotised; saccus curved dorsally, tapering, apex rounded (Figure 2.23); aedeagus (Figure 2.29) stout, short, apex rounded; cornuti absent from vesica.

3.7.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, short,

anteriores, absent; lamella postvaginalis (sternite 8) membranous, deeply invaginated, rugose, adorned with minute spicules; lamella antevaginalis median, moderately large, well sclerotised, rhomboidal, transverse plate; sternite 7 sclerotised; antrum membranous, funnel shaped; colliculum not well defined; ductus seminalis inserted medially dorsally; ductus bursae long, moderately slender; corpus bursae, moderate size, 'boot' shaped, apex rounded, membranous, well differentiated from ductus; signum absent (Figure 2.35).

3.7.5 Remarks

Three subspecies of *O. kershawi* are currently recognised *O. k. kanunda, O. k. ella,* and *O. k. kershawi. O. k. kanunda* is listed in South Australia as vulnerable and has a national conservation status of lower risk (Tindale 1949; Fisher 1978; Common & Waterhouse 1981; Braby 2000; New & Sands 2002a; Sands & New 2002).

O. k. ella has more pronounced brownish orange dorsal side markings than *O. k. kershawi. O. k. kanunda* is the smallest subspecies and is considerably brighter than the other subspecies (Sands & New 2002).

The likelihood of clinal variation within this species has been noted (Fisher 1978; Common & Waterhouse 1981; Dunn & Dunn 1991; Braby 2000; Sands & New 2002).

3.7.6 Diagnosis

O. kershawi is a distinctive species in which the hindwing is much more elongated than any other species in the genus. *O. kershawi* has a striped pattern on the ventral side of the hindwing with particularly obvious silvery-white bands. Males have a patch of sex-scales that is absent in other species (Braby 2000).

The male *O. kershawi* genitalia are distinguished by the valva which are uniformly broad tapering gradually, the dorsal subapical lobe is spinose, but not well developed. The aedeagus is short and stout.

Figure 2.13 *O. orichora* Canal Drive, Liawenee, Tasmania.

Figure 2.14 *O correae* male, Lake Mountain, Victoria

Figure 2.15 *O correae* male, Lake Mountain, Victoria

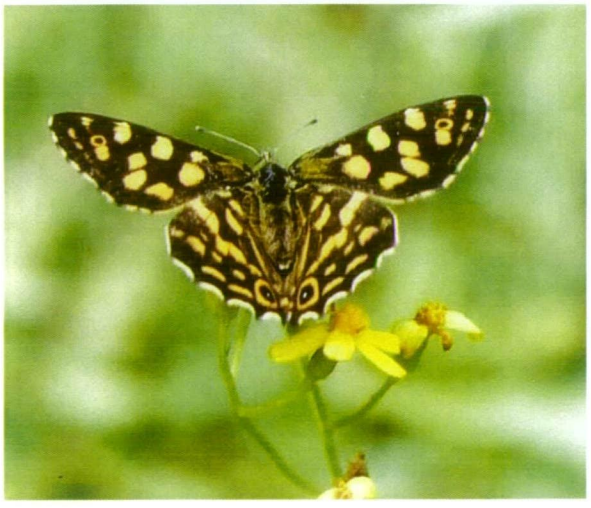


Figure 2.16 *O kershawi,* dorsal side, Mt Donna Buang, Victoria

Figure 2.17 *O kershawi*, ventral side, Mt Donna Buang, Victoria

Figure 2.18 *O. ptunarra* male genitalia

Figure 2.19 *O. latialis* male genitalia

Figure 2.20 *O. lathoniella* male genitalia

Figure 2.21 *O. orichora* male genitalia

Figure 2.22 *O. correae* male genitalia

Figure 2.23 *O. kershawi* male genitalia

Figure 2.24 *O. ptunarra* aedeagus

Figure 2.25 *O. latialis* aedeagus

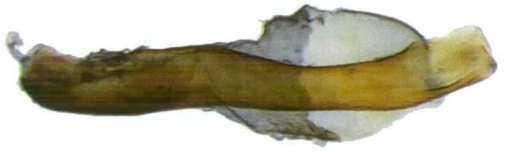


Figure 2.26 *O. lathoniella* aedeagus

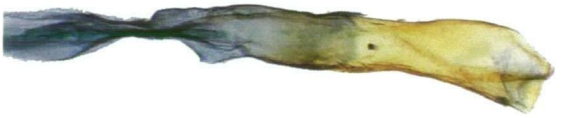


Figure 2.27 *O. orichora* aedeagus

Figure 2.28 *O. correae* aedeagus

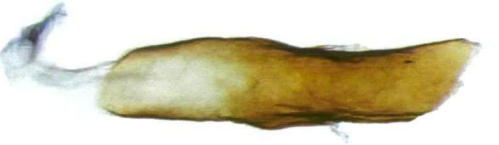


Figure 2.29 *O. kershawi* aedeagus

Figure 2.30 *O. ptunarra* female genitalia

Figure 2.31 *O. latialis* female genitalia

Figure 2.32 *O. lathoniella* female genitalia

Figure 2.33 *O. orichora* female genitalia

Figure 2.34 *O. correae* female genitalia

Figure 2.35 *O. kershawi* female genitalia

3.8 *Nesoxenica* Waterhouse & Lyell

The genus *Nesoxenica* (Waterhouse & Lyell 1914) is endemic to Tasmania and comprises a single species *N. leprea*. *N. leprea* (Hewitson 1864 [1863-1878]), the Tasmanian xenica (
Figure 2.36), has two recognised subspecies *N. l. leprea* and *N. l. elia*.

3.8.1 Habitat

Nesoxenica is restricted to the margins of cool temperate *Nothofagus* rainforest, habitat of the larval food plant *Uncinia* (Cyperaceae) sedge (Common & Waterhouse 1981; Braby 2000). Adults feed at the flowers of *Leptospermum lanigerum* (Myrtacae), *Prostanthera lasianthos* (Lamiaceae) and *Pentachondra pumila* (Epacidacae) (Prince 1988).

3.8.2 Habitus

Wingspan: ♂ ♀ 31 mm.
Male/female - dorsal side is black, with cream-pale yellow (*N. l. leprea*) or deep yellow-light orange (*N. l. elia*) markings, terminal scale fringe is chequered white. Ventral side hindwing black, with silvery-white markings, and a series of six black spots ringed with white. Main veins of forewings are strongly swollen at base. Hindwing cell is about half the length of the wing (Figure 2.36) (Couchman & Couchman 1978; Common & Waterhouse 1981; Braby 2000).

The adult has hairy eyes, relatively narrow wings, with termen rounded and basal area very hairy (Common & Waterhouse 1981). Antenna is about half the length of the costa of the forewing, with a broad club (Braby 2000).

The sexes are difficult to distinguish and can only be reliably separated by examination of the external genitalia (Couchman & Couchman 1978; Common & Waterhouse 1981; Prince 1988; Braby 2000).

N. leprea dorsal side

N. leprea ventral side

25mm

Figure 2.36 Habitus of *Nesoxenica*

3.8.3 Male genitalia

Uncus long, simple, parallel sided, apically acute; gnathos simple, lateral arms not joined medially, narrow, curved ventrally, short, acute apically; tegumen tall; valvae simple, broad basally, angled, tapering from mid point, apex truncated, squared, prominent, subapical dorsal spine present, distal ventral margin of valva serrated; transtilla well sclerotised; juxta small, rounded, well sclerotised; saccus long, curved dorsally, apex rounded (Figure 2.37); aedeagus (Figure 2.38) moderately long, slender, straight, apex simple, truncated, blunt; cornuti absent from vesica, numerous spicules on anterior surface of shaft.

3.8.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, short, anteriores, absent; lamella postvaginalis (sternite 8), deeply invaginated, membranous, rugose, adorned with spicules; lamella antevaginalis, broad, rhomboidal, transverse plate, posterior margin notched medially; antrum membranous, funnel shaped; colliculum membranous, not well defined; ductus seminalis inserted medially dorsally; ductus bursae membranous, long, slender; corpus bursae, moderate size, ovoid, membranous, well differentiated from ductus; signa, two, weak, long narrow, longitudinal, dorso-lateral, sclerotised bands adorned with numerous inward pointing spicules (Figure 2.39).

Figure 2.37 *N. leprea* male genitalia

Figure 2.38 *N. leprea* aedeagus

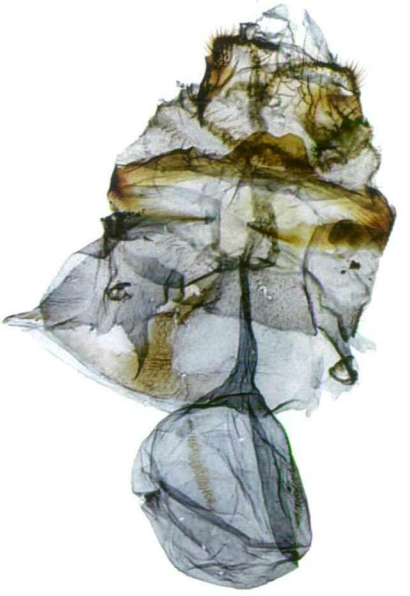


Figure 2.39 *N. leprea* female genitalia

3.9 *Argynnina* Butler

The genus *Argynnina* (Butler 1867) comprises two species, *A. hobartia* (Westwood 1851 [1850-1852]) which is endemic to Tasmania (Figure 2.40), and the other *A. cyrila* (Waterhouse & Lyell 1914), is restricted to the temperate zone of the southeast Australian mainland (Common & Waterhouse 1981; Dunn & Dunn 1991; Braby 2000).

3.9.1 Habitat

The different *Argynnina* species favour distinct habitats: *A. cyrila* favouring wetter tall open eucalypt forests and edges of cool and warm temperate rainforest, occasionally intruding into the drier eucalypt open forests via moist gullies and slopes; where as *A. hobartia* favours habitats with a relative dense, tall ground cover of native grasses, a sparse understorey of small shrubs and young trees, with an open canopy (Common & Waterhouse 1981; Braby 2000).

3.9.2 Habitus

Argynnina are moderate sized butterflies with densely hairy eyes; antenna is about half the length of the costa of the forewing with a broad club (Common & Waterhouse 1981). Forewing, only veins Sc and CuA are strongly swollen at base (Braby 2000). Hindwing, the cell is more than half the length of the wing. The basal area of the wings is vary hairy (Braby 2000).

3.9.3 Diagnosis

Argynnina can be defined from other southeast Australian Satyrinae by the veins of the forewing; only veins Sc and CuA re strongly swollen at the base.

3.10 *A. hobartia* Butler

3.10.1 Habitat

A. hobartia is prevalent in a wide range of habitats, from sea level to around 900 m, including open eucalypt forest, woodland and the margins of grasslands and heath-sedgelands. Adults generally prefer habitats with a relatively dense, tall ground cover of native grasses, especially *Poa labillardieri* and *Austrodanthonia*, a sparse understorey of small shrubs and young trees, and an open canopy (Prince 1988; Braby 2000). In western Tasmania *A. hobartia* is found in high rainfall areas characterised by button-grass plains on acid bogs associated with patches of rainforest (Couchman & Couchman 1978; Prince 1988; Braby 2000).

3.10.2 Habitus

Wingspan: ♂ 32 mm ♀ 35 mm.
Male - dorsal side black, with orange-yellow or brownish-orange spots and markings, and grey-brown basal hairs suffused with greenish-orange; forewing with three indistinct bluish-white centred black eyespots, followed by a narrow brownish-orange band of confluent spots; hindwing with three bluish-white centred black eyespots (Figure 2.40). Ventral side forewing similar to dorsal side but duller, a central black spot in cell, apex suffused with reddish-brown; hindwing base colour dull reddish-brown with obscure darker markings and striations, eyespots very small. Broad clubbed antenna about half the length of the costa of the forewing (Braby 2000) (Figure 2.40). The eyes are densely hairy (Common & Waterhouse 1981). In the forewing veins Sc and CuA are strongly swollen at the base (Couchman & Couchman 1978; Common & Waterhouse 1981; Braby 2000).

Female - has broader wings than the male and the ventral side base colour is generally paler (Couchman & Couchman 1978; Common & Waterhouse 1981; Braby 2000).

Figure 2.40 Habitus of *A hobartia*

3.10.3 Male genitalia

Uncus simple, parallel sided, tapered, rounded apically; gnathos simple, lateral arms not joined medially, narrow, short, acute apically, curving dorsally; tegumen tall; valva very broad basally, almost meeting medially, ventral margin strongly curved inwards, tapering markedly from midpoint, apex expanded, flattened, dorsal margin finely serrated, apex curved inwards, serrated; transtilla membranous; juxta a round lobe, weakly sclerotised; saccus moderately long, curved dorsally, apex rounded (Figure 2.41); aedeagus (Figure 2.42) long, slender, curved, sinuate, apex acute; cornuti absent from vesica, numerous spicules on anterior surface of shaft.

3.10.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised distally, with slightly rounded, membranous lobes, setae moderately long, well developed; apophyses posteriores moderately long, anteriores absent; lamella postvaginalis (sternite 8), membranous, lightly rugose, deeply invaginated, adorned with spicules; lamella antevaginalis, sclerotised band, much wider medially; antrum membranous, funnel shaped; colliculum not well defined; ductus bursae short, moderately broad; corpus bursae, moderate size, ovoid, membranous, well differentiated from ductus; signa, two, weak longitudinal, long, narrow, dorso-lateral, ventro-lateral sclerotised bands adorned with numerous inward pointing spicules, running to midpoint of corpus bursae. Sternite A7 well sclerotised (Figure 2.43).

Figure 2.41 *A. hobartia* male genitalia

Figure 2.42 *A. hobartia* aedeagus

Figure 2.43 *A. hobartia* female genitalia

3.10.5 Remarks

Couchman and Couchman (1978) recognised three subspecies of *A. hobartia*: *A. h. hobartia*, *A. h. tasmanica* and *A. h. montana.* A transition zone occurs between the distributional boundaries of *A. h. hobartia* and *A. h. tasmanica* where extremely variable intermediate forms have been collected (Braby 2000).

3.10.6 Diagnosis

A. hobartia males are distinguished from *A. cyrila* males by the absence of sex-scales on the forewing. *A. hobartia* is smaller than *A. cyrila* and has broader and shorter forewings (Braby 2000).

The genitalia of male *A. hobartia* are distinguished by the short tapering uncus, very basally broad valva with a finely serrated dorsal margin and the vesica is adorned with numerous spicules.

The genitalia of female *A. hobartia* are characterised by the sclerotised band of the lamella antevaginalis and the short wide ductus bursae. The signa are two weak longitudinal sclerotised bands adorned with numerous inward pointing spicules running to the midpoint of corpus bursae. In *A. cyrila* the signa are prominent and run the full length of the corpus bursae (Common & Waterhouse 1981; Braby 2000).

3.11 *Heteronympha* Wallengren

The genus *Heteronympha* (Wallengren 1858) currently comprises seven species, all restricted to the temperate zone of southern Australia. All seven species are found in New South Wales and Victoria, with five extending into southeast Queensland. Three species occur in Tasmania; *H. merope* (Fabricius 1807), *H. penelope* (Waterhouse 1937) and *H. cordace* (Geyer 1832 [1827-1837]) (Figure 2.44). Only *H. merope* extends into South Australia and south-western Western Australia (Braby 2000).

3.11.1 Habitat

Heteronympha occurs mainly in mountainous tall eucalypt open forest and in woodland. Many species occur together and show pronounced differences in seasonal timing of adult appearance, preferred habitat and larval food plants, and to a lesser extent altitude range (Braby 2000).

3.11.2 Habitus

Heteronympha are moderate to large butterflies, the eye is hairy, forewing main veins are strongly swollen to the base; hindwing cell is about half (male) or less than half (female) the length of the wing; narrow club antenna less than half the length of the costa of the forewing (Figure 2.44). Male usually has sex-scales consisting of a black patch in or below the cell on the dorsal side of the forewing (Common & Waterhouse 1981; Braby 2000).

3.11.3 Male genitalia

Uncus short to moderately long, simple, apically acute; gnathos simple, lateral arms not joined medially, narrow, relatively short, straight, apically acute, slightly curved dorsally; tegumen relatively tall; valvae simple, short, tapering to apex, rounded distally, prominent apical spine present; transtilla membranous, juxta small, sclerotised, rounded; saccus long, apex rounded, well sclerotised; aedeagus medium to long, slender to stout, straight to sinuous, apex truncated, rounded; vesica adorned with numerous spicules.

3.11.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae moderately long to long, well developed; apophyses posteriores short to moderately long, anteriores absent; lamella postvaginalis (sternite 8) markedly varied; lamella antevaginalis sclerotised, medial band; antrum membranous, funnel shaped; colliculum membranous, not well defined; ductus seminalis inserted medially, dorsally; ductus bursae membranous, long, moderately slender; corpus bursae, moderate size, ovoid to globular, membranous, well differentiated from ductus; signa, two, weak to strong, sclerotised bands, adorned with numerous inwardly pointing spicules. Sternite A7 lightly sclerotised.

3.11.5 Summary of Morphological Characters

Heteronympha differs from other southeast Australian Satyrinae genera by possession of a narrow clubbed antenna with is less than half the length of the costa of the forewing and hairy eyes. In males the saccus is long, apex rounded, well sclerotised; a prominent dorsal sub apical spine is present.

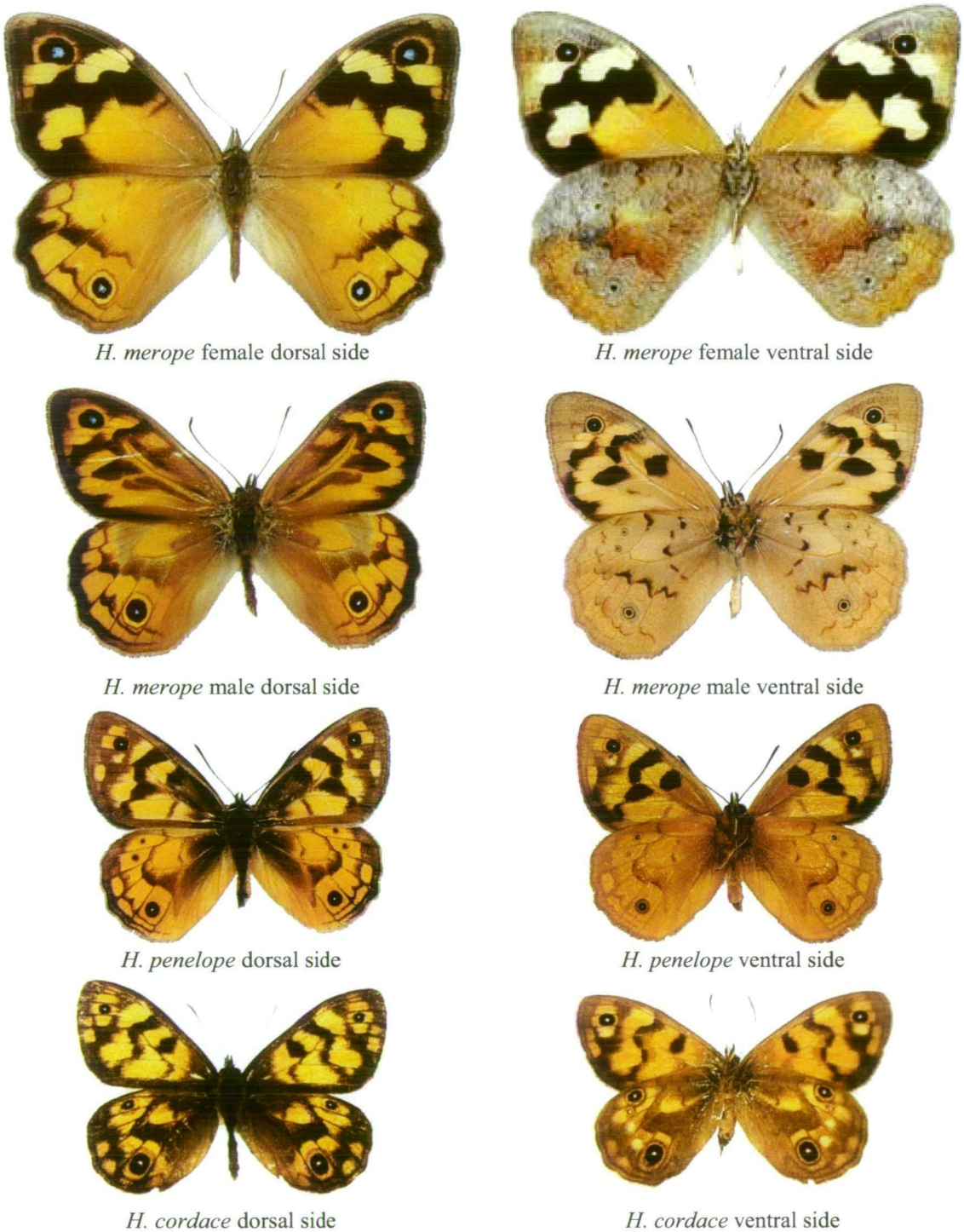


Figure 2.44 Habitus of *Heteronympha* species

3.12 *H. cordace* Geyer

3.12.1 Habitat

H. cordace occurs in open swampy areas, usually with a sparse cover of *Melaleuca* and *Leptospermum* shrubs, where dense stands of the larval food plant grow. Due to the patchy distribution of habitat, *H. cordace* tends to occur in fairly discrete areas in which it may be locally abundant. This is in contrast to other species of *Heteronympha* which are generally more widespread over larger areas of habitat (Braby 2000).

3.12.2 Habitus

Wingspan: ♂ 38 mm ♀ 42 mm.

Males - dorsal side black, with orange markings; forewing with a blue-centred black eyespot; hindwing with a blue-centred black eyespot and a blue-centred black eyespot, each ringed with orange then faintly with black. Ventral side: forewing similar to dorsal side but orange areas more extensive and with a dull orange band; hindwing base colour yellow, with irregular brownish-grey markings, eyespots similar to dorsal side, more obvious with two bluish-white spots between them (Figure 2.44).

Female – similar to male, larger, with abdomen stouter, termen of wings more rounded, hindwing often with an extra small spot below apical eyespot (Figure 2.44).

3.12.3 Male genitalia

Uncus moderately long, simple, parallel sided, apically acute; gnathos simple, lateral arms not joined medially, moderately narrow, tapered, relatively short, straight, acute apically, slightly curved dorsally; tegumen moderately tall; valvae simple, short, basally broad, tapering abruptly from approximate midpoint on ventral margin, rounded distally, apex not expanded, prominent dorsal sub-apical spine present; saccus long, apex rounded, well sclerotised (Figure 2.48); aedeagus (Figure 2.49) medium length, stout, straight, apex truncated, rounded; vesica adorned with numerous spicules.

3.12.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores short, anteriores absent; lamella postvaginalis (sternite 8) posteriorly, membranous, with deep longitudinal sharply defined channels, anterior channels coalesce forming circles, loosely gathered on anterior margin, lightly sclerotised, adorned with numerous moderately long spicules; lamella antevaginalis wide, well sclerotised, medially narrowing band; antrum membranous, funnel shaped; colliculum membranous, not well defined; ductus seminalis inserted medially dorsally; ductus bursae membranous, long, slender, plicate; corpus bursae, moderate size, elongate, ovoid, thickly membranous, plicate, well differentiated from ductus; signa, two, strong, sclerotised bands on venter, long, wide, almost extending length of corpus, with numerous transverse rows of inwardly directed spines. Sternite A7 lightly sclerotised (Figure 2.54).

3.12.5 Remarks

Five subspecies have been recognised which reflect considerable variation in the extent of orange markings on the dorsal side, the size of the eyespots, the extent of the blue centre within the eyespots, and ventral side base colour and markings. *H. c. cordace* occurs widely throughout New South Wales and Victoria. *H. c. wilsoni* is restricted to south-western Victoria where its national conservation status is listed as critically endangered (Sands & New 2002). The remaining three subspecies are restricted to Tasmania, isolated by geography, climate and topography: *H. c. comptena* is restricted to the wet coastal areas of western and southern Tasmania at altitudes up to 395m; *H. c. kurena* occurs in the high rainfall areas of the Central Plateau, at altitudes between 610m and 1030m; and *H. c. legana* occurs in north-eastern Tasmania at altitudes up to 760m (Burns 1948; Couchman 1954; Burns 1956; Couchman 1962; Couchman & Couchman 1978; Common & Waterhouse 1981; Dunn & Dunn 1991; Braby 2000; Grund & Hunt 2000).

3.12.6 Diagnosis

In *H. cordace* the antenna is proportionally longer and the termen of the wings more rounded than in other *Heteronympha* species, there is also a prominent blue-centred eyespot on the hindwing of *H. cordace*. The ventral side markings are a different pattern with much larger eyespots. Sex-scales are absent in the male (Burns 1956; Braby 2000). Flight behaviour: in *H. cordace* adults have a slow, meandering flight close to the ground amongst clumps of the larval food plants occasionally feeding from the flowers of *Melaleuca* and *Leptospermum*; other species tend to display an erratic, rapid flight. Larval food plant specialisation: *H. cordace* feeds on *Carex appressa* and possibly *C. gaudichaudiana*; other *Heteronympha* feed predominantly on *Poa* species (Burns 1956; Common & Waterhouse 1981; Braby 2000).

In male *H. cordace* the valva is basally broad, tapering abruptly from midpoint on ventral margin; *H. penelope* and *H. merope* valvae are narrow, tapering gradually. The uncus in *H. cordace* is moderately long; *H. penelope* and *H. merope* short.

Female *H. cordace* genitalia are most clearly differentiated from *H. penelope* and *H. merope* by the lamella postvaginalis (sternite 8). In *H. cordace* the lamella postvaginalis is posteriorly membranous, with deep longitudinal sharply defined channels, the anterior channels coalesce forming circles, loosely gathered on anterior margin, lightly sclerotised, adorned with numerous moderately long spicules; anteriorly a small medial lightly sclerotised sub rectangular plate. In *H. penelope* and *H. merope* the lamella postvaginalis is posteriorly membranous, and extremely deeply invaginated forming a large convoluted sac. In female *H. cordace* the lamella antevaginalis is a wide, well sclerotised, medially narrowing band in *H. merope* the lamella antevaginalis is a lightly sclerotised narrow band. The ductus seminalis is inserted medially dorsally in *H. cordace* compared to medially ventrally in *H. penelope* and *H. merope*. Signa, two strong, sclerotised bands in *H. cordace* contrasting the weak bands in *H. penelope* and *H. merope*.

3.13 *H. penelope* Waterhouse

3.13.1 Habitat

Four subspecies of *H. penelope* are currently recognised: *H. p. penelope* occurs in the mountains and lowlands of southern Queensland / northern New South Wales, extending into the Australian Capital Territory and western Victoria in a wide range of habitats, particularly in lowland grassy woodland, drier eucalypt open-forest with a grassy understorey and subalpine woodland; *H. p. alope* is restricted to south-western Victoria and the south-eastern corner of South Australia; *H. p. diemeni* occurs on King Island and widely throughout the lowland of north-western, northern and eastern Tasmania; *H. p. panope* is restricted to the central plateau and near sea level on the west coast of Tasmania (Couchman & Couchman 1978; Common & Waterhouse 1981; Dunn & Dunn 1991; Braby 2000).

3.13.2 Habitus

Wingspan: ♂ 54 mm ♀ 56 mm.
Males - dorsal side black, with brownish-orange markings; forewing with a prominent bluish-white-centred black eyespot, and a large patch of grey-black sex-scales in basal half of cell; hindwing with a prominent bluish-black subtornal eyespot, and black subapical eyespot. Ventral side forewing dull brownish-orange, with dull black markings, a round black spot in cell, and apex orange-brown enclosing an obvious bluish-white-centred black eyespot; hindwing base colour dull orange-brown, with irregular series of dark brown wavy markings and eyespots (Common & Waterhouse 1981; Braby 2000) (Figure 2.44).

Females - dorsal side black, with orange markings; forewing with an obvious bluish-white-centred black subapical eyespot; hindwing with a white-centred black subapical eyespot; tornus slightly produced. Ventral side forewing similar to dorsal side but duller, a conspicuous round black spot in cell, and apex slightly suffused with dull purple or pink enclosing a prominent bluish-white-centred black eyespot; hindwing base colour variable dull yellowish-brown, pale brown or orange-grey, sometimes suffused with lilac or rich purplish-pink, with a series of irregular dark brown wavy markings and eyespots (Common & Waterhouse 1981; Braby 2000) (Figure 2.44).

3.13.3 Male genitalia

Uncus moderately short, simple, apically acute; gnathos simple, lateral arms not joined medially, narrow, relatively short, straight, apically acute, slightly curved dorsally; tegumen relatively tall; valvae simple, short, narrow, tapering gradually to apex, rounded distally, apex not expanded, prominent sub-apical spine present; transtilla membranous, juxta small, sclerotised, rounded; saccus long, apex rounded, well sclerotised (Figure 2.50); aedeagus (Figure 2.51) long, slender, moderately straight, apex truncated, rounded; vesica adorned with numerous spicules.

3.13.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae moderately long, well developed; apophyses posteriores, moderately short, moderately slender, anteriores, absent; lamella postvaginalis (sternite 8) posteriorly, membranous, rugose, with longitudinal channels, extremely deeply invaginated forming large convoluted sac, adorned with minute spicules at entrance to sac, anteriorly sclerotised; lamella antevaginalis, wide sclerotised band, narrow medially; antrum membranous, funnel shaped, rugose; colliculum not well defined; ductus seminalis inserted medially dorsally; ductus bursae membranous, long, moderately slender, weakly plicate; corpus bursae, moderate size, ovoid, membranous, well differentiated from ductus; signa weak, two longitudinal, long narrow, ventral, sclerotised bands adorned with numerous inward pointing spicules. Sternite A7 well sclerotised (Figure 2.55).

3.13.5 Remarks

Male *H. penelope* deposit a mating plug (sphragis) (Figure 2.45) around the genital opening of the female (Common & Waterhouse 1981; Braby 2000).

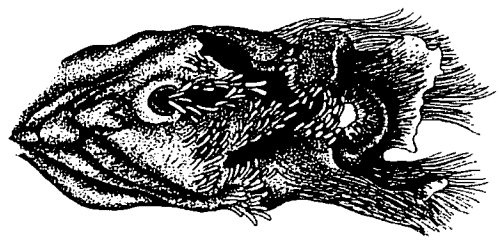


Figure 2.45 Sphragis attached beneath female *H. penelope* abdomen
[After Braby (2000)]

3.13.6 Diagnosis

Male *H. penelope* can be distinguished from male *H. merope* by the single large patch of sex-scales in the cell on the dorsal side of the forewing, and the white centred black subtornal eyespot on the dorsal side of the hindwing (Figure 2.46) (Braby 2000).

In male *H. penelope* the uncus is moderately short, compared to *H. cordace* moderately long. The valva is short, tapering gradually to apex with a prominent apical spine present in *H. cordace* tapering abruptly. The aedeagus is slender and moderately straight, where as in *H. cordace* stout; *H. morope* slightly sinuous.

In the female the posterior apophyses are moderately short. The lamella postvaginalis (sternite 8) is posteriorly membranous, rugose, extremely deeply invaginated forming large convoluted sac, adorned with minute spicules at entrance to sac; anteriorly sclerotised, compared to *H. cordace* deep longitudinal sharply defined channels; . Lamella antevaginalis, wide well sclerotised band, extremely narrow medially where as in *H. cordace* wide well sclerotised, medially narrowing band; *H. merope* lightly sclerotised narrow band, widening medially. In *H. penelope* the signa are two, weak, longitudinal, long narrow, ventral, sclerotised bands adorned with numerous inward pointing spicules, in *H. cordace* two strong, sclerotised bands on venter, and *H. merope* two, weak, long narrow bands, one dorsal, one ventral.

Figure 2.46 *H penelope* male, Lake Crescent, Interlaken, Tasmania.

3.14 *H. merope* Fabricius

3.14.1 Habitat

Three subspecies of *H. merope* are recognised: *H. m. merope* occurs widely in the east and southeast of mainland Australia; *H. m. salazar* is restricted to Flinders Island, King Island and mainland Tasmania; *H. m. duboulayi* is restricted to southwest Western Australia (Fisher 1978; Common & Waterhouse 1981; Braby 2000).

H. merope occurs in a wide range of habitats, frequenting grassy woodlands and dry eucalypt open-forest with a grassy understory in both coastal and mountainous terrain up to 1250 m on the mainland and from sea level to 760 m in Tasmania. At the northern end of its range in central Queensland *H. merope* flies only in the central highlands, where it is scarce (Fisher 1978; Common & Waterhouse 1981; Braby 2000).

3.14.2 Habitus

Wingspan: ♂ 56 mm ♀ 64 mm.
Males - dorsal side brownish-orange, with brown-black markings; forewing blue-centred black subapical eyespot, and large patch of grey-brown sex scales in four discrete linear areas. Hindwing prominent blue-centred black subtornal eyespot, two irregular black subterminal lines, followed by a broader black terminal band. Ventral side forewing dull orange, with a few black markings, apex yellow-brown enclosing a small subapical eyespot; hindwing yellowish-brown with a series of wavy dark brown lines (Fisher 1978; Common & Waterhouse 1981; Braby 2000) (Figure 2.44, Figure 2.47) .

Female - dorsal side forewing orange, outer half black enclosing three irregular yellow patches, one near costa, one near tornus and a smaller one near apex, and a prominent blue-centred subapical eyespot. Hindwing orange, with prominent blue-centred black subtornal eyespot, two irregular black subterminal lines, followed by a broader black terminal band. Ventral side forewing apex greyish-brown; hindwing ground colour varies from purplish-brown , through greyish-brown to yellow-brown, variably marked or striated with darker brown or grey lines, eyespots small and obscure (Fisher 1978; Common & Waterhouse 1981; Pearse & Murray 1981; 1982; Braby 2000) (Figure 2.44).

3.14.3 Male genitalia

Uncus short, simple, parallel sided, apically acute; gnathos simple, lateral arms not joined medially, narrow, parallel sided, relatively short, straight, apically acute, slightly curved dorsally; tegumen tall; valvae simple, relatively short, narrow, tapering gradually to apex, rounded distally; prominent sub-apical spine present; saccus long, apex rounded, well sclerotised (Figure 2.52); aedeagus (Figure 2.53) long, slightly sinuous, apex truncated, rounded; vesica adorned with numerous spicules .

3.14.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae moderately long, well developed; apophyses posteriores, moderately long, moderately slender, anteriores, absent; lamella postvaginalis (sternite 8), membranous, extremely deeply invaginated forming large convoluted sac, adorned with minute spicules at entrance to sac; lamella antevaginalis, lightly sclerotised, narrow band much wider medially; antrum membranous, funnel shaped; colliculum not well defined; ductus seminalis inserted medially dorsally; ductus bursae, membranous, long, moderately slender; corpus bursae, large, globular, membranous, well differentiated from ductus; signa two, weak, long narrow, one dorsal, one ventral, sclerotised bands adorned with numerous inward pointing spicules; sternite A7 weakly sclerotised (Figure 2.56).

3.14.5 Remarks

H. merope is the most common and widely distributed *Heteronympha.* Aided by the ability of the larvae to feed on some introduced grasses, it has been able to adapt successfully to suburban environments. *H. merope* often flies with *G. klugii* (Fisher 1978; Pearse 1978; Common & Waterhouse 1981; Braby 2000).

3.14.6 Diagnosis

Male *H. merope* can be distinguished from male *H. penelope* by the broken patch of sex-scales on the dorsal side of the forewing, and the blue centred black subtornal eyespot on the dorsal side of the hindwing (Braby 2000).

In male *H. merope* the uncus is short, parallel sided and apically acute cf *H. cordace* moderately long. The valva is relatively short, tapering gradually to apex with a prominent sub-apical spine present cf *H. cordace* tapering abruptly. The aedeagus is long and slightly sinuous cf *H. cordace* stout and *H. penelope* slender and moderately straight.

In the female the posterior apophyses are moderately long cf *H. cordace* short and *H. penelope* moderately short. The lamella postvaginalis (sternite 8) is membranous, extremely deeply invaginated forming large convoluted sac, adorned with minute spicules at entrance to sac cf *H. cordace* deep longitudinal sharply defined channels. Lamella antevaginalis, lightly sclerotised, narrow band much wider medially cf *H. cordace* wide well sclerotised, medially narrowing band; *H. penelope* wide well sclerotised band, extremely narrow medially. Signa two, weak, long narrow, one dorsal, one ventral, sclerotised bands adorned with numerous inward pointing spicules cf. *H. cordace* two strong, sclerotised bands on venter, and *H. penelope* two, weak, longitudinal, long narrow, ventral, sclerotised bands.

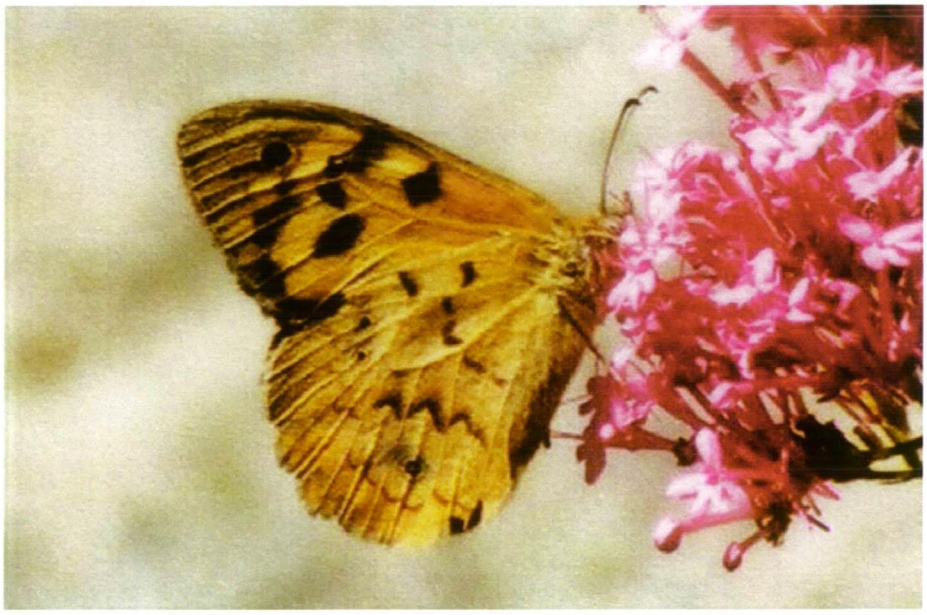


Figure 2.47 *H merope* male, Glenlusk, Tasmania.

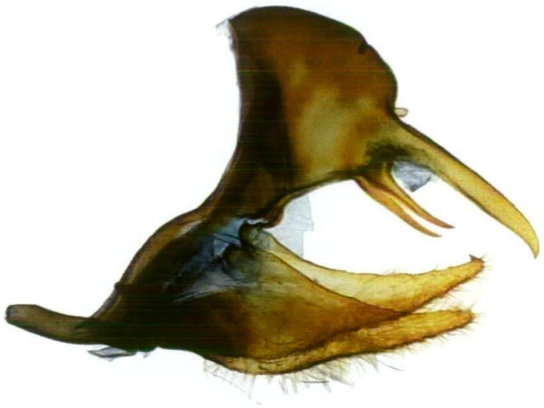


Figure 2.48 *H. cordace* male genitalia

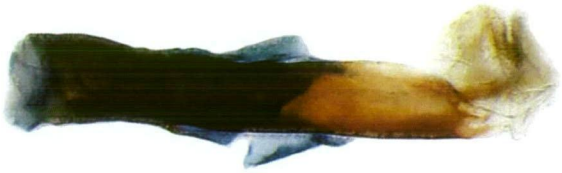


Figure 2.49 *H. cordace* aedeagus

Figure 2.50 *H. penelope* male genitalia

Figure 2.51 *H. penelope* aedeagus

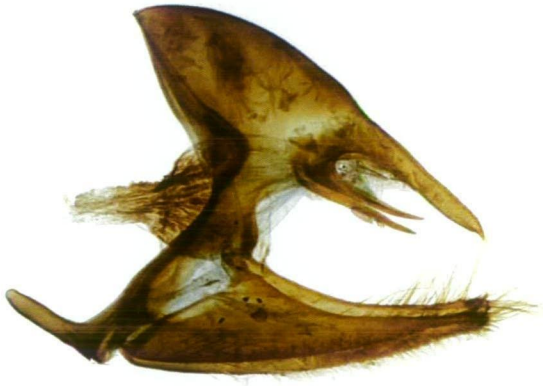


Figure 2.52 *H. merope* male genitalia

Figure 2.53 *H. merope* aedeagus

Figure 2.54 *H. cordace* female genitalia

Figure 2.55 *H. penelope* female genitalia

Figure 2.56 *H. merope* female genitalia

3.15 *Geitoneura* Butler

The genus *Geitoneura* (Butler 1867) comprises three species. *G. klugii* (Guérin-Méneville 1830 [1830-32]), is widely distributed across the temperate zone of mainland Australia extending from the east through southern Australia to the west and down into Tasmania. *G. acantha* (Donovan 1805) is restricted to southern and eastern temperate zone mainland Australia. *G. minyas* (Waterhouse & Lyell 1914), is endemic to south-western Western Australia (Common & Waterhouse 1981; Braby 2000).

3.15.1 Habitat

Geitoneura are found both on the lowlands and tablelands of southern Australia flying in a mixture of habitats, dominated by a variety of eucalypt open forest and woodlands with a grassy understory, and montane grasslands occasionally extending into subalpine and alpine woodlands. Two *Geitoneura* species can occur together, showing some differences in seasonal timing of adult appearance and preferred habitat (Common & Waterhouse 1981; Braby 2000).

3.15.2 Habitus

Geitoneura is characterised by smooth eyes and narrow clubbed antenna half the length of the costa of the forewing. The main veins in forewing are strongly swollen at base, and in hindwing, the cell is about half the length of the wing. The male has sex-scales consisting of a linear oblique dull black patch, which extends from near the base of vein M_3 to the dorsum on the upperside of forewing (Fisher 1978; Common & Waterhouse 1981; Braby & New 1988a; 1988b; 1999; Braby 2000).

3.15.3 Summary of Morphological Characters

Geitoneura differs from other southeast Australian Satyrinae genera by possession of a narrow clubbed antenna and smooth eyes.

3.16 *G. klugii* Guérin-Méneville

3.16.1 Habitat

G. klugii occurs in a wide range of habitats including eucalypt open forest and woodlands with a grassy understory, montane areas, occasionally extending into subalpine and alpine woodlands or grassy areas amongst sand-dunes shrublands and malee open scrub. *G. klugii* is extends from the coast up to 1400 m on mainland Australia and to 900 m in Tasmania (Fisher 1978; Common & Waterhouse 1981; Braby 2000).

G. klugii often flies with *H. merope* and with *G. minyas* and *G. acantha* where their habitat ranges overlap (Braby 2000).

3.16.2 Habitus

Wingspan: ♂ 39 mm ♀ 42 mm.
Dorsal side black, with brownish-orange markings; forewing, white-centred black subapical eyespot; hindwing, short black median band towards end of cell, a distinct white centred black subtornal eyespot and a broad black terminal band enclosing a row of brownish-orange subterminal spots. Ventral side forewing similar to dorsal side, apex dark grey; hindwing base colour ashy-grey to grey-brown or brown, with dark striations, and an irregular median band (Figure 2.57) (Fisher 1978; Common & Waterhouse 1981; Braby & New 1988a; 1988b; 1999; Braby 2000).

G. klugii dorsal side

G. klugii ventral side

Figure 2.57 Habitus of *G. klugii*

3.16.3 Male genitalia

Uncus moderately long, simple, parallel sided, truncated, apically acute; gnathos simple, lateral arms not joined medially, narrow, relatively long, acute apically; tegumen moderately tall; valvae simple, long, parallel sided, not markedly tapering, rounded apically, dorsal sub apical lobe present, lobe with spicules on apex; saccus moderately long, apex rounded (Figure 2.58); aedeagus (Figure 2.60) long, straight, slender, tapering, apex rounded, truncated; cornuti absent from vesica.

3.16.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores short, slender, anteriores absent; lamella postvaginalis (sternite 8) posteriorly, membranous, adorned with minute spicules, shallowly invaginated; lamella antevaginalis, weakly sclerotised narrow band, with a well-developed subrectangular medial plate; antrum membranous, funnel shaped, colliculum not well defined. Ductus bursae long, slender, plicate, membranous; corpus bursae, moderate size, elongate, ovoid, thickly membranous, well differentiated from ductus; signa weak, two long relatively narrow, dorsal ventral, sclerotised bands adorned with numerous inward pointing spicules. Sternite A7 weakly sclerotised (Figure 2.62).

3.16.5 Summary of morphological characteristics

In male *G. klugii* the gnathos is relatively long, valvae long, parallel sided and not tapering; saccus moderately long. Aedeagus tapers distally.

In female *G. klugii* the lamella postvaginalis is posteriorly membranous, adorned with minute spicules, shallowly invaginated; anteriorly a well-developed subrectangular medial plate. Lamella antevaginalis, a weakly sclerotised narrow band with medial plate. Signa, two, weak, long relatively narrow, dorsal ventral, sclerotised bands adorned with numerous inward pointing spicules.

3.17 *G. acantha* Donovan

3.17.1 Habitat

G. acantha (Donovan 1805) is restricted to mainland Australia where it occurs on the coast and tablelands of the east and south-east. *G. acantha* flies together with *G. klugii* in some places, however it favours damp shady gullies, sheltered slopes and riparian habitats where the larval food plants grow and avoiding the more open sunny areas (Fisher 1978; Common & Waterhouse 1981; Braby & New 1988a; 1988b; 1999; Braby 2000).

3.17.2 Habitus

Wingspan: ♂ 39 mm ♀ 44 mm.
Dorsal side: brown black, with extensive orange markings; forewings with a white-centred black subapical eyespot; hindwing with a white-centred black subtornal eyespot, and an obscure black apical spot. Ventral side: forewings similar to dorsal side; hindwing base colour brown, sometimes suffused with cream, with extensive pale yellow or creamish-white markings, a prominent white-centred black subtornal eyespot and a white–centred black apical eyespot, each ringed with pale yellow (Fisher 1978; Common & Waterhouse 1981; Braby & New 1988a; 1988b; 1999; Braby 2000)

3.17.3 Male genitalia

Uncus long, simple, parallel sided, tapered, apically acute; gnathos simple, lateral arms not joined medially, narrow, curved dorsally, short, acute apically; tegumen moderately tall; valvae simple, elongated, tapering abruptly from midpoint on ventral margin, rounded distally; well defined dorsal sub apical lobe present, with spicules on apex, lobe angle from valva; vinculum moderately short; saccus moderately short, apex broad, rounded (Figure 2.59); aedeagus (Figure 2.61) long, slender, slightly sinuous, apex rounded, cornuti absent from vesica.

3.17.4 Summary of morphological characteristics

In male *G. acantha* the gnathos is short, valvae elongated, tapering abruptly from midpoint on ventral margin. Saccus moderately short and the aedeagus long, slender, slightly sinuous.

Figure 2.58 *G. klugii* male genitalia

Figure 2.59 *G. acantha* male genitalia

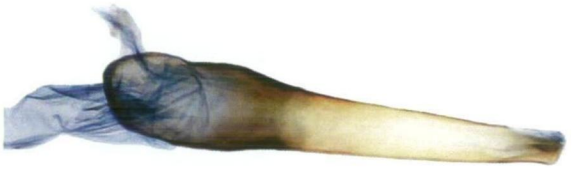


Figure 2.60 *G. klugii* aedeagus

Figure 2.61 *G. acantha* aedeagus

Figure 2.62 *G. klugii* female genitalia

3.18 *Vanessa* Fabricius

The genus *Vanessa* (Fabricius 1807) has a worldwide distribution and several wide-ranging species. Three migratory species are found in Australia; *V. kershawi* (McCoy 1868); *V. itea* (Fabricius 1775); and *V. cardui* (Linnaeus 1758). *V. cardui* seems to be dispersing from Africa as it does not appear to be permanently established in Australia (Braby 2000).

3.19 *V. kershawi* McCoy

3.19.1 Habitat

V. kershawi, a migratory species occurs from northern Queensland to Tasmania and into Western Australia in a wide variety of habitats, both natural and modified including suburban gardens, and is generally common throughout its range, except in northern Queensland where adults appear only occasionally, usually in spring (Braby 2000).

3.19.2 Habitus

Wingspan: ♂ 43 mm ♀ 47 mm.

Dorsal side, black with pinkish-orange markings; forewing base brown, anterior to cell reaching costa white band of spots, series of four small, white subapical spots (Figure 2.63 Figure 2.64). Hindwing base brown, series of four black subterminal spots three have blue centres, black broken subterminal line, blue tornal streak. Ventral side forewing similar to dorsal side, base colour brown, paler markings, pinkish-orange markings richer reddish-orange, white bar in cell. Hindwing brown intricately patterned, cream and yellow markings, series of four or five obscure subterminal eye spots (Figure 2.64) (Common & Waterhouse 1981; Braby 2000).

Figure 2.63 Habitus of *V. kershawi*

3.19.3 Male genitalia

Uncus very short, simple, broad based, tapering, rounded apically; gnathos simple, lateral arms not joined medially, very broad, relatively short, terminally rounded, tapering apically, ventrally-medially curved, hook like; tegumen moderately long; valvae complex, short, truncated, very broad, long setae scattered on inner surface, joined basally; ampulla enlarged, occupying most of valva, moderately concave, fused with harpe along ventral margin, well sclerotised, dorsal margin triangular with well developed proximal, mesal spines, proximal half sub-serrated; harpe process-like, extending perpendicularly from ampulla base, robust spine extending medially at apex, medial margin wavy; sacculus narrow, extended into free arm, terminating in dorsally directed rounded spine; valva ventral margin distally serrate, subapical small triangular process, margin serrate; vinculum relatively short; juxta small rounded lobe, well sclerotised; saccus moderately long, broad basally, curved dorsally, tapering, apex rounded (Figure 2.65); aedeagus (Figure 2.66) long, slender, sinuous, constricted medially, distal half very well sclerotised, apex rounded; cornuti absent from vesica.

3.19.4 Female genitalia

Ovipositor short, broad; papillae anales, sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, long, slender, anteriores, absent; lamella postvaginalis (sternite 8), well sclerotised plate, lamella antevaginalis, well sclerotised plate, anterior margin "M" shaped; antrum not well defined; colliculum not well defined, ostium bursae, very well sclerotised, very small. Ductus seminalis inserted medially dorsally; ductus bursae long, very slender, membranous; corpus bursae, moderate size, rounded, apex rounded, thickly membranous, well differentiated from ductus; signa weak, two longitudinal, long narrow, ventral sclerotised bands adorned with numerous inward pointing spicules. Sternite A7 very well sclerotised (Figure 2.67).

Figure 2.64 *V kershawi,* Lake Catania, Mt Buffalo Victoria

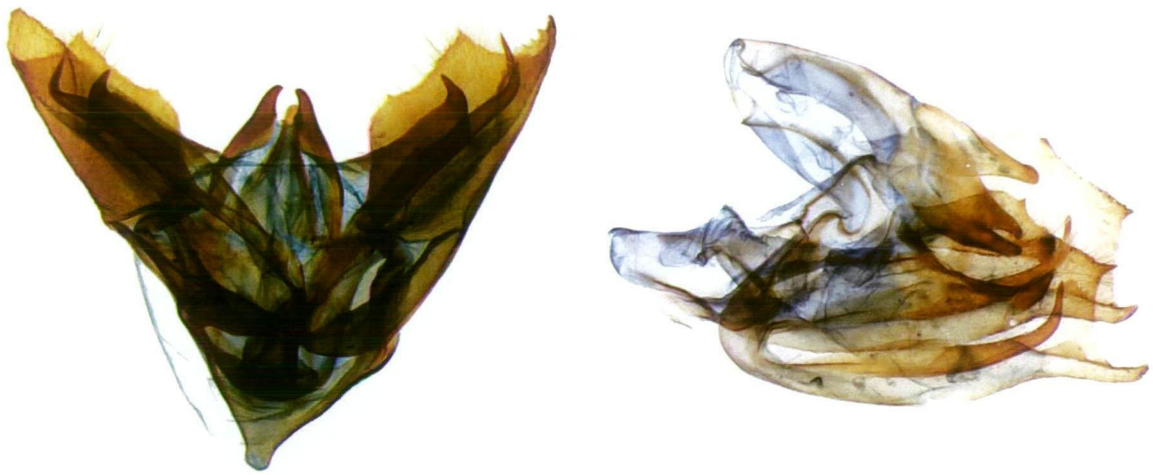


Figure 2.65 *V. kershawi* male genitalia

Figure 2.66 *V. kershawi* aedeagus

Figure 2.67 *V. kershawi* female genitalia

3.20 *Junonia* Hübner

The genus *Junonia* (Hübner 1819) has a very wide distribution in the tropical and subtropical regions of Australia. Species include: *J. orithya* (Linnaeus, 1758), *J. hedonia* (Linneaus, 1764) and *J. erigone* (Cramer, [1775]), however only *J. villida* (Fabricius 1787), extends into the temperate zone (Braby 2000).

3.21 *J. villida* Godart

3.21.1 Habitat

J. villida a migratory species is common in a wide variety of habitats, particularly woodlands, open-woodlands and grasslands, in both coastal and inland areas. *J. villida* occurs in both natural and modified habitats including suburban gardens (Braby 2000).

3.21.2 Habitus

Wingspan: ♂ 40 mm ♀ 43 mm.

Dorsal side is brown; forewing with two orange bars in cell edged with dark brown and separated by a dull blue area. A narrow cream band of spots stretches from costa to termen, followed by a smaller cream subapical band, and two blue subterminal eyespots broadly ringed with black then orange, near tornus. Hindwing has two large subterminal eyespots broadly ringed with orange, largest near costa, followed by two broken cream subterminal lines. Ventral side, base colour pale brown or buff; forewing with markings similar to dorsal side but subapical eyespot reduced to minute spot. Hindwing with narrow brown irregular postmedian band or wavy line followed by two small eyespots and sometimes two or three very small obscure dark brown spots (Figure 2.68) (Braby 2000).

J. villida dorsal side

J. villida ventral side

30mm

Figure 2.68 Habitus of *J. villida*

3.21.3 Male genitalia

Uncus moderately short, simple, broad based, tapering, pointed apically; gnathos complex, lateral arms joined medially, very broad, with very large medial process, consisting dorsally of large, oval, membranous process, concave dorsally, covered with stout, long spines, process ventrally fused with lateral arms of vinculum; valvae complex, very short, truncated; ampulla, harpe fused; ampulla dorso-subapical process curving inwards, apex recurved, medial margin with stout robust pointed spines, apical spines, long setae on dorsal surface; harpe with dorso-apical process, curving inwards, apex ventrally directed, 3 spines apically, 2 very large proximally, small spines distally; posterior margin of valva, wavy, numerous long setae on inner margin; sacculi of 2 valvae fused; vinculum long; saccus very narrow, very long, curved dorsally, apex rounded (Figure 2.69); aedeagus (Figure 2.70) long, slender, well sclerotised, apex acute; cornuti absent from vesica.

3.21.4 Female genitalia

Ovipositor short, broad; papillae anales, very well sclerotised, distally with slightly rounded, membranous lobes, setae long, well developed; apophyses posteriores, very long, slender, anteriores, moderately long, slender; lamella postvaginalis (sternite 8) posteriorly membranous, adorned with minute spicules, evaginated to form large sac; anteriorly a small well sclerotised, concave plate, continuous with sclerotised section of sternite A8; lamella antevaginalis, not distinct; antrum sclerotised, funnel shaped, colliculum not well defined, vaginal opening small. Ductus seminalis inserted medially dorsally at base of antrum; ductus bursae moderately long, membranous, very slender; corpus bursae, thickly membranous, moderate size, very elongate, narrow, apex rounded, moderately well differentiated from ductus; signum absent. Sternite A7 well sclerotised (Figure 2.71).

Figure 2.69 *J. villida* male genitalia

Figure 2.70 *J. villida* aedeagus

Figure 2.71 *J. villida* female genitalia

4 KEY TO SPECIES BASED UPON GENITALIC CHARACTERS

4.1 *Male*

1. Valva complex **2**

Valva simple **3**

2. Gnathos complex, lateral arms joined medially ..... *J. villida*

Gnathos simple, lateral arms not joined medially ..... *V. kershawi*

3. Valva long, parallel sided, not markedly tapering ..... *G. klugii*

Valva tapering **4**

4. Valva broad basally, tapering from mid point on ventral margin **5**

Valva narrow tapering **6**

5. Dorsal sub-apical spine present, distal ventral margin of valva serrated ..... *N. leprea*

Ventral margin of valva strongly curved inwards, apex expanded, flattened, dorsal margin finely serrated, apex curved inwards, serrated ..... *A. hobartia*

Prominent dorsal sub-apical spine present, valvae rounded distally, apex not expanded, ... *H. cordace*

6. Valva short, narrow, tapering **7**

Valva long, narrow, tapering **8**

7. Aedeagus long, slender, moderately straight ..... *H. penelope*

Aedeagus long, slightly sinuate ..... *H. merope*

8. Valva tapers markedly **9**

Valva relatively uniformly broad, gradually tapering **12**

9. Uncus, long, simple, parallel sided, truncated, rounded apically **10**

Uncus, long, simple, parallel sided, tapered, acute apically ..... *G. acantha*

10. Saccus curved dorsally, apex rounded **11**
Saccus curved dorsally, tapering, apex rounded ..... *O. latialis*

11. Aedeagus long, slender, slightly sinuate ..... *O. lathoniella*
Aedeagus long, stout, markedly sinuate ..... *O. ptunarra*

12. Aedeagus long, slender, slightly sinuate ..... *O. correae*
Aedeagus short, stout **13**

13. Valva very small, dorsal sub-apical lobe present, apex not spinose ..... *O. orichora*
Valva normal, dorsal sub apical lobe present, apex spinose ..... *O. kershawi*

4.2 *Female*

1. Apophyses anteriores present **2**
Apophyses anteriores absent **3**

2. Signa present **3**
Signa absent ..... *J. villida*

3. Lamella antevaginalis distinct **5**
Lamella antevaginalis not distinct **4**

4. Vaginal opening very well sclerotised ..... *V. kershawi*
Vaginal opening not well sclerotised **5**

5. Signa present **6**
Signa absent **10**

6. Apophyses posteriores extremely short to short **7**
Apophyses posteriores moderately long to long **9**

7. Ductus bursae membranous, moderately long, moderately slender **8**
Ductus bursae relatively broad ..... *O. orichora*

8. Corpus bursae elongated ..... *O. correae*
Corpus bursae rounded ..... *O. latialis*
Corpus bursae boot shaped ..... *O. kershawi*

9. Signa present **11**
Signa absent **10**

10. Lamella antevaginalis, rhomboidal transverse plate ..... *O. ptunarra*

Lamella antevaginalis, subrectangular plate, with medially indented posterior margin ..... *O. lathoniella*

11. Apophyses posteriores short to moderately short **13**

Apophyses posteriores moderately long to long **12**

12. Signa, two, weak, long, narrow, longitudinal, dorso-lateral, ventro-lateral sclerotised bands, running to midpoint of corpus bursae..... *A. hobartia*

Signa, two, weak, long, narrow, one dorsal, one ventral, sclerotised bands adorned with numerous inward pointing spicules ..... *H. merope*

13. Signa weak **14**

Signa strong ..... *H. cordace*

14. Lamella antevaginalis broad, rhomboidal, transverse plate, posterior margin notched medially ..... *N. leprea*

Lamella antevaginalis weakly sclerotised narrow band ..... *G. klugii*

Lamella antevaginalis wide sclerotised band extremely narrow medially ..... *H. penelope*

5 DISCUSSION

5.1 *Morphology*

Marked inherited phenotypic sexual dimorphism is unusual in Australian Lepidoptera and is most commonly seen in Lycaenidae (Braby 2000). Within the Australian satyrine fauna, only species in the genus *Oreixenica* and *Heteronympha* display marked sexual dimorphism. Two of the six species in the genus *Oreixenica*: *O. ptunarra* and *O. correae*; and two of the seven species in the genus *Heteronympha*: *H. merope* and *H. mirifica* (a north-eastern temperate zone species from the northeast corner of Victoria, New South Wales and southern Queensland) exhibit marked sexual dimorphism. Phenotypic plasticity in tropical satyrine species between wet / dry season forms is well documented (Brakefield 1987; Brakefield & Reitsma 1991; Braby 1994b; Kooi *et al.* 1994; Ruiter & Brakefield 1994; Windig *et al.* 1994; Braby 1995c; Kooi & Brakefield 1999; Roskam & Brakefield 1999; Kemp 2000; Braby 2002; Lyytinen *et al.* 2004; Pijpe *et al.* 2007). In the temperate zone nymphaline species, James (1987) observed phenotypic plasticity in *V. kershawi* and *J. villida* in relation to body size and weight. Neither of these species show marked sexual dimorphism in their seasonal morphological phenotypic plasticity.

Melanitis leda is a tropical satyrine which exhibits seasonal polyphenism. There is a wet season form, characterised by uniform colouration and large, conspicuous submarginal eyespots; and a dry season form which lacks eyespots but displays remarkable variety in colour and pattern (Ruiter & Brakefield 1994). Ruiter & Brakefield (1994) found that part of the variation within the dry season form was genetically based. This species therefore provides an interesting example of an interaction between the phenotypic plasticity expressed in the wet season form and genetic polymorphism within the dry season form. McQuillan & Ek (1997) and Anderson & McQuillan (2000) in their studies of *O. ptunarra* and Berry (1997) in her study of *O. lathoniella* observed clinal variation in phenotype plasticity along climatic gradients. Sexual dimorphism as exhibited in *O. ptunarra* and *O. correae* is related to genetic polymorphism.

Phenotypic differences between the seasonal forms of tropical satyrine such as *Bicyclus* and *Mycalesis* imply that selection for cryptic colouration is very strong in the dry season when butterflies tend to rest inactively on a ground layer of dead brown leaves. In the wet season when an environment of lush growth promotes an active lifestyle, pattern elements, especially marginal eyespots, which are active anti-predator devices are favoured (Brakefield & Larsen 1984; Brakefield 1987; Brakefield & Reitsma 1991; Holloway *et al.* 1993 ; Braby 1994b; Kooi & Brakefield 1999). It is interesting to note that the phenotypic variation expressed between the wet and dry season forms of tropical Satyrinae species are not as extreme as the sexual dimorphism expressed between the male and female phenotype in *Oreixenica* and *Heteronympha*.

Sexual dimorphism in *Oreixenica* and *Heteronympha* species is associated with differences in flight behaviour between male and female butterflies. *H. mirifica* and *H. merope* female butterflies aestivate during summer, resting in cool shady places amongst dry leaf litter (Braby 2004). Male *H. mirifica* fly high and perch 6-7 metres above the ground on foliage of trees overhanging gullies in more open sunlit areas to establish territories. Male *H. merope* fly slowly close to the ground over grasses early in the flight season; later flying higher, patrolling the mid to upper canopy with a faster erratic flight and commonly hilltop (Braby 2004).

There is compelling evidence from field observations to suggest that male *O. ptunarra* are territorial and that females are not (Anderson 2001a; Anderson & McQuillan 2003). Male territories are based around patches of *Poa* tussocks. The size of territory appears to be largely determined by *Poa* patch size. Territories are centred around *Poa* patches rather than nectar sources, many territories seem to be preferentially adopted in areas with few to no nectar sources (Anderson 2001b). Male *O. ptunarra* are more active, spending most of their time flying in low search patterns around and between tussocks seeking females and defending territory. The dark cryptic colouration of male *O. ptunarra* aids in camouflaging the butterfly against the *Poa* tussocks, whilst assisting with heat absorption to aid flight. At higher altitudes darker colouration may be advantageous in males which need to be able to rapidly absorb heat to facilitate a high level of activity (Anderson & McQuillan 2000).

Female *O. ptunarra* are relatively sedentary, spending most of their time basking on *Poa* tussocks, and occasionally flying short distances to adjacent tussocks (Anderson 2001a; Anderson & McQuillan 2003). Anderson & McQuillan (2003) found a negative cline indicating that females are lighter at higher altitudes, this maybe a response to exposure. At higher altitudes the females are more exposed whilst basking therefore lighter colouration prevents rapid heating. Furthermore pale colouration may be advantageous in assisting with camouflage against the light coloured grass tussocks with the marginal eyespots serving as active anti-predator devices.

O. correae males fly in the understorey close to small shrubs, herbs and grasses with a slow weak flight; feeding on the nectar of Asteraceae. *O. correae* males display flight behaviour akin to individuals flying in the tropical wet season, when ready food sources are available and individuals display uniform colouration and large and conspicuous submarginal eyespots. Female *O. correae* tend to be more sedentary confined to shady perches seldom venturing out into the open to feed. Flight behaviour akin to that displayed in the tropical dry season; when there is limited food resources available, individuals tend to rest inactively and cryptic colourations dominate. In some tropical Satyrinae species adults resulting from larvae reared on stressed plants had more dry season wing patterning than those reared on fresh material (Kooi *et al.* 1998).

The placement of *H. cordace* within the genus *Heteronympha* has been questioned by some authors (Burns 1948; 1956; Braby 2000). *H. cordace* differs considerably in adult morphology, flight behaviour, larval and pupal morphology and food plant specialisation to the other species of *Heteronympha* (Burns 1956). In many respects *H. cordace* phenotypicially and in flight behaviour is more similar to *Oreixenica* species than *Heteronympha* species. When both the male and female genitalia of *H. cordace* are compared with other *Heteronympha* species there is no doubt that *H. cordace* is a conventional *Heteronympha* based on genitalia because they share the male *Heteronympha* synapomorphies of the saccus being long, apex rounded, well sclerotised; and a prominent dorsal sub apical spine is present and female *H. cordace* signa is present.

5.2 *Genitalia*

The genitalia of temperate zone southeast Australian Satyrinae are fairly homogenous with only subtle interspecies differences within most genera. Within some genera, e.g. *Argynnina*, species are almost unrecognizable by examination of genitalia alone. In addition, some species resemble the genitalic features of species from other genera. This pattern of some species within a genus showing marked differences, and others very little has been documented previously in other studies of Satyrinae. The temperate northern hemisphere satyrine genus *Maniola* exhibits this pattern in both sexes (Grill *et al.* 2004). This pattern was also reported by Peña & Lamas (2005) in their review of the Neotropical satyrine genus *Forsterinaria.* Braby (1993) in his study of the Australian tropical Satyrine genus *Tisiphone* noted the genitalia of *T. helena* shows a close resemblance to that of *T. abeona* but significant morphological differences in the uncus, gnathos, saccus and valvae to *T. abeona.* Mutanen (2006) in his work on moths noted external genital traits express varying amounts of variability and that the genital structures that do show variation in closely related species may show structural overlap. He also observed that the amount of variation in internal genitalia was equal to that in non-genital traits (2006).

5.2.1 Male Genitalia

Kuznetzov& Stekol'nikov (2001) identified the main autapomorphies for male Satyrinae genitalia as: (1) the tegumen having distinct articulatory processes providing dorsal connection of valvae with segment; (2) the valvae are narrowed, heavily sclerotised, and their distal ends bear groups, or a row, of strong teeth; (3) modification of sub-uncus; and (4) the intra-valval muscles m7 are hypertrophied, and additionally contribute, their own autapomorphic characters.

5.2.1.1 Male Genitalic Autapomorphy 1:

In the southeast Australian satyrine, extended processes of the tegumen are not present nor are they present in the Neotropical *Forsterinaria* (Peña & Lamas 2005). In the species studied by Kuznetzov& Stekol'nikov (2001) the articulatory processes only appear to be extended in *Ypthima motschulskyi.*

5.2.1.2 Male Genitalic Autapomorphy 2:

The valva of all Satyrinae in my study were simple, narrow and sclerotised consistent with the findings of Kuznetzov& Stekol'nikov (2001). In several species, autapomorphies were related to characteristics of the valva, particularly the degree of tapering and characteristics of the distal apex. The valvae of *V. kershawi* and *J. villida* are complex in contrast to the simple valvae of satyrines. In a global study Willmott *et al.* (2001) found that within the subfamily Nymphalinae the valvae vary from simple to complex among genera.

Goulson (1993) noted that individuals of *M. jurtina* exhibited significant variation in the male genitalia particularly in the distal and dorsal margins of the valva, leading him to question the reliability of characteristics of the valva. However, characteristics of the valva have been identified in a number of studies discussing the morphology of Satyrinae genitalia as key to identifying individual species (Braby 1993; Johnson & Hedges 1998; Jutzeler *et al.* 1998; Sourakov 1999; Wakeham-Dawson & Dennis 2001; Belik & Zamolodchikov 2002; Peña & Lamas 2005; Penz 2007). In particular, autapomorphies are identified in the width of the valvae, degree of tapering, the presence or absence of a dorsal sub-apical lobe, and if present the shape and size of the lobe, and the presence or absence of spines towards the apex of the valva. Genera in my study that show the most significant variation in valva complexity are *Nesoxenica*, *Argynnina*, *Heteronympha,* and *Geitoneura.*

5.2.1.3 Male Genitalic Autapomorphy 3:

The subunci referred to by Kuznetzov & Stekol'nikov (2001) can be interpreted as the arms of the gnathos (Beljaev 2009). Kuznetzov & Stekol'nikov (2001) consider the presence of paired subunci a characteristic feature of Satyrinae as they state *these appendages are absent in the closely related family Nymphalidae, while being present in other diurnal Lepidoptera.* Gnathos or subunci are present in other closely related Nymphalidae, for example the subfamily Charaxinae (Miller & Miller 1976; Willmott & Hall 2004). Furthermore, subunci or gnathos are also present in more distantly related Nymphalidae for example species of the genus *Boloria* (subfamily Heliconiinae) (Warren 1944).

In all the Satyrinae studied and in *V. kershawi*, the gnathos was simple whereas in *J. villida* the lateral arms of the gnathos are joined medially. Willmott *et al* (2001) in their review of the Neotropical Nymphalinae butterflies noted variation in the gnathos ranges from: a simple 'U' shape, with projections connected by soft tissue; to lateral arms joined and continuously sclerotised; to heavily sclerotised, forming 2 long, posteriorly pointing projections.

5.2.1.4 Other Male Genitalic Apomorphies

The uncus is generally long, simple, parallel sided and truncated, the main exception being *Heteronympha*. In *H. penelope* and *H. merope* the uncus is short, as also seen in *J. villida* and *V. kershawi*. Characteristics of the uncus, particularly distal variations in the uncus, predominantly apical variations such as rounded or acute are often used as autapomorphies to define species for example the neotropical genus *Calisto* (Gail 1985). In *Henotesia* the uncus is strongly curved and broad (Usher 1985) whereas in *Yphthimoides cipoensis* the uncus forms a dorso-ventrally flattened process, in the form of a wide spatula, an unusual shape for the Satyrinae (Freitas 2004). In *Pseudohaetera*, a Neotropical genus which appears to share a similar ecological niche as *Oreixenica*, the uncus is curved and elongate (Constantino 1992) as in *Oreixenica*.

Where possible limited emphasis has been placed on characteristics of the aedeagus as the aedeagus changes shape according to the orientation in which it is studied, and as it is a rather soft structure, it can vary in shape.

5.2.2 Female Genitalia

The autapomorphies identified by Kuznetzov & Stekol'nikov (2001) for the female Satyrinae genitalia are: (1) frequently with shortened, vestigial posterior apophyses; and (2) a single pair of long strip-shaped dentate or spinulous signa.

Overall the female southeastern Australian Satyrinae documented in this study, conformed to the Kuznetzov & Stekol'nikov (2001) autapomorphies, with a notable exception regarding the signa. An additional autapomorphy that could be described for the temperate zone southeast Australian Satyrinae is (3) apophyses anteriores absent.

5.2.2.1 Female Genitalic Autapomorphy 1:

The length of the posterior apophyses ranged from extremely short to very long and showed interspecies variation within most genera especially within *Oreixenica*. In *O. ptunarra* the posterior apophyses are moderately long. Sharma (2003) described the apophyses posteriores in *Elymnias hypermnestra undularis* as moderately long measuring these to be approximately 0.5mm long, a similar length to *O. ptunarra*.

5.2.2.2 Female Genitalic Autapomorphy 2:

Significantly signa are absent in *Oreixenica*; but all other Satyrinae studied had some form of signum. Most species had either one or two longitudinal strips of signa as described by Kuznetzov & Stekol'nikov (2001) and documented in other Satyrinae (Johnson *et al.* 1986(87); Grill *et al.* 2004).

5.2.2.3 Female Genitalic Autapomorphy 3:

Comments referring to the condition of Satyrinae apophyses anteriores in the literature are scarce. None of the southeast Australian Satyrinae studied had apophyses anteriores present. In *E. h. undularis* the apophyses anteriores are also wanting (Sharma 2003). Apophyses anteriores were present in *J. villida* and absent in *V kershawi*. In the Nymphalidae tribe Argynnini (subfamily Heliconiinae) the apophyses anteriores are usually small and membranous, but some variation occurs (Simonsen 2006a).

5.2.2.4 Other Female Genitalic Apomorphies

The lamella postvaginalis and lamella antevaginalis was recognised by Sourakov (1999) as being of taxonomic value in the genus *Calisto*. Sourakov (1999) noted several different shapes in the lamella postvaginalis and lamella antevaginalis, including some similar to those observed in the southeast Australian Satyrinae.

6 CONCLUSION

The southeast Australian Satyrinae appear to be a monophyletic group based upon morphological evidence.

Chapter 3

The Immature Stages of *Oreixenica* with notes on associated Temperate Zone Southeast Australian Satyrinae

1 INTRODUCTION

1.1 *Brief history of Satyrinae taxonomy*

The use of egg morphology in lepidopteran systematics dates back to the late nineteenth century. Chapman (1896) was one of the first authors to discuss the phylogenetic significance of the eggs in Lepidoptera (Common 1975). Comparative studies published in the mid twentieth century suggested that little could be gained from external chorion morphology, except at low taxonomic levels. However, the introduction of Scanning Electron Microscopy (SEM) increased the potential of comparative egg morphology as utilised by Downey & Allyn (1981; 1984) and Kitching (1985).

The few comprehensive studies of Satyrinae eggs have mostly been limited to the northern hemisphere fauna (Garcia-Barros & Martin 1991; Garcia-Barros 1994; Garcia-Barros & Martin 1995; Garcia-Barros & Munguira 1997; Garcia-Barros 2000; 2006) or tropical species (Braby 1993; 1994a). The pioneering study by Garcia-Barros and Martin (1995) on the eggs of European Satyrinae butterflies, provided a preliminary comparative study of the satyrine external chorionic morphology.

The majority of other studies have focused on a single species or genus in isolation (Salkeld 1975; 1976; Downey & Allyn 1981; 1984; Brower 1997; Freitas *et al.* 2002) or addressed particular research questions (Ruohomaki *et al.* 1993; Resetarits 1996; Oberhauser 1997; Clark & Faeth 1998; Bergman 1999; Carter & Feeny 1999; O'Brien *et al.* 2004; Steigenga & Fischer 2007).

Early descriptions of lepidopteran larvae were generally confined to superficial characteristics such as colour, shape and size (Hinton 1946; 1948; 1955). These characteristics are useful in distinguishing between species (Stehr *et al.* 1987) but are subject to convergence, and are therefore limited in their utility in the separation of higher taxonomic divisions. However, larvae have been invaluable in demonstrating

weaknesses in adult classification and providing some resolution (Scoble 1995). Dyar (1894), Fracker (1915), and Hinton (1946) all carried out significant pioneering studies of lepidopteran larvae. Dayar and Fracker found that with certain significant exceptions their work supported and complemented existing classifications based on adult morphology (Scoble 1995). A study by DeVries *et al.* (1985) emphasising larval characters in the Nymphalidae led to hypotheses suggesting that many accepted taxa within the Nymphalidae were untenable in a phylogenetic system (Scoble 1995).

The limited number of studies that examine Satyrinae larvae are restricted to discussing and describing individual species or genus, and generally lack an evolutionary component (Braby 1993; 1994a; James 1999; Freitas *et al.* 2002; Murray 2003).

The most significant work on Satyrinae pupae compared the pupal structures of 10 species and their associated mode of pupation (Starnecker 1999). Pupal taxonomy has chiefly been limited to describing species and genera (Aiello 1991; Braby 1993; 1994a; Murray 2003; Freitas 2006). A limited number of authors have considered controls of pupal colour (Van Dyck *et al.* 1998; Jones *et al.* 2007).

1.2 *Aims*

The main aims of this study are threefold. Firstly, to comprehensively describe the eggs of *Nesoxenica,* the Tasmanian *Heteronympha, Geitoneura,* and *Argynnina* and all the species from the genus *Oreixenica.* Secondly, to describe and document the larva and pupa of *Oreixenica ptunarra.* Finally to revise the immature biology of selected Tasmanian Satyrinae. This will add greatly to the available information about immature *Oreixenica*, in particular *O ptunarra.*

2 MATERIALS AND METHODS

2.1 *Fresh Egg Collection*

Eggs were obtained from adult butterflies collected in the field using a hand net between 2000 and 2005. After capture, female butterflies were transferred as soon as possible to oviposition containers. These containers consisted of a plastic drinking cup (66mm wide and 95mm deep) or takeaway food container (115mm wide and 60mm deep) covered by a piece of stocking held in place by a rubber band. Within the container was placed a folded piece of tissue paper and cuttings of *Poa*. A glass vial 10 mm in diameter and 50mm in height was attached to the base of the container with a piece of adhesive putty. Packed inside the vial was a tissue paper wick that fanned out over the edge of the vial 2 – 3 cm. The wicks were sodden with a 2 - 5% sugar solution. The oviposition containers were stored in the laboratory at room temperature.

Eggs were removed from the oviposition containers shortly after oviposition and stored in plastic, well ventilated containers, in a cool, dry location. Eggs that were laid on the sides of the containers were removed with a moistened camel hair brush or egg (swan beak) forceps.

The following information was recorded for each species: adult collection details, batch size and number of batches, the date of oviposition of each batch, the overall egg colour and colour changes during maturity, egg arrangement and orientation to the substrate and incubation period. The number of eggs laid per female was counted. Where possible, a minimum of 10 eggs per female, were measured for three dimensions: length, width and height following Young (2006a). When available, eggs from more than one female were measured to account for differences in egg size between individuals, as significant differences in egg size have been found between females of the same species of Lepidoptera (Syme 1961; Young 2006a).

Eggs and larvae were measured using a binocular microscope and an eyepiece micrometer. The measurements were expressed as mean ± S.E. in mm. In each description, batch size is expressed as the mean ± S.E., unless the batch number was small in which case the range of batch size is given.

2.2 *Egg Collection from Pinned / Dried Specimens*

As fresh eggs were not available for every species, eggs were collected from dried pinned specimens housed at the Australian National Insect Collection (ANIC) and the Tasmanian Department of Primary Industries and Water (DPIW). Eggs were collected using an adaptation of the Protease Digestion Method first described by Junker *et al.* (2006)

2.2.1 Protease digestion

The abdomen was detached from the metathorax of each specimen and placed in 140µL LIFTON-buffer (refer section 2.2.2) in 1.5 mL Eppendorf microcentrifugation tubes (Eppendorf tubes). After incubation for 30 mins in a 55 °C waterbath, 0.5 µL protease K (PK) (20 mg/mL) was added and the samples incubated for a further 18 hours. After 18 hours of incubation the abdomens were transferred into small glass vials containing a drop of buffer solution and the skin of the abdomen was split open at the anterior end to determine the degree of digestion. Free eggs were transferred with a camel hair brush into a 1.5 mL Eppendorf tube containing 500 µL milliQ. If the abdomens required further digestion they were returned to the original Eppendorf tubes which had been rinsed with milliQ. 140 µL clean LIFTON-buffer solution was then added to the Eppendorf tubes along with 2.0 µL PK. The samples were again incubated at 55 °C. This supplementary digestion was monitored regularly and terminated when eggs could be easily removed from the surrounding tissue.

The extracted eggs were washed in 500µL milliQ and then dehydrated in a gradual acetone series consisting of 10 mins each in 30%, 50%, 70%, 80%, 90% and for two 30 min. periods in 100% acetone. After the acetone dehydration the samples were immersed in 1000 µL of hexamethyldisilazane (HMDS) for final drying (Laforsch & Tollrian 2000). After a 30 minute soak in HMDS, 90% of the HMDS was removed and the vials were immediately transferred to a vacuum desiccator. The bottom of the desiccator was covered by silica gel beads and the desiccator evacuated. The remaining HMDS was allowed to evaporate overnight under anhydrous conditions. All steps with HMDS were conducted under a fume hood due to the strong irritant nature of this reagent.

Several dried eggs were mounted on aluminium SEM stubs in different positions using clear nail polish (Young 2006a). If necessary the eggs were cleaned using a fine camel

hair brush dipped in water and then all were splatter coated with gold using a Bal-Tec SCD 050 Sputter Coater for 220 seconds at 40 milliamps.

2.2.2 LIFTON Buffer

LIFTON buffer consists of 6.8g sucrose, 50mL 200mM Tris, 10mL 0.5M EDTA and 2.5mL 20%w/v SDS made up to 100mL with MilliQ.

2.3 *Egg and Larva Photography*

Unless otherwise stated in the text all fresh and mature eggs and larva were photographed by the author using a Wild MPS52 photoautomat camera attached to a Wild M8 zoom stereo-microscope.

Eggs of each species were also photographed at high magnification using an Environmental Scanning Electron Microscope (ESEM), Electroscan Corporation, Wilmington, Massachusetts, U.S.A., or FEI Quanta 600 ESEM, located in the Central Science Laboratory of the University of Tasmania.

2.4 *Larva Data Collection*

Upon hatching neonates were offered fresh *Poa* cuttings. These were monitored and the food plant was refreshed daily. The tissue paper lining in the bottom of the containers was changed twice a week and the frass and other debris removed. Every couple of days they were lightly sprayed with fresh water to maintain humidity within the containers.

Other caterpillars were carefully placed onto live food plants with a dampened brush. Both the caterpillars in containers and those on live food plants were stored at ambient room temperature within the laboratory under prevailing diurnal cycles.
First instar larvae were described and photographed from laboratory hatched specimens. Mature descriptions are based on field collected caterpillars and previously published works.

2.5 *Glossary of terms used to describe eggs*

Term	Definition
Aeropyle	Opening connecting outer surface of chorion with inner respiratory plastron
Anterior pole	End of egg on which the micropylar areas is located
Batch	Group of eggs laid in one session of oviposition activity. This generally occurs in short bursts of activity as the female moves from one location to the next. For the purposes of this study, a batch is defined as the number of eggs laid in a 24 hour period.
Cell	Termed areolae by Downey and Allyn (1981). This characteristic hexagonal patination on the surface of eggs most likely results from the dense crowding of inner epithelian cells in the ovarian follicles (García-Barros & Martin 1995). Cells are usually but not always defined by cell walls and Aeropyles at the wall junctions.
Cell Wall	Linear boundaries that define the outline of the cells.
Chorion	Outer shell or covering of egg, produced by follicle cells
Loose	Eggs that are not attached to the substrate
Loosely	Easily detached from substrate
Attached	Securely glued to substrate
Micropylar Area	Area including the external openings of the Micropylar Areas, the rosette of cells immediately surrounding the Micropylar Areas and several rows of cells extending concentrically outwards. The cells in these rows are usually well defined, have no Aeropyles at their junctions and frequently have reticulated walls
Micropylar Areas	Funnel-shaped canal through which spermatozoa enter the egg
Plastron	Respiratory layers of air below the outer surface of the chorion which consist of gas-filled spaces in the inner chorion and also numerous, very thin, gas-filled layers between the endochorion and the exochorion.
Posterior pole	End of egg opposite anterior pole.
Realised Fecundity	Total number of eggs laid by one female.
Reticulation	The elevation of cell walls. A reticulated wall is one with well-defined and elevated cell walls.
Ribs	Elevated, linear extensions along the margins between columns of cells.
Rosette	Inner ring of cells surrounding the micropylar areas that forms a characteristic flower-shaped arrangement of tear-shaped cells.

Table 3.1 Glossary of terms used to describe eggs

(Downey & Allyn 1981; Hinton 1981; Salkeld 1983; Downey & Allyn 1984; Stehr *et al.* 1987; Torre-Bueno 1989; Garcia-Barros & Martin 1995; Scoble 1995; Young 2006a).

3 RESULTS

3.1 *Egg Descriptions*

Terminology used to describe features of the egg is detailed in Table 3.1; definitions are drawn from Downey & Allyn (1981; 1984), Garcia-Barros & Martin (1995), Hinton (1981), Salkeld (1983), Scoble (1995), Stehr *et al.* (1987), Torre-Bueno (1989), and Young (2006a).

3.1.1 Oreixenica

Oreixenica eggs are globular, spherical to sub-barrel, marked on anterior pole by hexagonal, slightly convex cells with narrow, elevated walls. Lateral sides marked by convex hexagonal cells arranged in longitudinal rows outlined by slightly elevated aeropyles with moderately small openings, situated at cell junctions. Chorion is smooth, inset with leaf shaped forms.

3.1.1.1 O. ptunarra

Micropylar area: distinct, number of openings: obscured. Cells in rosette = 13, rows of cells in micropylar area = 10.

Shape: Globular upright eggs, with longitudinal axis perpendicular to substrate (Figure 3.2a), posterior pole flattened, anterior pole circular, apex slightly pointed (Figure 3.2b) centred by a circular micropylar area (Figure 3.2b,c).

Characteristics: Egg marked on anterior pole by hexagonal, slightly convex cells, with narrow elevated walls (Figure 3.2c). Anterior pole circular, centred by circular micropylar area (Figure 3.2b,c). Lateral sides marked by convex hexagonal cells, arranged in longitudinal rows outlined by areopyles only at cell junction (Figure 3.2e,f). Lateral cell walls not discernible (Figure 3.2f). Broad, rounded, elevated, longitudinal ribs run from anterior pole to two-thirds way down side of egg to widest point (Figure 3.2a-f). Aeropyles located in valleys between ribs on lateral sides, slightly elevated, opening moderately small (Figure 3.2d,f). Chorion, smooth, gently undulating with numerous regularly spaced, inset, leaf shaped forms, sparse short narrow slight elevated ridges in rib area only (Figure 3.2f). Chorion on anterior pole rough (Figure 3.2c,d).

Eggs are laid singly, firmly attached to substrate by posterior pole. Newly laid eggs grass green in colour (Figure 3.8) translucent on maturity (Figure 3.9) (Couchman 1953, 1954, 1956; Common & Waterhouse 1981; McQuillan & Ek 1997; Braby 2000; Anderson 2001b; Anderson & McQuillan 2003; New & Sands 2003).

Oviposition: mean total eggs laid by one female = 26 ± 5.0 (SE) (n=25);
Mean batch size = 4.16 ± 0.5 (SE) (n=25); batch range = 0-9.
Mean egg size (μm) length = 739.8 ± 8.3 (SE) (n=85); width = 733.8 ± 8.1 (SE) (n=85); height = 737.7 ± 8.23 (SE) (n=85);
Incubation period = 23 ± 3 days (n=25).

Figure 3.1 *Oriexenica ptunarra*, mating pair.

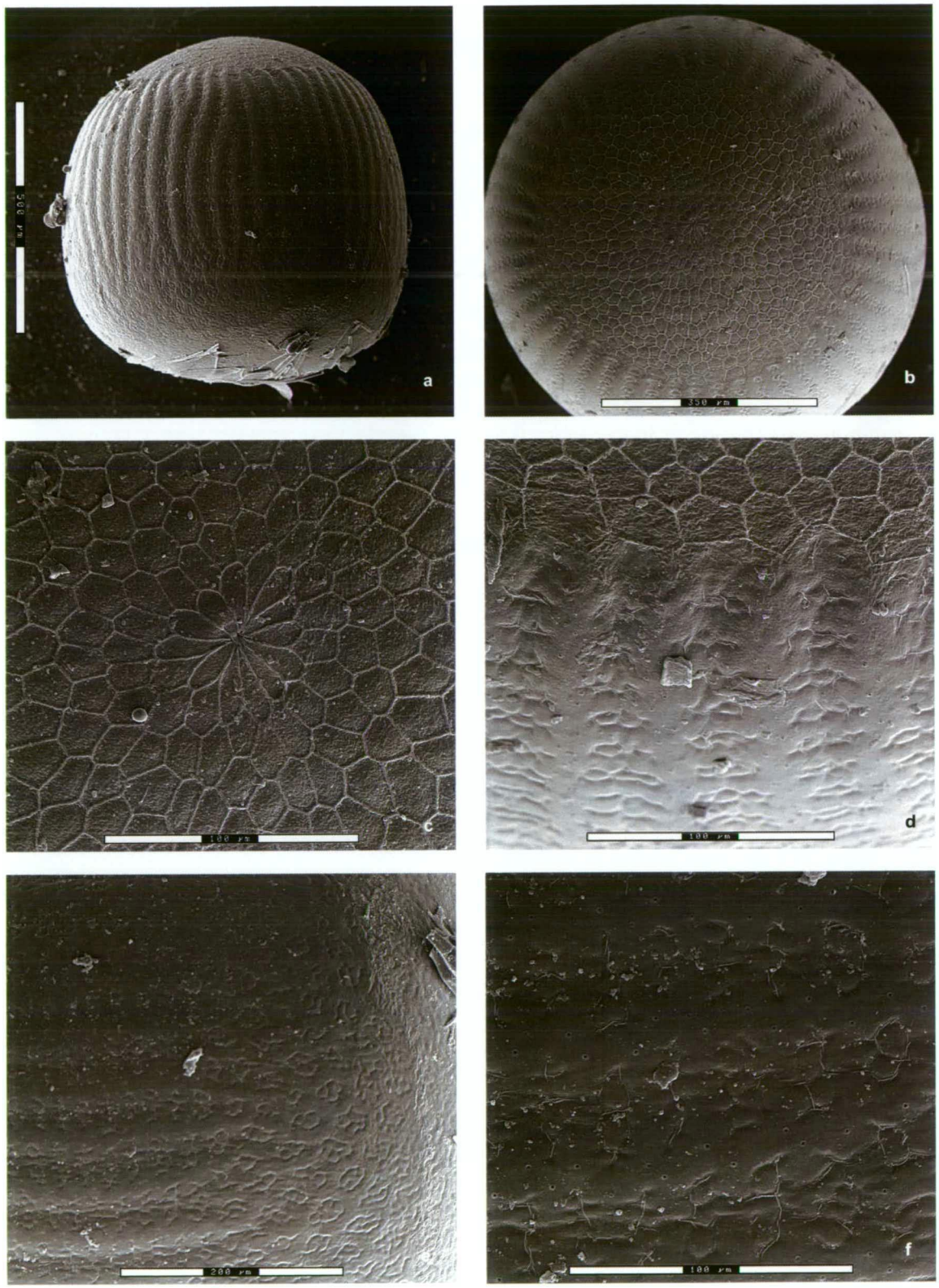


Figure 3.2 *O. ptunarra*, SEM egg

(a) lateral view of whole egg, scale bar 500 µm; (b) anterior pole, scale bar 350 µm; (c) micropylar area, scale bar 100 µm; (d) junction of lateral side with anterior pole, scale bar 100 µm; (e) posterior end of lateral side, scale bar 200 µm; (f) chorion of middle of lateral side, scale bar 100 µm.

3.1.1.2 O. latialis

Micropylar area: Distinct, number of openings: obscured. Cells in rosette = 9, rows of cells in micropylar area = 16.

Shape: Spherical, upright, with longitudinal axis perpendicular to substrate (Figure 3.3a), anterior pole circular, convex (Figure 3.3b), centred by circular micropylar area (Figure 3.3c).

Characteristics: Egg marked on anterior pole by hexagonal, slightly convex cells, with narrow elevated walls (Figure 3.3a-c). Anterior pole circular, centred by circular micropylar area (Figure 3.3b,c). Lateral sides marked by convex hexagonal cells, arranged in longitudinal rows (Figure 3.3e,f) cells outlined by areopyles (Figure 3.3d-f). Broad, rounded, elevated, longitudinal ribs run from anterior pole to the posterior pole (Figure 3.3a,f). Aeropyles slightly elevated, opening moderately small, located in valleys of ribs on lateral side. Chorion, smooth, sparse short narrow slight elevated ridges in rib area only (Figure 3.3e,f). Chorion on anterior pole rough (Figure 3.3c).

Eggs are laid singly whilst female is settled, dropped amongst tussock grass, and attached to substrate by posterior pole. Newly laid eggs are grass green in colour (Figure 3.10) and become translucent on maturity (Figure 3.11) (Waterhouse 1923; 1928; 1932; McCubbin 1971; Kitching *et al.* 1978; Common & Waterhouse 1981; Crosby 1998; Braby 2000).

Oviposition: mean total eggs laid by one female = 18 ± 0.5 (SE) (n=3);
Mean batch size = 2 ± 0.5 (SE) (n=3); batch range = 0 - 4.
Mean egg size (μm) length = 720 ± 10.0 (SE) (n=10); width = 716.5 ± 10.5 (SE) (n=10); height = 499.3 ± 10.5 (SE) (n=10);
Incubation period = 21 ± 3 days (n=3).

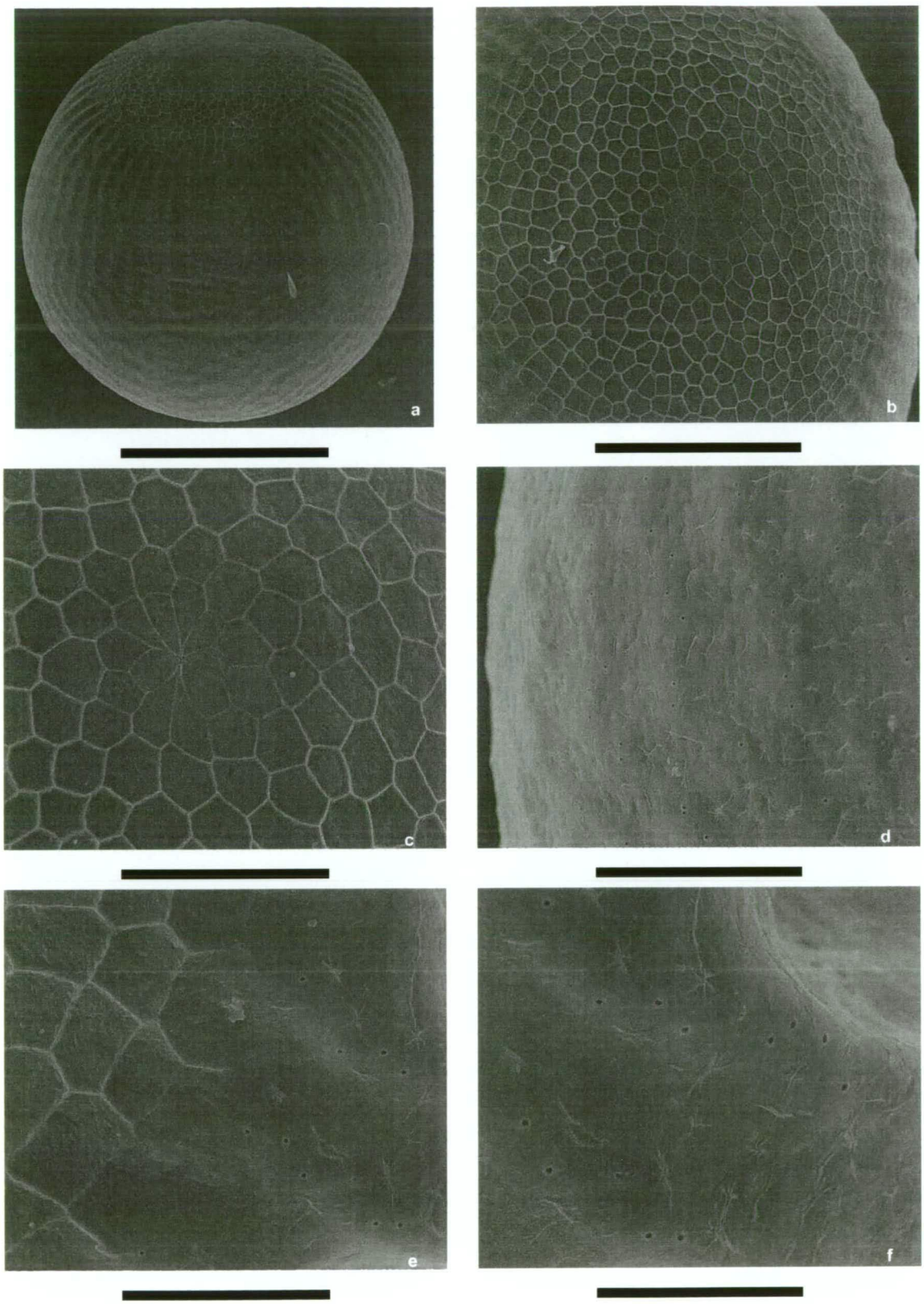


Figure 3.3 *O. latialis*, SEM egg

(a) lateral view of whole egg, scale bar 500 μm; (b) anterior pole, scale bar 350 μm; (c) micropylar area, scale bar 100 μm; (d) posterior pole, scale bar 150 μm; (e) chorion at junction of anterior pole and lateral side, scale bar 100 μm; (f) chorion of lateral side towards posterior pole, scale bar 200 μm.

3.1.1.3 O. lathoniella

Micropylar area: distinct, number of openings = 4, cells in rosette = 9 rows of cells in micropylar area = 18.

Shape: Sub-barrel (hemi-elliptical), upright, with longitudinal axis perpendicular to substrate (Figure 3.4a), anterior pole circular, shallowly convex (Figure 3.4a,b), centred by circular micropylar area (Figure 3.4b,c).

Characteristics: Egg marked on anterior pole by hexagonal, slightly convex cells, with narrow elevated walls (Figure 3.4c). Anterior pole circular, centred by circular micropylar area (Figure 3.4b,c). Lateral sides marked by concave hexagonal cells, arranged in longitudinal rows (Figure 3.4a-f) cells outlined by areopyles (Figure 3.4d). Broad, rounded, elevated, longitudinal ribs run from anterior pole to widest point (Figure 3.4d-f). Aeropyles slightly elevated, opening moderately small, located in valleys of ribs on lateral side (Figure 3.4d), not visible on anterior or posterior poles. Chorion divided into two regions; upper ribbed area smooth, gently undulating with numerous regularly spaced, inset, leaf shaped forms (Figure 3.4f), and lower smooth, non-ribbed area.

Eggs are generally laid singly, firmly attached to substrate by posterior pole. Newly laid eggs yellowish green in colour (Figure 3.12) translucent on maturity (Figure 3.12 & Figure 3.13). Emerging larva cut circular area around anterior pole (Figure 3.14) (Waterhouse 1923; 1932; Crosby 1965; McCubbin 1971; Couchman & Couchman 1978; Common & Waterhouse 1981; Braby 2000).

Oviposition: mean total eggs laid by one female = 23 ± 4.3 (SE) (n=15);
Mean batch size = 3.87 ± 0.7 (SE) (n=15); batch range = 1-10.
Mean egg size (μm) length = 730.0 ± 8.0 (SE) (n=13); width = 757.7 ± 8.2 (SE) (n=13); height = 761.5 ± 7.8 (SE) (n=13);
Incubation period = 17 ± 2 days (n=15).

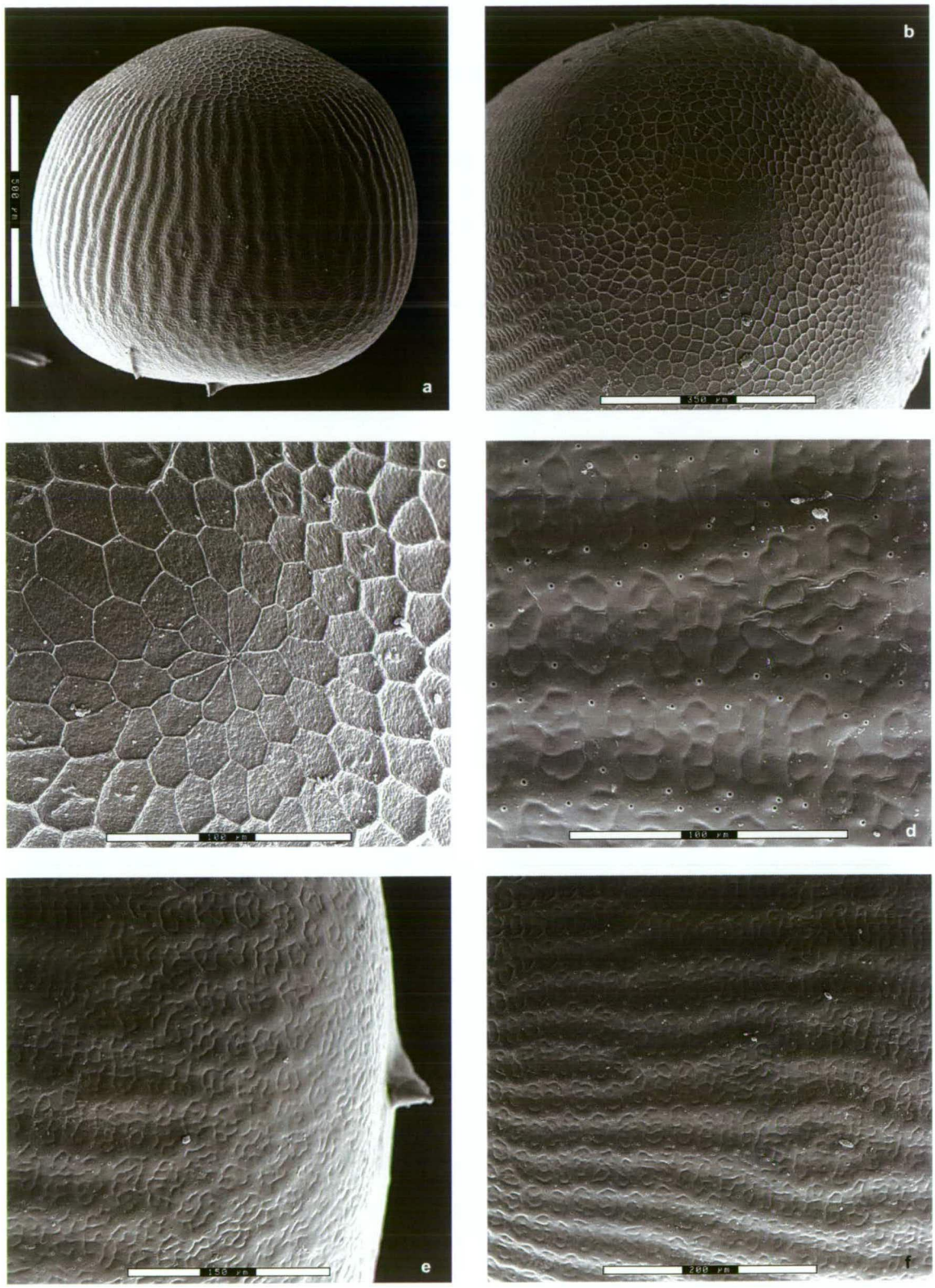


Figure 3.4 *O. lathoniella*, SEM egg

(a) lateral view of whole egg, scale bar 500 µm; (b) anterior pole, scale bar 350 µm; (c) micropylar area, scale bar 100 µm; (d) chorion towards posterior end, scale bar 150 µm; (e) chorion detailing aeropyles towards posterior pole, scale bar 100 µm; (f) chorion of middle of lateral side, scale bar 200 µm.

3.1.1.4 O. orichora paludosa

Micropylar area: distinct, number of openings = 5, cells in rosette = 9, rows of cells in micropylar area = 11.

Shape: Sub-barrel (hemi-elliptical), upright, with longitudinal axis perpendicular to substrate (Figure 3.5a). Anterior pole circular, shallowly convex (Figure 3.5b), centred by circular micropylar area (Figure 3.5c);

Characteristics: Egg marked on anterior pole by hexagonal, slightly convex cells, with narrow elevated walls (Figure 3.5b). Anterior pole circular, centred by circular micropylar area (Figure 3.5b,c). Lateral sides marked by concave hexagonal cells, arranged in longitudinal rows, cells outlined by areopyles and multiple pores (Figure 3.5d,e), cell form not as obvious near posterior pole (Figure 3.5f). Broad, rounded, slightly elevated, longitudinal ribs run from anterior pole to half way down lateral side of egg to widest point (Figure 3.5a,d). Aeropyles slightly elevated with multiple pores (Figure 3.5e). Chorion shallowly undulating, with numerous regularly spaced, inset leaf shaped forms.

Eggs are generally dropped amongst grass tussocks by females whilst in flight but do not adhere to substrate. They are straw yellow in colour (Figure 3.15) and become translucent on maturity (Waterhouse 1923; 1932; Kitching *et al.* 1978; Common & Waterhouse 1981; Braby 2000).

Oviposition: mean total eggs laid by one female = 18.5 ± 4.14 (SE) (n=11);
Mean batch size = 4.38 ± 0.5 (SE) (n=11); batch range = 0-9.
Mean egg size (μm) length = 737.5 ± 3.5 (SE) (n=14); width = 739.3 ± 3.4 (SE) (n=14); height = 742.9 ± 3.1 (SE) (n=14);
Incubation period = 16 ± 3 days (n=11).

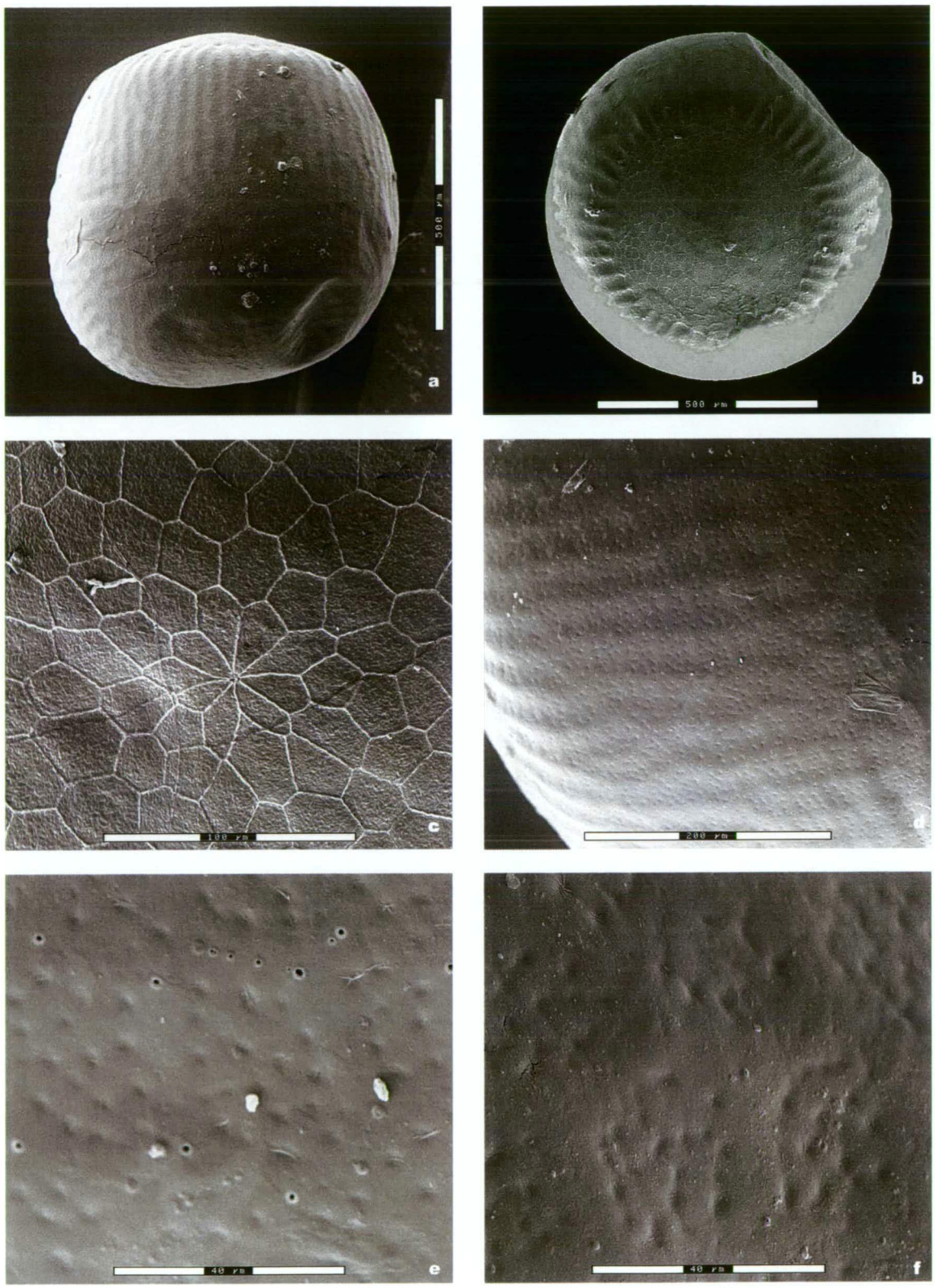


Figure 3.5 *O. orichora*, SEM egg

(a) lateral view of whole egg, scale bar 500 µm; (b) anterior pole, scale bar 500 µm; (c) micropylar area, scale bar 100 µm; (d) chorion towards anterior pole, scale bar 200 µm; (e) chorion detailing aeropyles note multiple pores, scale bar 40 µm; (f) chorion near posterior pole, scale bar 40 µm.

3.1.1.5 O. correae

Micropylar area: distinct, number of openings: obscured, cells in rosette 8, rows of cells in micropylar area: 14.

Shape: Sub-barrel (hemi-elliptical), upright, with longitudinal axis perpendicular to the substrate (Figure 3.6a), posterior pole flattened, anterior pole circular, apex slightly pointed (Figure 3.6a,b), centred by a circular micropylar area (Figure 3.6b,c).

Characteristics: Egg marked on anterior pole by hexagonal, slightly convex cells, with narrow elevated walls (Figure 3.6b). Anterior pole circular, centred by circular micropylar area (Figure 3.6b,c). Lateral sides marked by concave hexagonal cells, arranged in longitudinal rows (Figure 3.6b a,d-f) cells outlined by areopyles. Broad, rounded, elevated, longitudinal ribs run from anterior pole to posterior pole (Figure 3.6d,e). Aeropyles slightly raised, opening moderately small, located in valleys of ribs on lateral side (Figure 3.6e,f), not visible on anterior or posterior poles. Chorion smooth with regularly spaced, inset, leaf shaped forms (Figure 3.6e).

Newly laid eggs are pale green (Figure 3.16) (Waterhouse 1923; 1932; McCubbin 1971; Quick 1971; Kitching *et al.* 1978; Common & Waterhouse 1981; Braby 2000) becoming translucent on maturity.

Incubation period = 10-14 days (Quick 1971)
Incubation period = 12-22 days (McCubbin 1971)

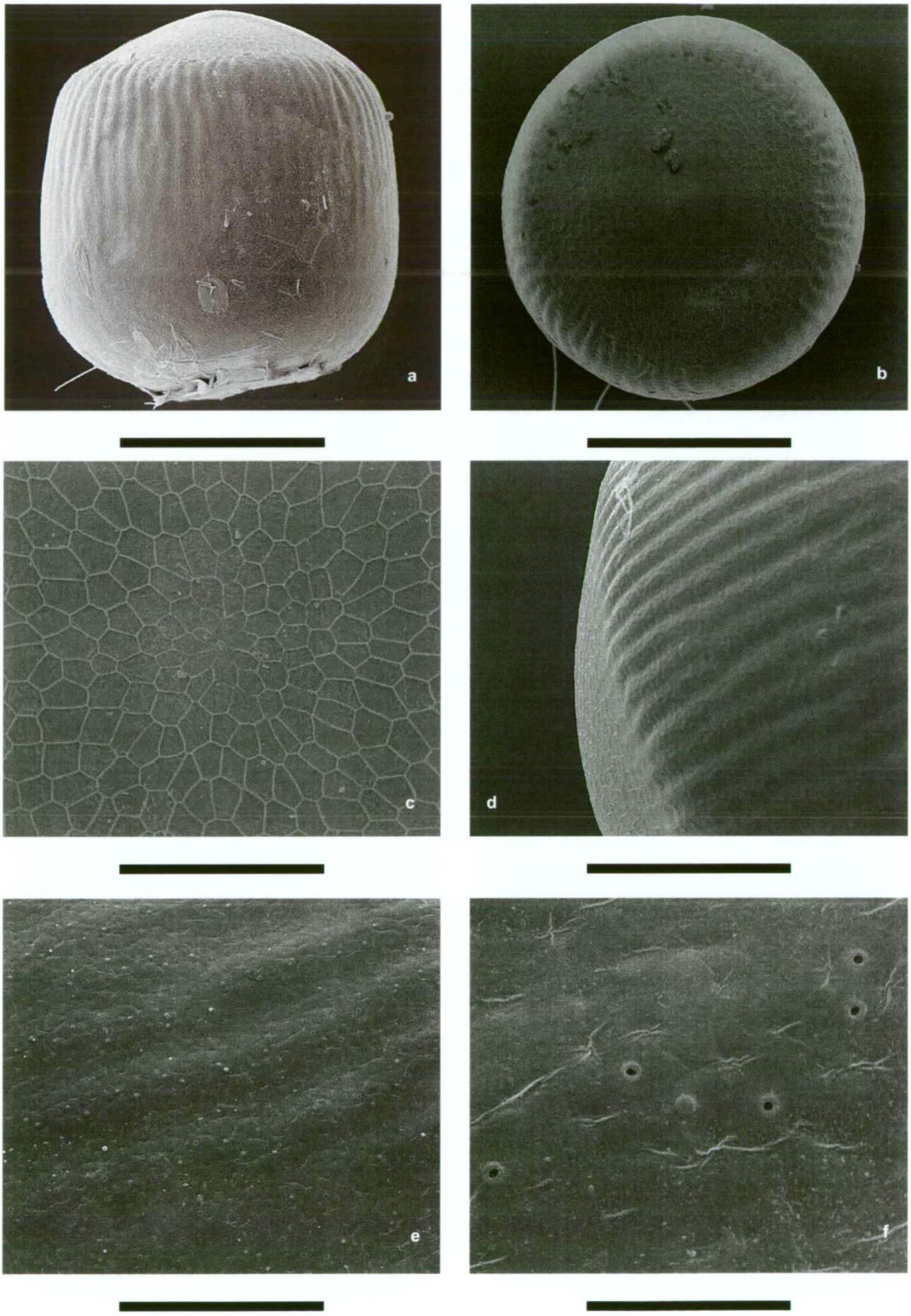


Figure 3.6 *O. correae*, SEM egg

(a) lateral view of whole egg, scale bar 500μm; (b) anterior pole, scale bar 500μm; (c) micropylar area, scale bar 100μm; (d) chorion towards anterior pole, scale bar 200μm; (e) chorion on lateral side scale bar 40μm; (f) chorion on lateral side detailing aeropyles, scale bar 40μm

3.1.1.6 O. kershawi

Micropylar area: distinct, number of openings: obscured, cells in rosette = 9, rows of cells in micropylar area = 13.

Shape: Sub-barrel (hemi-elliptical), upright, with longitudinal axis perpendicular to the substrate (Figure 3.7a), posterior and anterior poles convex (Figure 3.7b).

Characteristics: Egg marked on anterior pole by hexagonal, slightly convex cells with narrow elevated walls (Figure 3.7d). Anterior pole circular, centred by circular micropylar area (Figure 3.7d). Lateral sides marked by concave hexagonal cells, arranged in longitudinal rows (Figure 3.7c) cells outlined by areopyles. Broad, rounded, elevated, longitudinal ribs run from anterior pole to posterior pole (Figure 3.7c,e). Aeropyles slightly raised, opening moderately small, located in valleys of ribs on lateral side, not visible on anterior or posterior poles. Chorion smooth with regularly spaced, inset, leaf shaped forms (Figure 3.7c).

Eggs are laid singly, firmly attached to substrate. Newly laid eggs are pale green in colour, and become translucent on maturity (Figure 3.17) (Waterhouse 1923; 1932; Kitching *et al.* 1978; Common & Waterhouse 1981; Braby 2000).

Oviposition: mean total eggs laid by one female = 31 ± 7.0 (SE) (n=4);
Mean batch size = 5.0 ± 0.68 (SE) (n=4); batch range = 3-7.
Mean egg size (μm) length = 764 ± 3.1 (SE) (n=17); width = 747 ± 3.6 (SE) (n=17)
height = 750 ± 4.3 (SE) (n=17);
Incubation period = 15 ± 3 days (n=4).

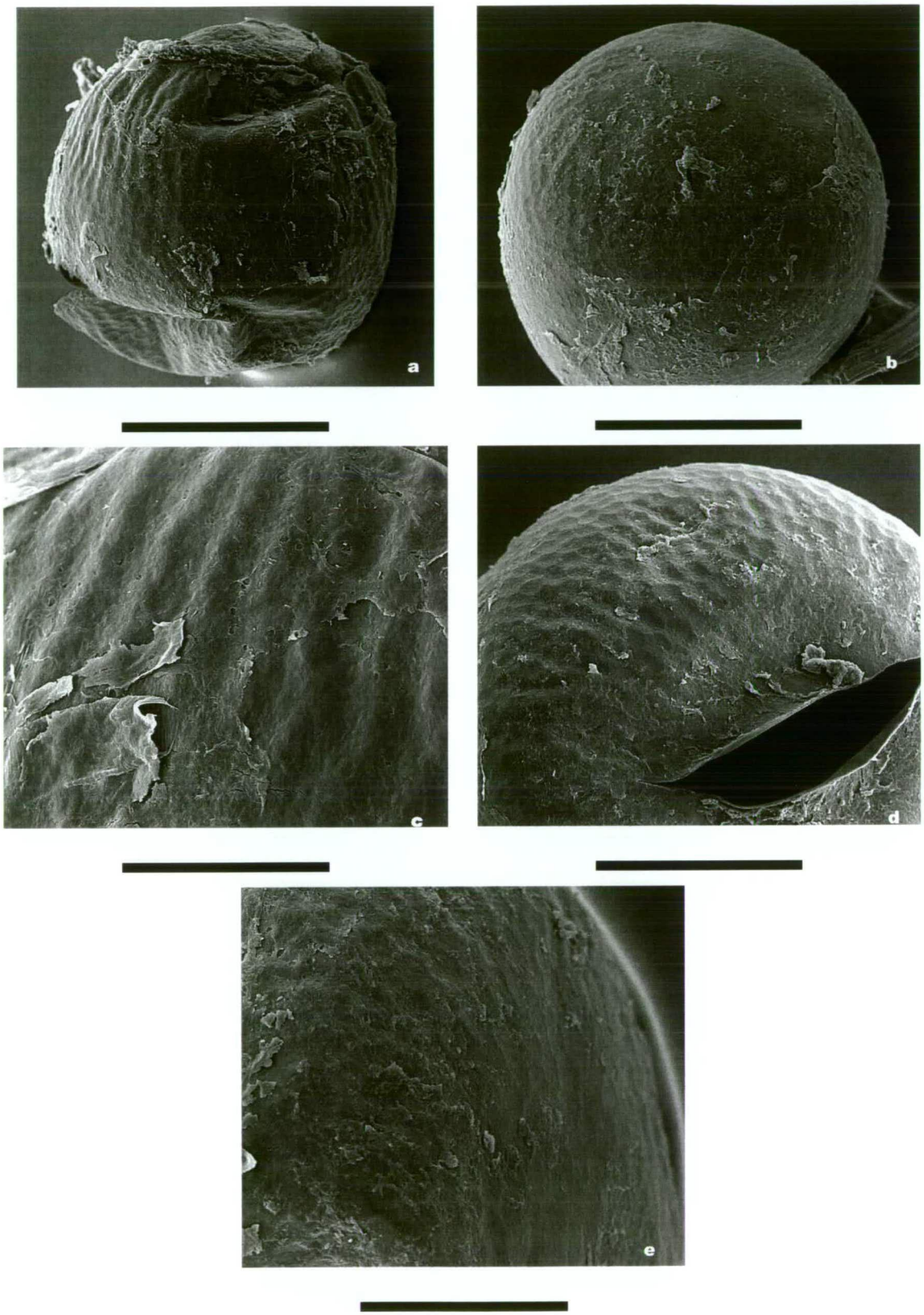


Figure 3.7 *O. kershawi*, SEM egg

(a) lateral view of whole egg, scale bar 500 μm; (b) posterior pole, scale bar 500 μm; (c) chorion towards anterior pole, scale bar 50 μm; (d) anterior pole 300μm; (e) chorion near posterior pole, scale bar 100 μm.

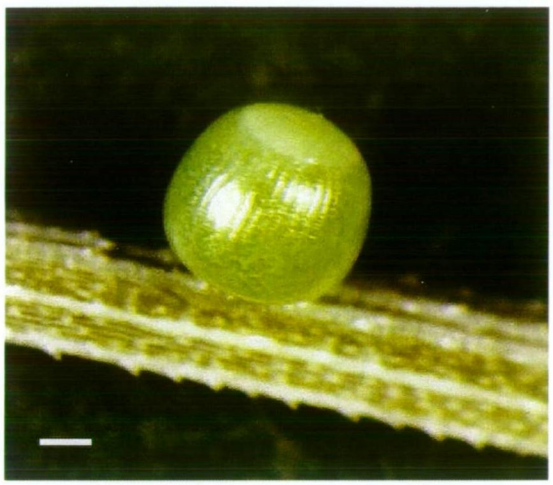


Figure 3.8 *O. ptunarra*, newly laid egg on a blade of *Poa* tussock grass. Scale bar 0.5 mm.

Figure 3.9 *O. ptunarra*, mature eggs on a blade of *Poa* tussock grass. Scale bar 0.5mm.

Figure 3.10 *O. latialis*, newly laid egg on a blade of *Poa* tussock grass. Scale bar 0.5 mm.

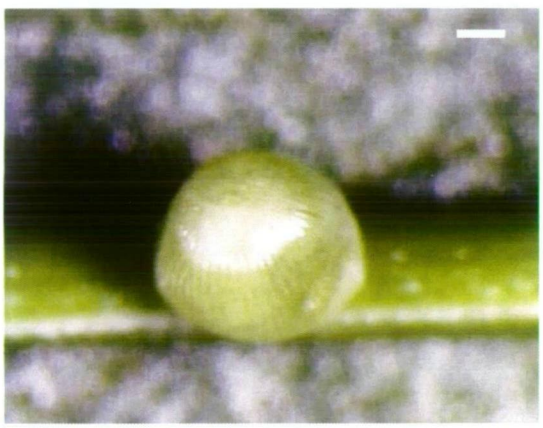


Figure 3.11 *O. latialis*, maturing eggs on a blade of *Poa* tussock grass. Scale bar 0.5mm.

Figure 3.12 *O. lathoniella*, eggs mature eggs left, fresh eggs centre, right. Scale bar 0.5mm

Figure 3.13 *O. lathoniella*, mature eggs on a blade of *Poa* tussock grass. Scale bar 0.5mm

Figure 3.14 *O. lathoniella*, eggs hatching
Scale bar 0.5mm

Figure 3.15 *O. orichora*, newly laid egg
on a blade of *Poa* tussock grass. Scale bar 0.5 mm.

Figure 3.16 *O. correae*, semi-mature egg
on a blade of *Poa* tussock grass. Scale bar 0.5 mm
(Field 2002).

Figure 3.17 *O. kershawi*, semi-mature eggs
on a blade of *Poa* tussock grass. Scale bar 0.5 mm
(Viridans 2006).

3.1.2 Nesoxenica leprea

Micropylar area: distinct, number of openings: 6, cells in rosette 8, rows of cells in micropylar area: 12.

Shape: Sub-quadrate, upright, with longitudinal axis perpendicular to substrate (Figure 3.18a), posterior and anterior poles convex (Figure 3.18b).

Characteristics: Egg marked on anterior pole by hexagonal, slightly convex cells with narrow, elevated, clearly defined walls (Figure 3.18b), anterior pole circular (Figure 3.18b,c), centred by circular micropylar area, rosette cells slightly raised (Figure 3.18c). Lateral sides by hexagonal flat cells with narrow, slightly elevated walls, cells outlined by areopyles (Figure 3.18c-f). Broad, rounded, elevated, longitudinal ribs run from anterior pole to posterior pole (Figure 3.18d). Aeropyles slightly elevated, with small openings, clearly present on top of ribs (Figure 3.18e) aeropyles are not present on anterior pole (Figure 3.18f). Chorion smooth with regularly spaced, inset, leaf shaped forms (Figure 3.18d)

Eggs are generally laid singly, firmly attached to substrate by posterior pole. Newly laid eggs are pale grass green in colour (Figure 3.20). Eggs are elongated along longitudinal axis (Waterhouse 1932; Couchman & Couchman 1978; Common & Waterhouse 1981; Prince 1988; Braby 2000).

Oviposition: mean total eggs laid by one female = 22 ± 4.0 (SE) (n=4);
Mean batch size = 20 ± 0.2 (SE) (n=4); batch range = 0-32.
Mean egg size (μm) length = 1025 ± 15 (SE) (n=10); width = 796.5 ± 10.5 (SE) (n=10); height = 840.2 ± 20.5 (SE) (n=10);
Incubation period = 14 ± 3 days (n=4).

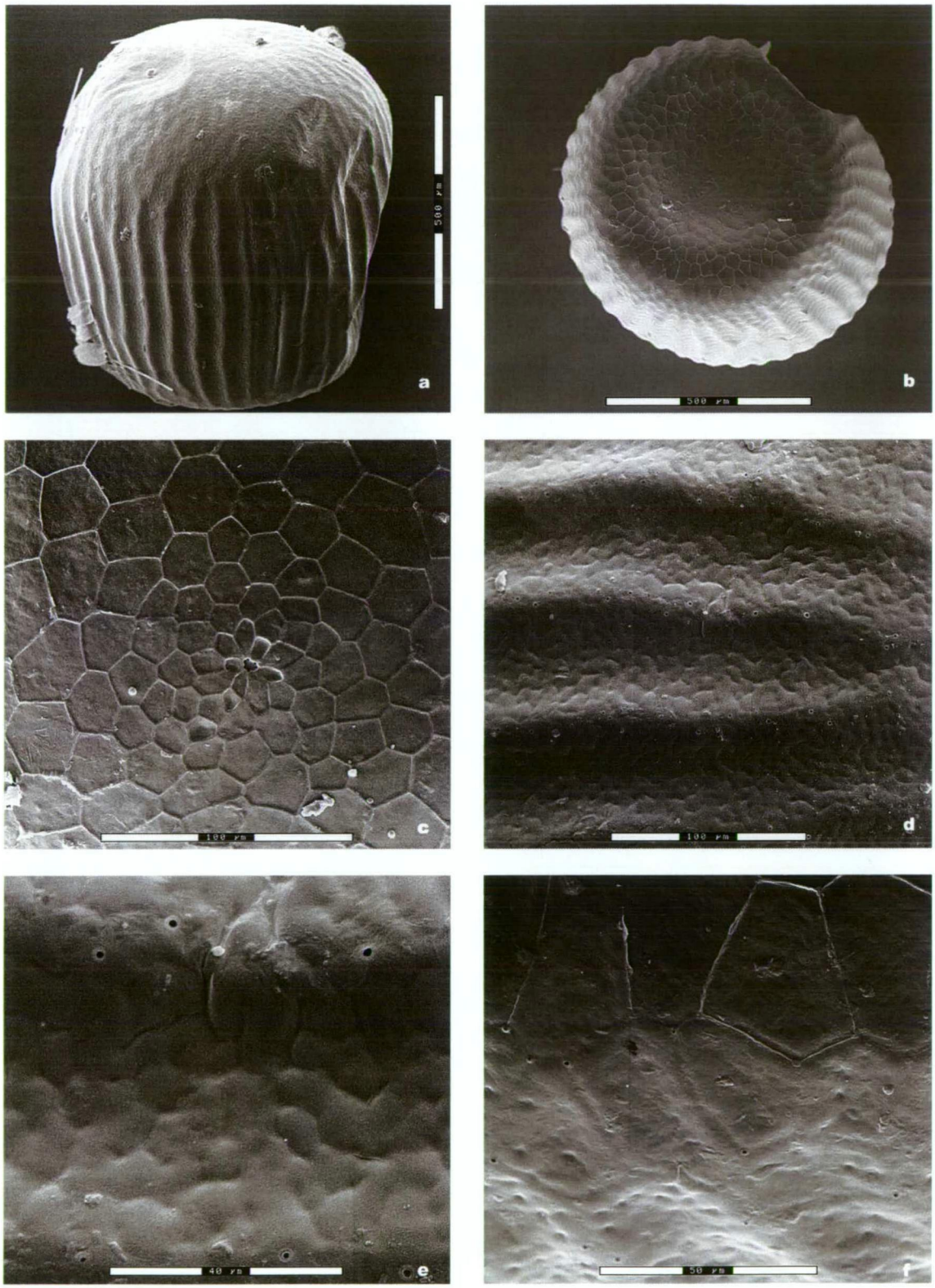


Figure 3.18 *N. leprea*, SEM egg

(a) lateral view of whole egg, scale bar 500 µm; (b) anterior pole, scale bar 500 µm; (c) micropylar area, scale bar 100 µm; (d)chorion middle of lateral side, scale bar 100 µm; (e) aeropyles along ribs, scale bar 40 µm; (f) chorion at the rim of anterior pole, note aeropyles not present on anterior pole scale bar 50 µm.

3.1.3 Argynnina hobartia

Micropylar area: distinct, number of openings = 5, cells in rosette = 12, rows of cells in micropylar area = 18.

Shape: Sub-hemi-spherical eggs, upright, with the longitudinal axis perpendicular to the substrate (Figure 3.19a,b), posterior and anterior poles convex (Figure 3.19a-c).

Characteristics: Egg marked on anterior pole by hexagonal, slightly convex cells with slightly elevated walls (Figure 3.19b,c). Anterior pole is circular, convex (Figure 3.19b,c), centred by circular micropylar area (Figure 3.19c-e). Lateral sides marked by concave, sub-quadrat cells, arranged in longitudinal rows cells outlined by areopyles (Figure 3.7f-i). Broad, rounded, shallow ribs run from anterior pole to posterior pole. Secondary ribs run perpendicular to main ribs, especially around centre of eggs (Figure 3.19f,g). Aeropyles slightly elevated, more conspicuous on ribs (Figure 3.19j), situated on elevated ridges of cell walls (Figure 3.19f,h,i). Chorion smooth.

Eggs are laid singly, firmly attached to substrate. Newly laid eggs are greenish yellow in colour (Figure 3.21).and become translucent on maturity (Figure 3.22 & Figure 3.23). (Waterhouse 1932; Couchman & Couchman 1978; Common & Waterhouse 1981; Prince 1988; Braby 2000).

Oviposition: mean total eggs laid by one female = 22 ± 4.0 (SE) (n=4);
Mean batch size = 67 ± 23.0 (SE) (n=4); batch range = 13-32.
Mean egg size (μm) length = 945 ± 5.0 (SE) (n=10); width = 906 ± 5.5 (SE) (n=10);
height = 903 ± 4.5 (SE) (n=10);
Incubation period = 16 ± 3 days (n=4).

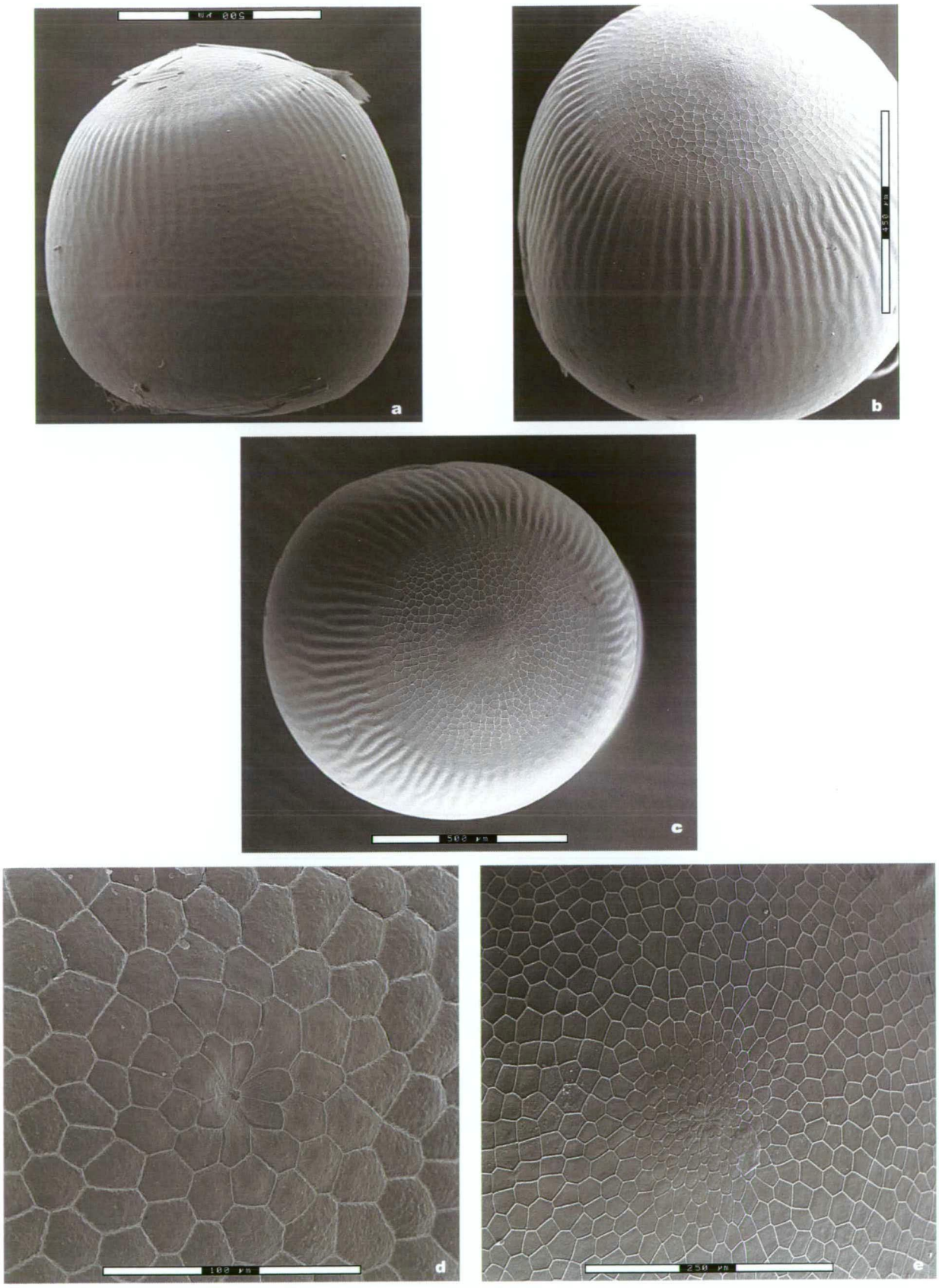


Figure 3.19 *Argynnina hobartia*, SEM egg

(a) lateral view of whole egg, scale bar 500 µm; (b) lateral view of whole egg, scale bar 450 µm; (c) anterior pole, scale bar 500 µm; (d) micropylar area, scale bar 100 µm; (e) micropylar area, scale bar 250 µm;

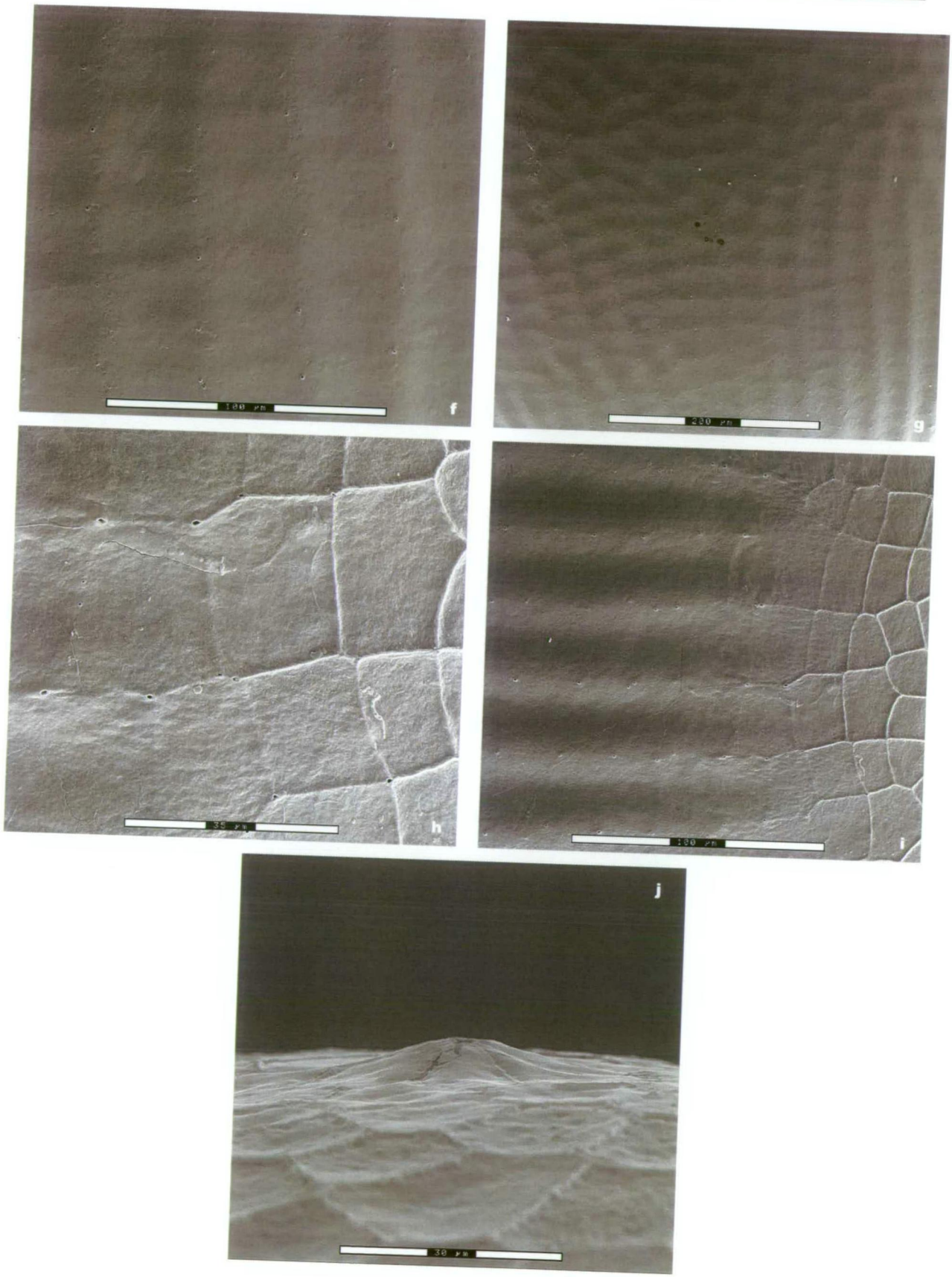


Figure 3.19 continued *Argynnina hobartia*, SEM egg

(f) chorion detailing sub-quadrat cell form, scale bar 100 µm; (g) chorion detailing ribs run from anterior pole to posterior pole note secondary ribs run perpendicular to the main ribs, scale bar 250 µm; (h) chorion near anterior pole, scale bar 35 µm; (i) chorion near anterior pole, scale bar 100 µm; (j) aeropyle lateral view, scale bar 30 µm.

Figure 3.20 *N. leprea*, fresh eggs.
Scale bar 0.5 mm.

Figure 3.21 *A. hobartia*, fresh eggs.
Scale bar 0.5 mm.

Figure 3.22 *A. hobartia*, maturing eggs.
Scale bar 0.5 mm.

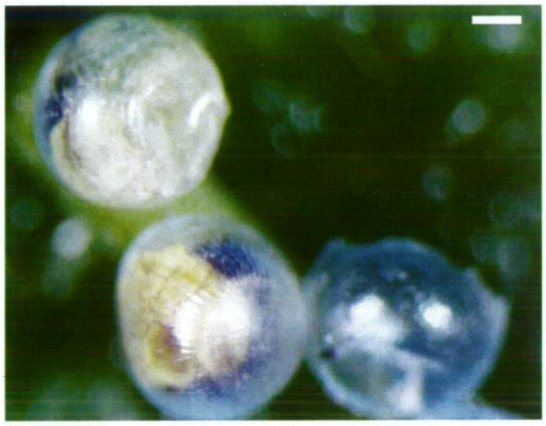


Figure 3.23 *A. hobartia*, mature eggs.
Scale bar 0.5 mm.

3.1.4 Heteronympha

Sub-hemispherical / dome to turbinate / sub-conical, upright, eggs. Markings on anterior pole vary between species. *Heteronympha* characterised by secondary sets of ribs running perpendicular to main ribs.

3.1.4.1 H. cordace

Micropylar area: distinct, number of openings: obscured, cells in rosette 7, rows of cells in micropylar area: 15.

Shape: Sub-hemispherical to dome shape, upright, longitudinal access perpendicular to substrate, flattened basally on posterior pole (Figure 3.24a) anterior pole convex forming a peak (Figure 3.24a,b).

Characteristics: Egg marked on anterior pole by flat cells with slightly elevated walls (Figure 3.24b). Anterior pole, circular, convex forming a peak (Figure 3.24b), centred by relatively small circular micropylar area (Figure 3.24c). Lateral sides marked by hexagonal cells, floors concave with aeropyles on elevated ribs (Figure 3.24d). Posterior pole cells hexagonal concave, cell wall not visible. Broad, rounded, shallow ribs run from anterior to half way to posterior pole (Figure 3.24e,f). Minor secondary ribs run perpendicular to main ribs especially around centre of egg. Aeropyles slightly elevated (Figure 3.24d,f), situated on elevated ridges of the cell walls between junction of the two sets of ribs (Figure 3.24f).

Eggs are usually laid singly, however they are occasionally in small batches of up to five eggs. Eggs are very loosely adhered to substrate. Newly laid eggs are straw green in colour (Figure 3.28) and become translucent on maturity (Figure 3.29) (Waterhouse 1932; Couchman & Couchman 1978; Common & Waterhouse 1981; Prince 1988; Braby 2000).

Oviposition: mean total eggs laid by one female = 28 ± 14.3 (SE) (n=4);
Mean batch size = 10 ± 1.3 (SE) (n=4); batch range = 7-13.
Mean egg size (μm) length = 935 ± 15 (SE) (n=10); width = 704.5 ± 12.5 (SE) (n=10); height = 840.5 ± 8.5 (SE) (n=10);
Incubation period = 12 ± 3 days (n=4).

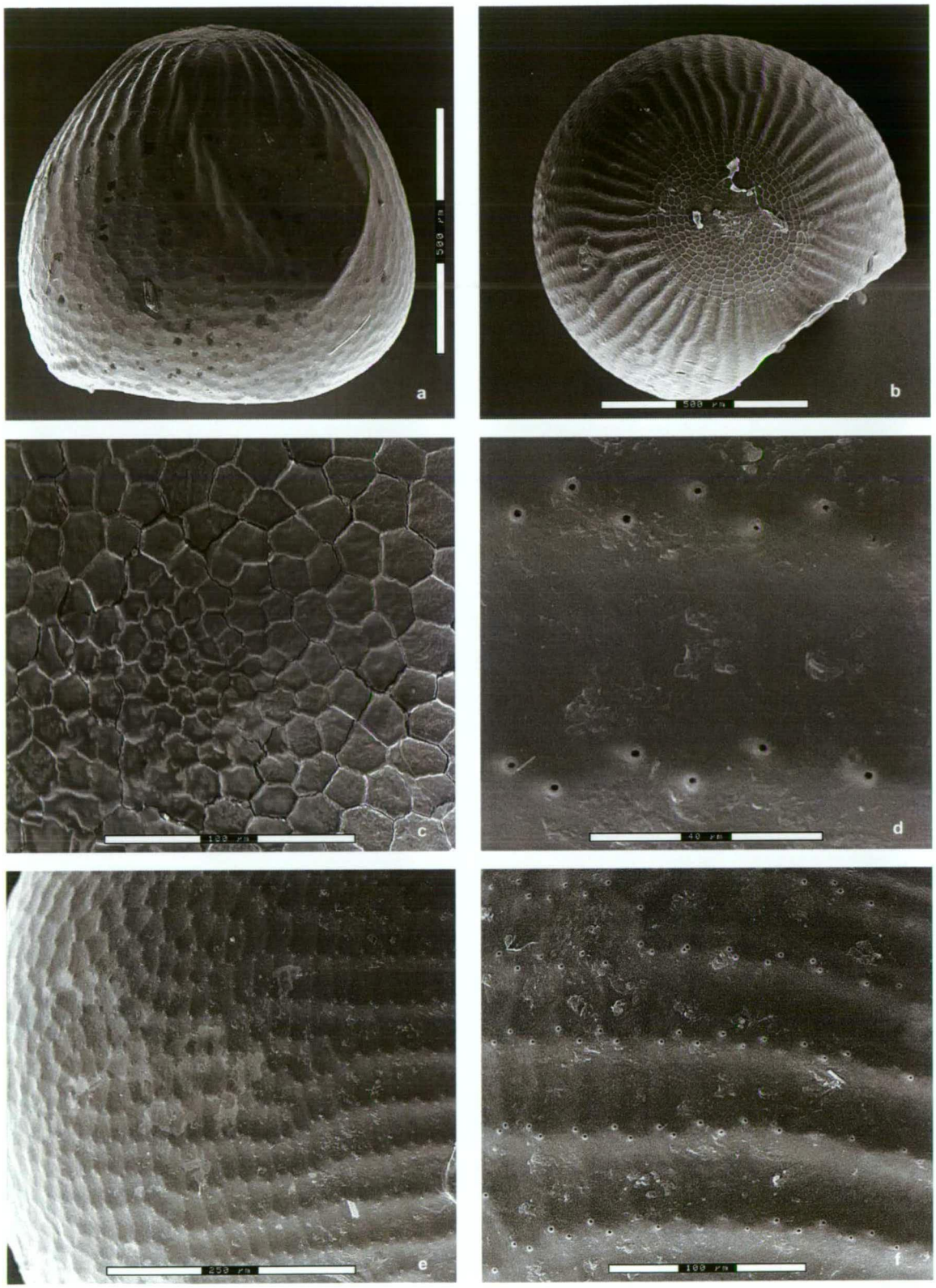


Figure 3.24 *H. cordace*, SEM egg

(a) lateral view of whole egg, scale bar 500 µm; (b) anterior pole, scale bar 500 µm; (c) micropylar area, scale bar 100 µm; (d) chorion towards anterior pole, scale bar 200 µm; (e) chorion lateral sde, scale bar 40 µm; (f) chorion near posterior pole, scale bar 40 µm

3.1.4.2 H. penelope

Micropylar area: distinct, number of openings: obscured, cells in rosette = 7, rows of cells in micropylar area = 6.

Shape: Turbinate to sub-conical (Figure 3.25a), upright, expanding basally, posterior pole flattened concave, anterior pole convex.

Characteristics: Egg marked on anterior pole by very fine indistinct dimpling, chorion nearly smooth (Figure 3.25b,d). Anterior pole is circular, convex, and centred by a circular micropylar area (Figure 3.25b). Lateral sides plain, smooth hexagonal cells, arranged in longitudinal rows (Figure 3.25e) cells outlined by areopyles (Figure 3.25f). Broad, rounded, shallow, ribs run from anterior pole to posterior pole. There is a secondary set of ribs that run perpendicular to main ribs especially around posterior end of eggs (Figure 3.25c). Aeropyles slightly raised, opening moderately small, situated on boundaries of cell walls on lateral side, not visible on anterior or posterior poles (Figure 3.25f). Chorion plain (Figure 3.25e).

Eggs are laid singly, dropped randomly amongst tussocks grass whilst female is perched on a stem of grass or low shrub. Newly laid eggs are pale yellowish white in colour, very loosely adhered to the substrate and become translucent on maturity (Waterhouse 1932; Couchman & Couchman 1978; Common & Waterhouse 1981; Prince 1988; Braby 2000) .

Oviposition: mean total eggs laid by one female = 88 ± 48.8 (SE) (n=3);
Mean batch size = 20 ± 9 (SE) (n=3); batch range = 2-30.
Mean egg size (μm) length = 1025 ± 6.4 (SE) (n=10); width = 984.5 ± 10.5 (SE) (n=10); height = 980.2 ± 20.5 (SE) (n=10);
Incubation period = 20 ± 7 days (n=3).

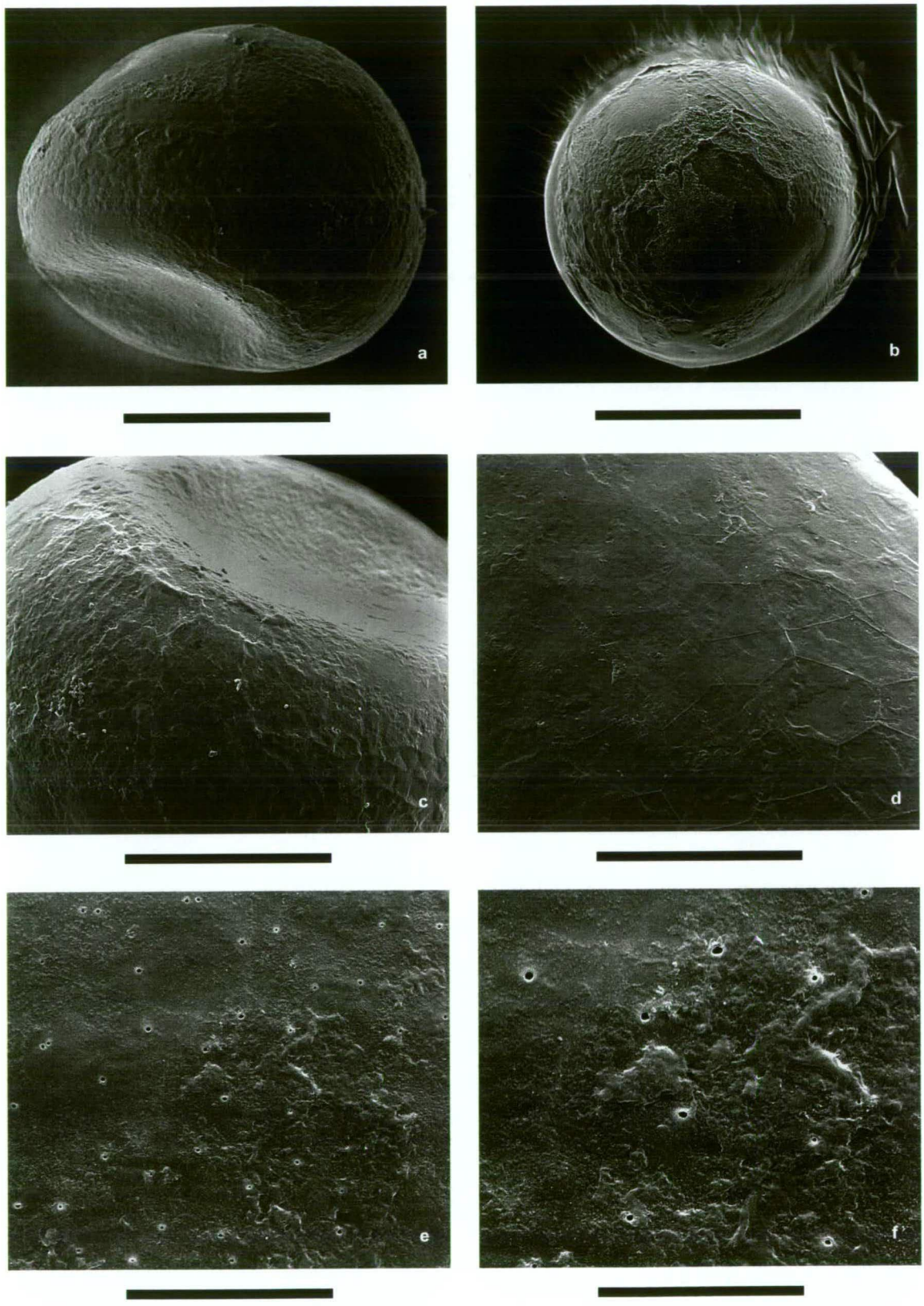


Figure 3.25 *H. penelope*, SEM egg

(a) lateral view of whole egg, scale bar 500 μm; (b) anterior pole, scale bar 500 μm; (c) posterior pole, scale bar 250 μm; (d) chorion towards anterior pole, scale bar 200 μm; (e) chorion lateral side, scale bar 100 μm; (f) chorion detailing aeropyles lateral side, scale bar 50 μm

3.1.4.3 H. merope salazar

Micropylar area: distinct, number of openings = 2, cells in rosette = 5, rows of cells in micropylar area = 6.

Shape: Turbinate to sub-conical, upright, expanding basally, base and apex are flattened (Figure 3.26a), posterior and anterior poles flattened.

Characteristics: Egg marked on anterior pole by hexagonal convex cells with narrow, elevated walls (Figure 3.26b), centred by a circular micropylar area (Figure 3.26c,d). Lateral sides marked by concave hexagonal cells, arranged in longitudinal rows creating indistinct vertical ridges running around the egg, cells outlined by areopyles. (Figure 3.26e). Broad, rounded, shallow ribs run from anterior pole to posterior pole. A secondary set of ribs run perpendicular to main ribs especially around centre of egg (Figure 3.26e). Aeropyles are raised, situated on elevated ridges of cell walls (Figure 3.26f). Chorion smooth with regularly spaced, shallowly inset, leaf shaped forms (Figure 3.26c).

Eggs are laid singly or in groups of up to 10 eggs, very loosely adhered to substrate. Newly laid eggs are cream in colour (Figure 3.30) and become translucent on maturity (Waterhouse 1932; Couchman & Couchman 1978; Common & Waterhouse 1981; Prince 1988; Braby 2000).

Oviposition: mean total eggs laid by one female = 131 ± 40 (SE) (n=2);
Mean batch size = 29 ± 1 (SE) (n=2); batch range = 28-30.
Mean egg size (μm) length = 925 ± 12.5 (SE) (n=10); width = 796.5 ± 10.5 (SE) (n=10); height = 905 ± 12.5 (SE) (n=10);
Incubation period = 23 ± 3 days (n=2).

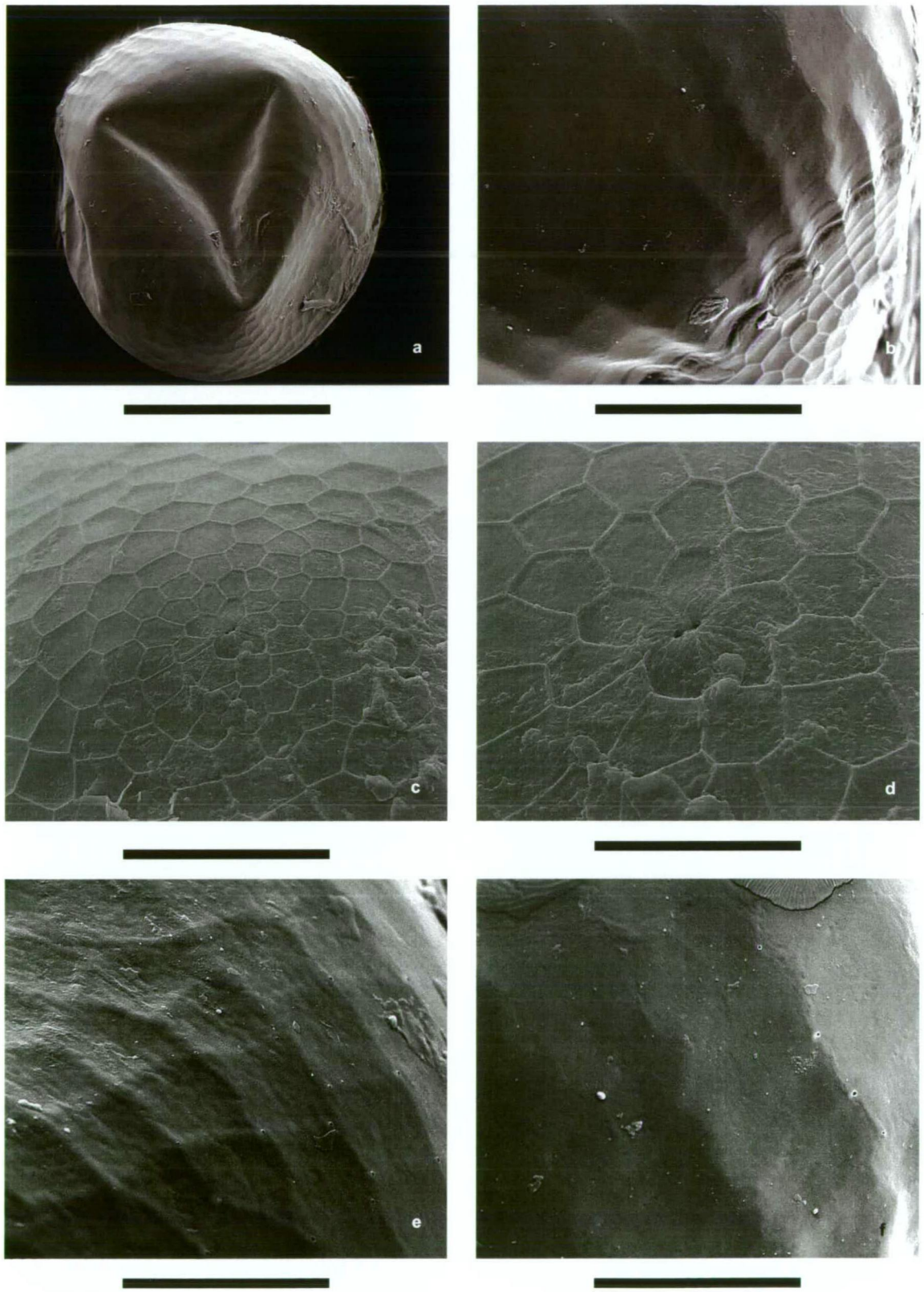


Figure 3.26 *H. merope*, SEM egg

(a) lateral view of whole egg, scale bar 500 μm; (b) anterior pole, scale bar 300 μm; (c) micropylar area, scale bar 100μm; (d) micropylar area, scale bar 50μm; (e) ribs lateral side, posterior end, scale bar 100μm;(f) chorion detailing aeropyles, scale bar 50μm.

3.1.5 Geitoneura klugii

Micropylar area: distinct, number of openings = 3, cells in rosette = 5, rows of cells in micropylar area = 8.

Shape: Approximately turbinate, upright, truncate, expanding basally (Figure 3.27a), posterior and anterior pole flat (Figure 3.27a-c), moderately thick shelled, with well developed broad longitudinal ribs (Figure 3.27a,e).

Characteristics: Egg marked on anterior pole by semi-hexagonal, slightly convex cells with elevated walls (Figure 3.27c,d). Anterior pole circular, convex, flattened, rimmed with beaded ridge due to extensions of vertical ridges (Figure 3.27c), centred by a circular micropylar area (Figure 3.27d). Lateral sides marked by concave elongate rectangular cells, arranged in broad longitudinal rows (Figure 3.27a,e). Posterior pole smooth marked with regularly spaced, inset, leaf shaped forms (Figure 3.27b). Broad, rounded, shallow, ribs run from anterior pole to posterior pole. A secondary set of ribs run perpendicular to main ribs especially around centre of egg (Figure 3.27a,e). Aeropyles are raised (Figure 3.27e,f), situated on elevated ridges of cell walls (Figure 3.27e,f).

Eggs are usually laid singly, occasionally in pairs, and are very pale green to cream in colour (Figure 3.31) becoming translucent on maturity.

Mean egg size (μm) length = 750 ± 15 (SE) (n=10); width = 800 ± 10.5 (SE) (n=10); height = 800 ± 10.5 (SE) (n=10);

The incubation period in *Geitoneura klugii* varies greatly (Common & Waterhouse 1981; Braby & New 1988a; 1999; Braby 2000)

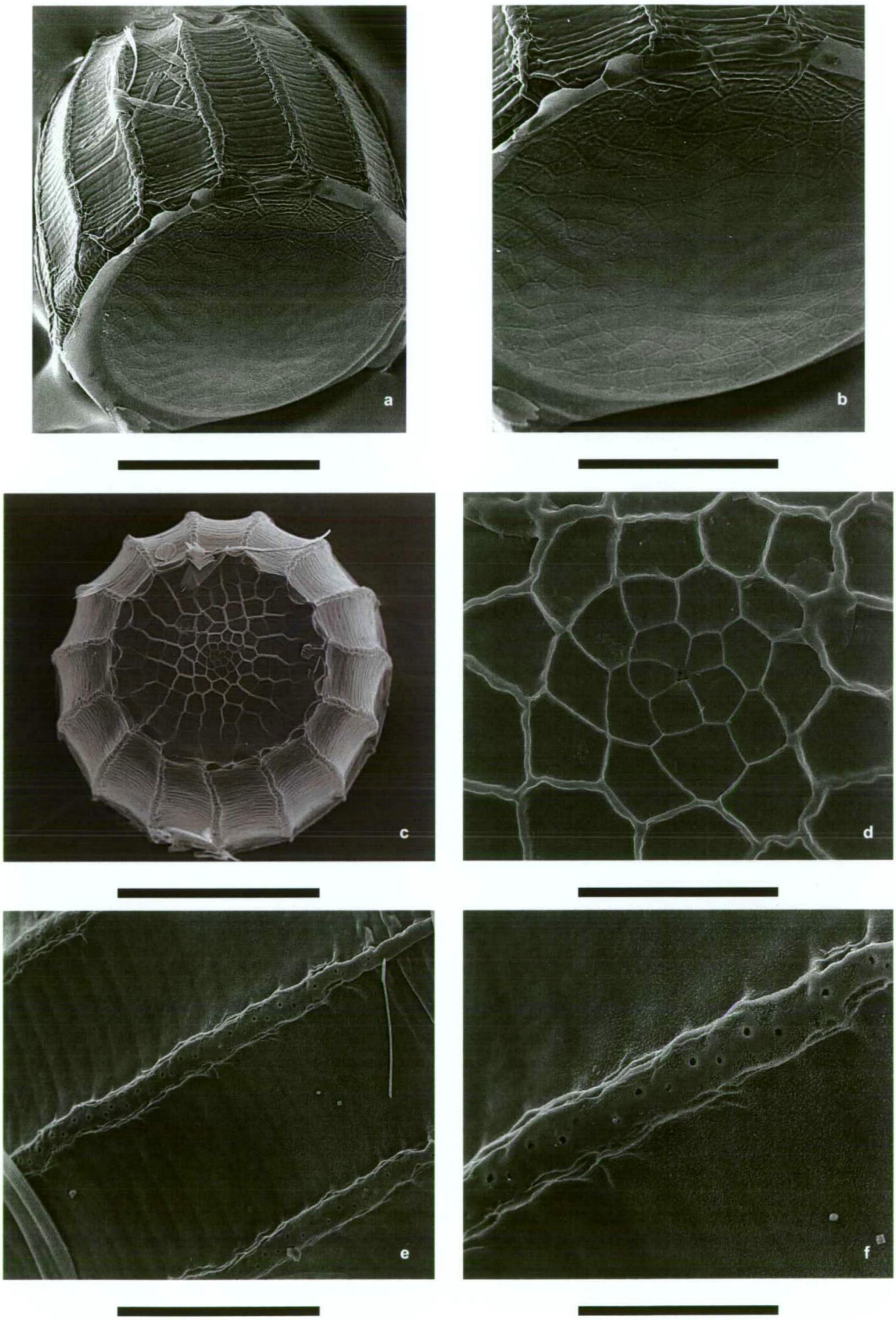


Figure 3.27 *G. klugii*, SEM egg

(a) lateral view of whole egg, scale bar 200 μm; (b) posterior pole, scale bar 100 μm; (c) anterior pole, scale bar 500 μm; (d) micropylar area, scale bar 100 μm; (e) chorion near anterior pole, scale bar 50 μm; (f) chorion near posterior pole, scale bar 50 μm.

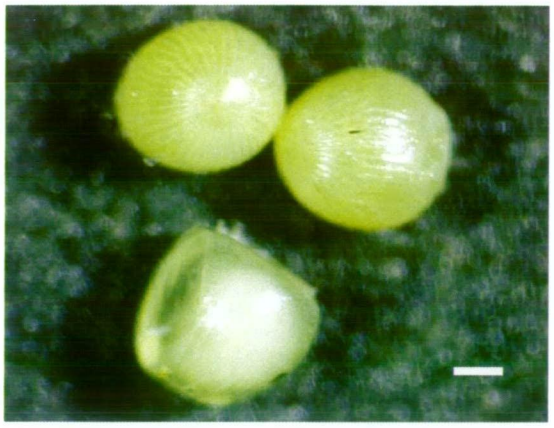


Figure 3.28 *H. cordace*, fresh eggs
Scale bar 0.5 mm.

Figure 3.29 *H. cordace*, mature eggs
Scale bar 0.5 mm.

Figure 3.30 *H. merope*, fresh eggs
Scale bar 0.5 mm.

Figure 3.31 *G. klugii*, maturing eggs
Scale bar 0.5 mm (Field 2002).

3.1.6 Vanessa kershawi

Shape: Barrel shaped, upright, height slightly greater than the width (Figure 3.34a), posterior pole flattened, anterior pole circular, apex concave (Figure 3.34b-d).

Characteristics: Anterior pole is circular, convex (Figure 3.34b), and centred by a circular micropylar area (Figure 3.34c). Lateral sides marked by well developed wing like transparent longitudinal ribs that enlarge apically and continue onto top edge of egg, numerous indistinct lateral ridges. Broad, rounded, shallow ribs run from anterior pole to posterior pole. A secondary set of ribs run perpendicular to main ribs especially around centre of egg (Figure 3.34d). Aeropyles are raised, opening moderately small, (Figure 3.34e), situated on elevated ridges of cell walls (Figure 3.34f).

Eggs are usually laid singly, and are pale green in colour (Figure 3.32, Figure 3.33) becoming greyish yellow as they mature.

Incubation period approximately 12 days (Common & Waterhouse 1981)

Figure 3.32 *V. kershawi*, fresh egg lateral view (Field 2002).

Figure 3.33 *V. kershawi*, fresh egg dorsal view (Field 2002)

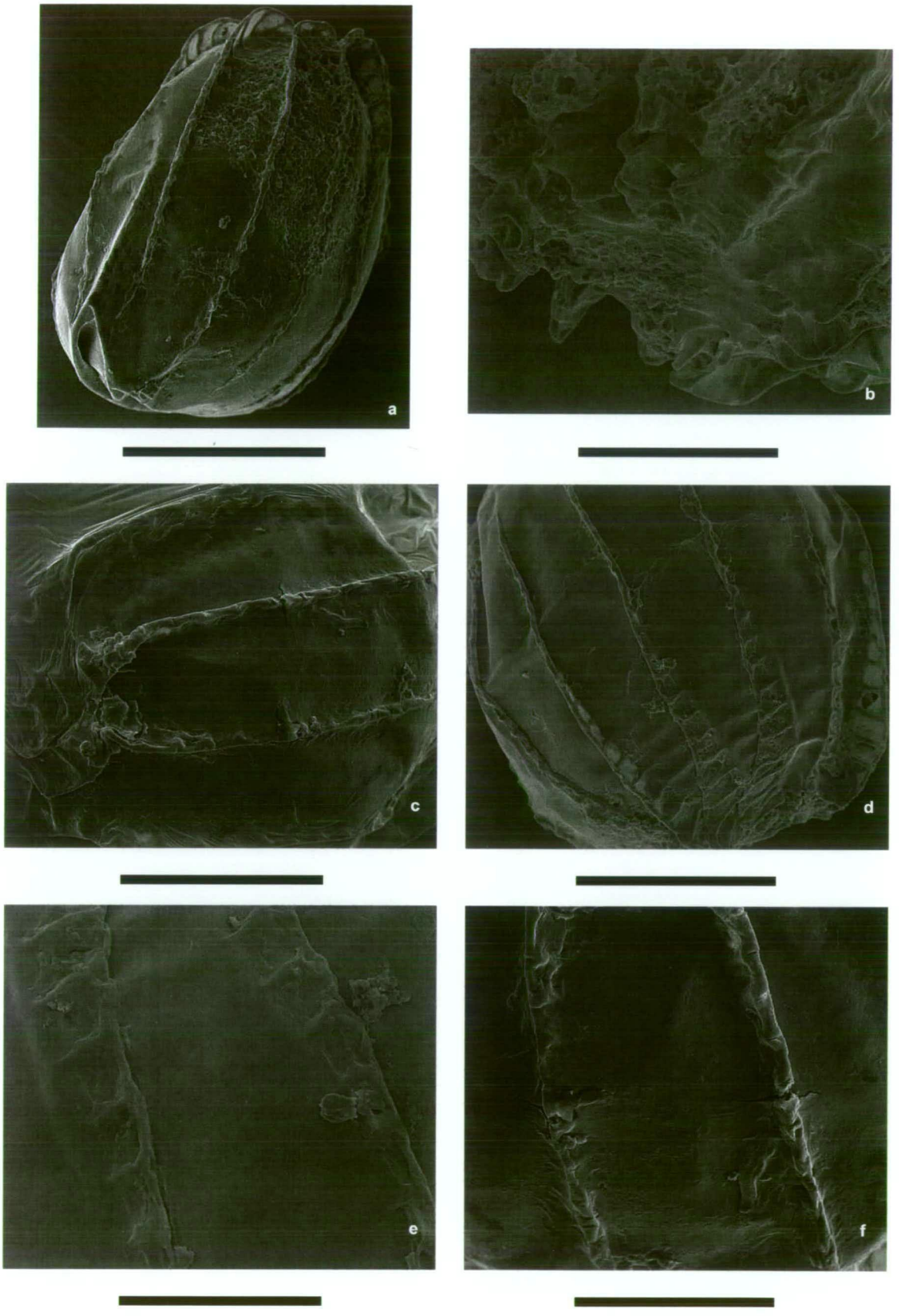


Figure 3.34 *V. kershawi*, SEM egg

(a) lateral view of whole egg, scale bar 500 μm; (b) anterior pole, scale bar 500 μm; (c) micropylar area, scale bar 100 μm; (d) chorion towards anterior pole, scale bar 200 μm; (e) chorion detailing aeropyles, scale bar 40 μm; (f) chorion near posterior pole, scale bar 40 μm.

3.1.7 Junonia villida

Shape: Dome shaped, upright, height about same as width (Figure 3.35, Figure 3.36), posterior pole flattened, anterior pole circular, apex concave.

Characteristics: Anterior pole is circular, convex , and centred by a circular micropylar area. Lateral sides marked by broad, rounded, shallow, well developed, transparent, longitudinal ribs that enlarge apically running from anterior pole to posterior pole. A secondary set of ribs run perpendicular to main ribs especially around centre of egg. Aeropyles are raised, situated on elevated ridges of cell walls.

Eggs usually laid singly, attached to substrate. Newly laid eggs are pale green in colour (Figure 3.35, Figure 3.36) becoming greyish yellow as they develop, then translucent on maturity (Figure 3.37). (Common & Waterhouse 1981; Braby 2000).

Egg size (μm) length = 800 ; width = 700 (Braby 2000).
Incubation period is approximately 12 days (Braby 2000).

Figure 3.35 *J. villida*, fresh egg lateral view (Grund 2003).

Figure 3.36 *J. villida*, fresh egg dorsal view (Grund 2003).

Figure 3.37 *J. villida*, mature egg with emerging larva (Grund 2003).

3.2 *O. ptunarra larval characteristics*

Below are descriptions of *O. ptunarra* larva based on field and laboratory observations.

3.2.1 O. ptunarra 1st Instar Larva-

Head – Light khaki in colour.

Mean head capsule = 0.56mm ± 0.001 (SE) (n=79) (Figure 3.40).

Stemmata – 5, arranged in a semi circle, darker brown in colour than head.

Body – straw yellow-green in colour, marked with a row of spots (~0.02mm in diameter) along lateral side.

Shape – Short and stout.

Setae – medium brown to tan in colour, bristle-like, slightly clubbed distally, ~0.27mm long.

Pinacula – positioned on slightly raised olive green tubercules.

Spiracles – pale yellow, periderm dark brown and raised, especially on abdominal segment 7 (A7) and thoracic segment 1 (T1).

Legs – 4 pairs of prolegs, 1 pair of anal claspers. Legs and prolegs same colour as body. Tan claws on the true legs (Figure 3.39).

Mean caterpillar length = 2.04mm ± 0.02 (SE) (n=33) (Figure 3.38).

Hatching – observed to take around 25 minutes from when micropyle split, until caterpillar was completely free.

Feeding – did not appear to commence directly after hatching; delay of a few hours.
Newly hatched caterpillars grazed on surface of *Poa* with a sideways movement of their head.
With increasing age and size deeper layers were grazed.
A preference for *P. hiemata* was noticed, younger larvae preferred younger shoots or broken ends of *Poa*.
Feeding was observed all hours of the day and night

Faeces – round, green globules, containing what appeared to be platelets of *Poa* epidermis.

Figure 3.38
O. ptunarra
1st instar larva.

Scale bar 0.5 mm

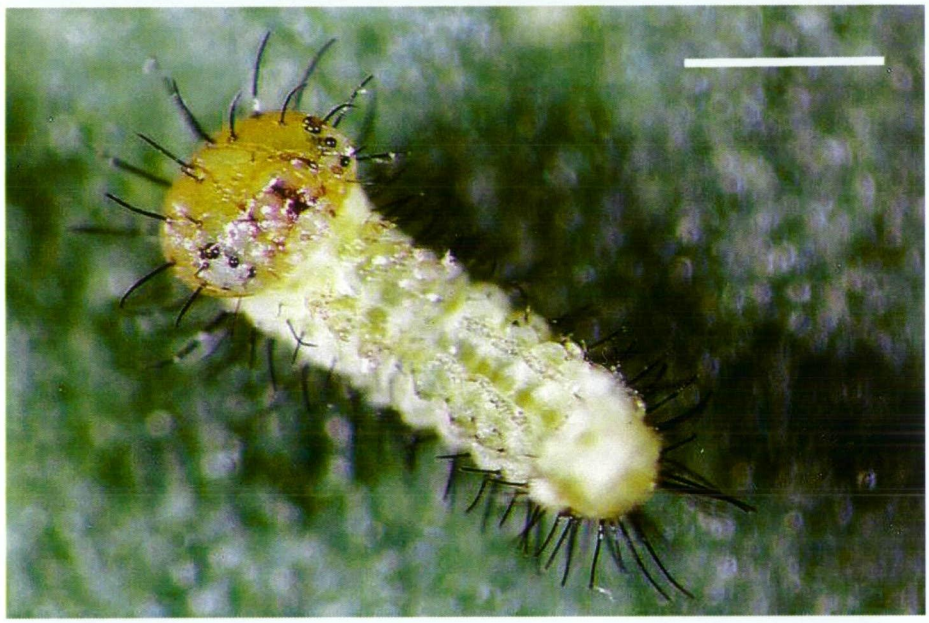


Figure 3.39
O. ptunarra
1st instar larva,
legs and claws.

Scale bar 0.5 mm

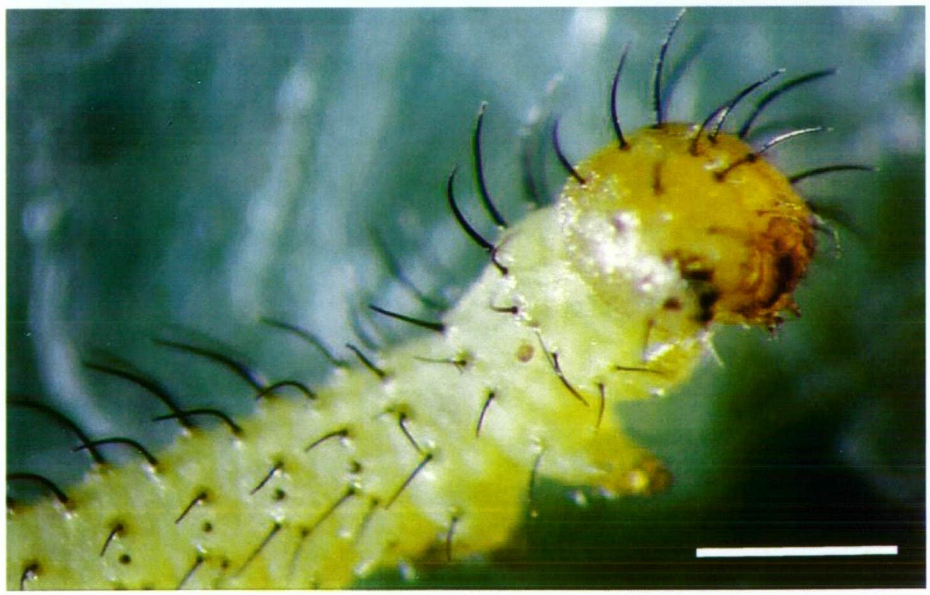


Figure 3.40
O. ptunarra
1st instar larva,
head and
abdominal
section.

Scale bar 0.5mm

3.2.2 O. ptunarra 5th Instar Larva

There are two distinct colour morphs in mature *Oreixenica ptunarra* larva; green (Figure 3.41, Figure 3.42, Figure 3.43, Figure 3.44, Figure 3.45, Figure 3.46) and brown (Figure 3.47, Figure 3.48, Figure 3.49).

3.2.2.1 Green Colour Morph

Head Capsule – shape rounded, olive green in colour with two pale green spots on middle of each side of vertex. Head is distinctively separated from thorax (Figure 3.41, Figure 3.42)

Blotches – absent

Mouth parts – dark reddish brown (Figure 3.43).

Prothoracic Shield – absent

Mean head capsule = ~5.0mm (n=2)

Body – ground colour grass green (Figure 3.44, Figure 3.45, Figure 3.46)

Shape – Short and stout (Figure 3.44).

Dorsum – semi transparent dark green mid dorsal band boarded by narrow yellow stripes (Figure 3.44, Figure 3.45)

Dorsolateral bands – dark green stripe boarded by yellow bands (Figure 3.44)

Lateral – Narrow yellow lateral stripes

Venter – Overall grass green in colour, same as dorsum; A1 and A2 venter pale green (Figure 3.43).

Tubercles – absent.

Epidermis – smooth, covered with numerous secondary setae (Figure 3.46).

Legs – Olive green, same shade as head.

Prolegs – well developed prolegs present on A3, A4, A5, A6, and A10, same ground colour as body.

Anal Claspers – same ground colour as body present on A10.

Anal Plate – same ground colour and patterning as body.

Paraprocts – very well developed become paler distally.

Hypoprocts – poorly developed.

Setae – Short yellowish green, bristle-like, slightly clubbed distally.

Mean caterpillar length = ~30mm (n=2)

Resting position is prostrate tightly clasped to substrate.

Figure 3.41 *O. ptunarra*, mature larva green colour morph, dorsal surface. Scale bar 20mm

Figure 3.42 *O. ptunarra*, mature larva green colour morph, dorsal surface. Scale bar 20mm

Figure 3.43 *O. ptunarra*, mature larva green colour morph, ventral surface. Scale bar 20mm

Figure 3.44 *O. ptunarra*, mature larva green colour morph, dorsal surface. Scale bar 20mm

Figure 3.45 *O. ptunarra*, mature larva green colour morph, ventral surface. Scale bar 20mm

Figure 3.46 *O. ptunarra*, mature larva green colour morph, dorsal surface. Scale bar 20mm

3.2.2.2 Brown Colour Morph

Head Capsule – shape rounded, terracotta brownish red in colour with two dark reddish brown spots on middle of each side of vertex. Head is distinctively separated from thorax (Figure 3.48).

Blotches – absent

Mouth parts – dark reddish brown.

Prothoracic Shield – absent

Mean head capsule = ~5.0mm (n=1)

Body – ground colour pinkish brown (Figure 3.47).

Shape – Short and stout.

Dorsum – semi transparent mid dorsal band, dark reddish brown, boarded by pale pink stripes.

Dorsolateral – pink strip boarded by pale pink bands, which are in turn boarded by dark pink stripes, ventral strip is very dark reddish brown.

Lateral – Narrow pale pink lateral stripes.

Venter – Overall same pinkish brown ground colour as dorsum; A1 and A2 venter pale pink.

Tubercles – absent.

Epidermis – smooth, covered with numerous secondary setae.

Legs – brownish red, same shade as head.

Prolegs – well developed prolegs present on A3, A4, A5, A6, and A10, same ground colour as body.

Anal Claspers – same ground colour as body present on A10 (Figure 3.49).

Anal Plate – same ground colour and patterning as body (Figure 3.49).

Paraprocts – very well developed become paler distally.

Hypoprocts – poorly developed.

Setae – Short pinkish brown, bristle-like, slightly clubbed distally.

Mean caterpillar length = ~25mm (n=1)

Resting position is prostrate tightly clasped to substrate.

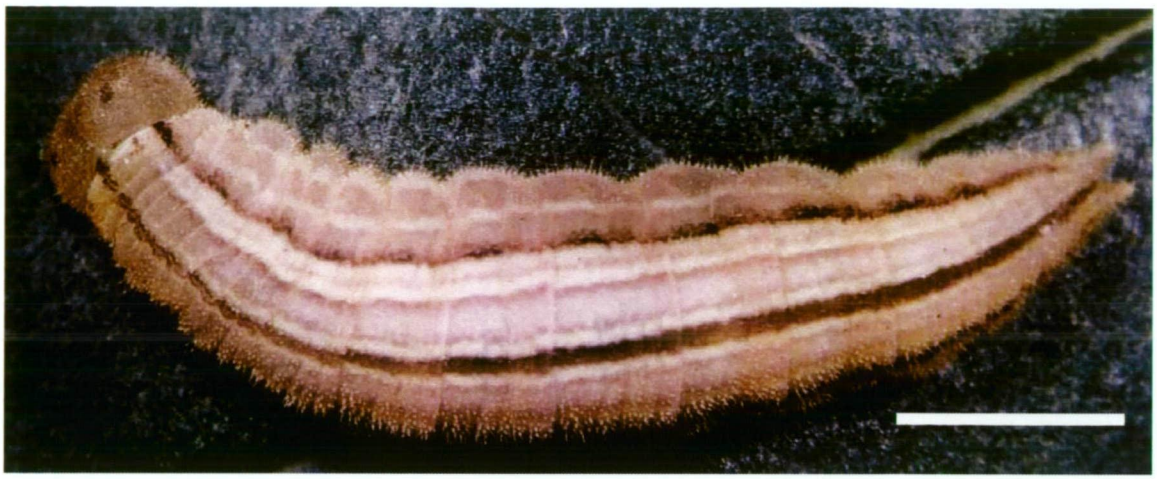


Figure 3.47 *O. ptunarra*, mature larva brown colour morph, dorsal surface

Scale bar 20mm

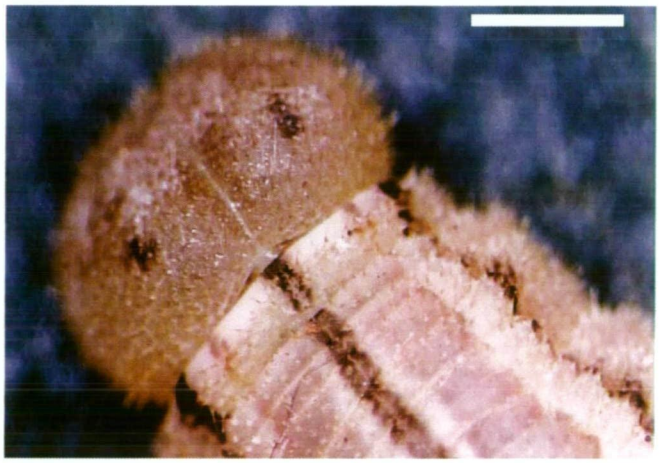


Figure 3.48 *O. ptunarra*, mature larva head capsule brown colour morph

Scale bar 3mm

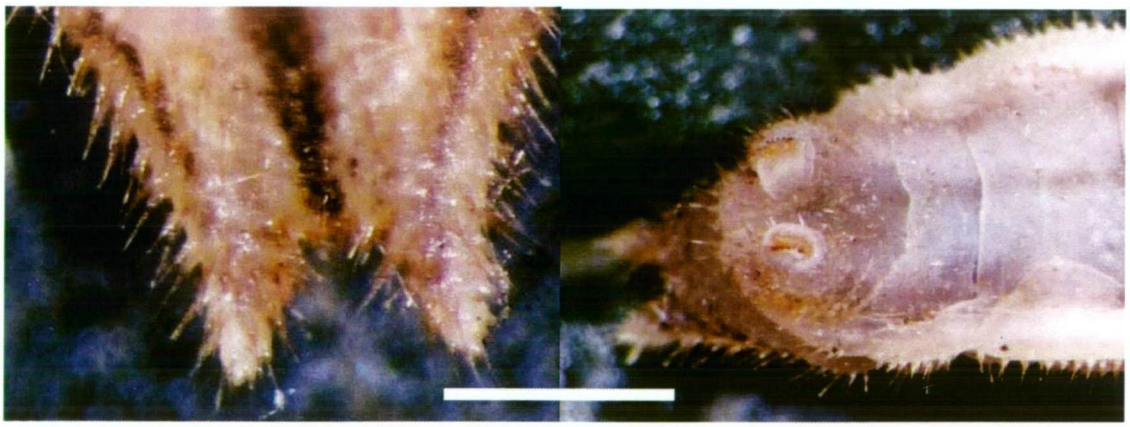


Figure 3.49 *O. ptunarra*, mature larva anal claspers brown colour morph

Scale bar 3mm

3.2.3 Field observations of mature O. ptunarra larva

Mature *Oreixenica ptunarra* larvae were found at Lake Crescent Interlaken [500125E 5330348N] (TASMAP 1992) (refer to Appendix 3 for further site details) on Wednesday 8th February 2006, approximately six weeks prior to the flight season commencing at this locality. Lake Crescent is an open *Poa* grassland boarded by open alpine woodland to the east (Figure 3.50) fresh water lake and road to the north, marshland and fresh water lake to the south and open grassland interspersed with marshland to the west. The weather conditions during collection were mild, very still with high cloud cover (Figure 3.51), ahead of a cold front which crossed the state around midnight. Daytime conditions were fine, still and mild to warm.

Figure 3.50 Field collection site looking towards the southeast, Lake Crescent, Interlaken, Tasmania.

Figure 3.51 Dusk Field collection site, Lake Crescent, Interlaken, Tasmania.

Figure 3.52 Field collecting mature *O. ptunarra* larva, Lake Crescent, Interlaken, Tasmania.

The larvae start to stir at sunset crawling to the tops of the tussocks to begin feeding (Figure 3.53, Figure 3.54). Larvae were most active within the first two hours after sun set. Larval activity dramatically declined within three hours of sunset and no larvae were seen after this time.

The most effective method to observe larvae is crawling through the tussocks with a head torch looking for a caterpillar feeding near the top of *Poa* (Figure 3.52).

When initially disturbed by light, the larvae freeze and remain motionless on the *Poa* (Figure 3.53). When physically disturbed, the larva would drop from the *Poa* shoot upon which they were feeding, down into the base of tussock and burrow down into the root mass.

Figure 3.53 *O. ptunarra*, mature larva

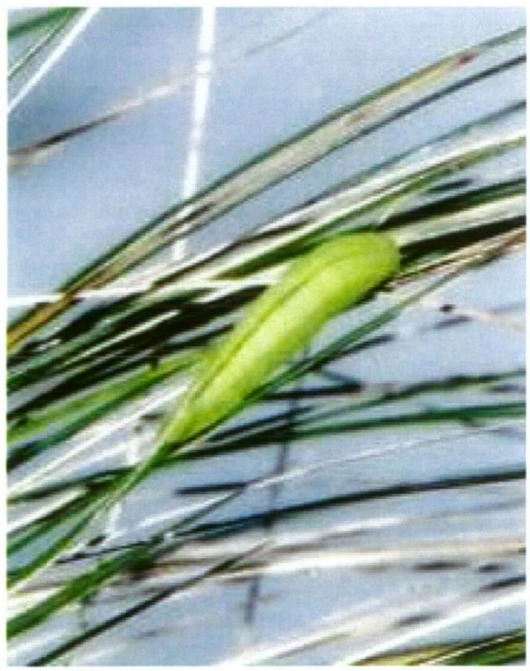


Figure 3.54 *O. ptunarra*, mature larva

3.3 *Satyrinae larval characteristics*

A comparison to temperate zone southeast Australian Satyrinae larvae is presented in Table 3.2. These notes are based on field observations augmented with descriptions from previously published works (Couchman 1953; Couchman & Couchman 1978; Common & Waterhouse 1981; Braby 2000)

Table 3.2 Comparison of Satyrinae larva

Species / Maturity	**Head**	**Body**
O. ptunarra 1st Instar Larva	Rounded, yellowish khaki green in colour. Short black hairs.	Pale green with long black setae
O. ptunarra Mature Larva	Olive green or terracotta brownish red colour, dorsal surface rounded with a few scattered short black setae.	Green or pinkish brown in colour, short and stout with a middorsal line edged by a narrow subdorsal line, a lateral line and a ventrolateral band. Hairy with short bristle like secondary setae. Anal segment with a forked posterior projection.
O. latialis 1st Instar Larva	Pale green in colour, dorsal surface rounded	Green in colour with long black hairs
O. latialis Mature Larva (Figure 3.57)	Pale brown in colour, dorsal surface rounded	Pale pinkish-brown or stone-brown / fawn, with darker longitudinal middorsal lines edged by a paler subdorsal line, and two dark lateral lines. Anal segment with a forked posterior projection.
O. lathoniella 1st Instar Larva (Figure 3.55)	Greenish brown in colour	Green, with yellowish green longitudinal lines
O. lathoniella Mature Larva	Green or light brown in colour, with faint darker markings; dorsal surface rounded.	Green with yellowish green longitudinal lines, or light pinkish brown with dark middorsal line edged by a narrow pale subdorsal line, prominent pale dorsolateral and ventrolateral lines, and two faint lateral lines. Sometimes, with a series of small black dorsolateral dots. Anal segment with a forked posterior projection.
O. orichora 1st Instar Larva (Figure 3.56)	Brown in colour with long whitish hairs, dorsal surface rounded	Green with very long brown hairs
O. orichora Mature Larva	Light green in colour, dorsal surface rounded.	Green with darker green longitudinal lines and minute white spots. Anal segment with a forked posterior projection.
O. correae 1st Instar Larva	Black in colour, dorsal surface rounded	Greenish with brown hairs
O. correae Mature Larva	Green in colour, dorsal surface rounded	Khaki green with darker green longitudinal lines or pale brown in colour with darker green longitudinal lines. Anal segment with a forked posterior projection.
O. kershawi 1st Instar Larva	Brown in colour, with a few black hairs.	Cream in colour with sparse short black hairs

O. kershawi Mature Larva (Figure 3.58)	Pale green in colour, slightly hairy, surface roughened, slightly concave.	Green with darker green longitudinal lines and minute white dots. Anal segment with forked posterior bifid processes tipped with pink.
N. leprea 1st Instar Larva (Figure 3.59 & Figure 3.60)	Broad, light brown with numerous setae longer than setae on the body.	Light green with a darker green dorsal line, and a pair of less distinct subdorsal lines, and an even less distinct lateral line joining a series of small black tubercles, one on each segment. Setae, medium brown to tan in colour, bristle-like, clubbed distally
N. leprea Mature Larva	Green darker than body.	Green with a dark green lateral line and a lower yellowish white lateral line joining tubercles.
A.. hobartia 1st Instar Larva (Figure 3.61 & Figure 3.62)	Dark brown, rounded, with numerous long dark brown setae, longer then the setae on the body.	Body light creamish green / grey brown to with an obscure black dorsal line, and a pale ventrolateral line. Two distinct spots in the dorsal lateral position on the pro-thoracic shield. Dense short brown setae clubbed distally. Anal segment with a forked posterior projection.
A.. hobartia Mature Larva	Rounded, dark brown	Grey-brown to chocolate brown, with an obscure black dorsal stripe, and a pale ventrolateral line. Anal segment with a forked posterior projection.
H. cordace 1st Instar Larva (Figure 3.63)	Rounded, blackish brown, absent of long setae.	Pale green with darker longitudinal lines and a blackish lateral line. Marked with rows of spots along the dorsal, dorsolateral and lateral sides. A prominent spot is present on the lateral side of the pro-thoracic shield and on the lateral side of segment A10.
H. cordace Mature Larva	Dark reddish –brown, with paler markings. Slightly concave dorsally without horns.	Green, greenish-brown, or dark brown, with a brown darker middorsal line, edged by a paler subdorsal line, and a pale lateral line; rough skin. Abdominal segments with a black lateral line, anal segment with a prominent forked posterior projection.
H. penelope Mature Larva	Dull brown or blackish brown, and hairy. Rounded, convex dorsally, almost circular when viewed anterioly.	Variably brown with darker brown markings and a middorsal line dark brown middorsal line edged with grey, and a greyish –brown dorsolateral line. Anal segment with a forked posterior projection.
H. merope 1st Instar Larva (Figure 3.64 &Figure 3.65)	Black to blackish brown with long setae.	Green to greenish cream, with very long black setae. Darker dorsal stripe, and distinct pro-thoracic shield
H. merope Mature Larva	Brown to reddish brown, rugose, head is flatter dorsally rather then concave. Numerous dense short setae.	Variable in colour, generally green, grey or light brown, mottled with darker brown and dense short setae and a darker broad brown broken middorsal line and narrower brown broken dorsolateral line. Anal segment with a forked posterior projection.
G. klugii Mature Larva (Figure 3.66)	Green, rounded with longer setae than body.	Green with a broad darker green mid-dorsal line, a thin pale dorsolateral line edged above with dark green, and a cream or pale yellow ventro-lateral line. Short erect setae, white. Anal segment with a forked posterior projection tipped with reddish-brown.
V. kershawi Mature Larva (Figure 3.67)	Black or brown, with numerous setae.	Variable in colour, usually a shade of brown but sometimes yellowish grey or green, with paler, yellowish or whitish middorsal, lateral and lines ventral stripes. Each segment has several branched spines.
J. villida Mature Larva (Figure 3.68)	Black with short setae and two short black branched spines.	Black with numerous short thick black branched spines, sometimes arising from paler areas. Prothorax dull orange.

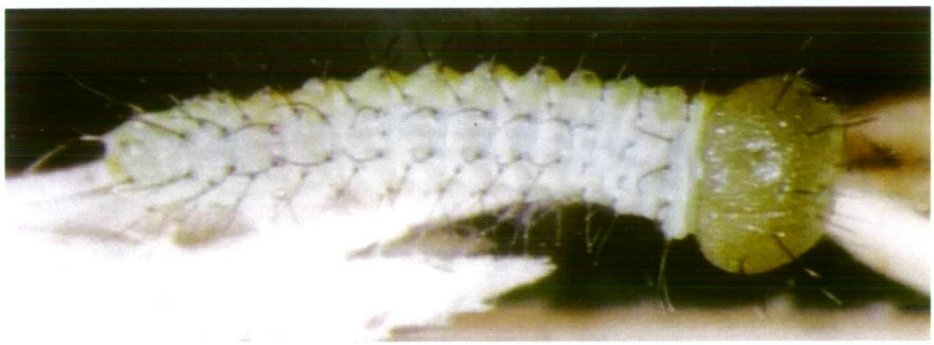


Figure 3.55
O. lathoniella, first Instar larva

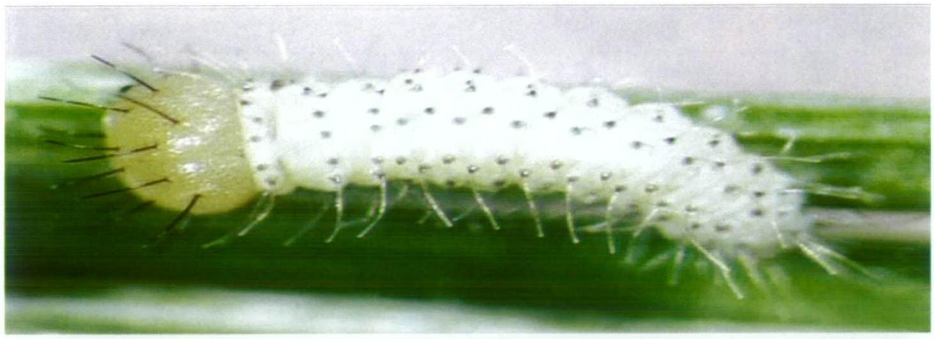


Figure 3.56
O. orichora, first Instar larva

Figure 3.57
O latialis, mature larva

(Viridans 2006)

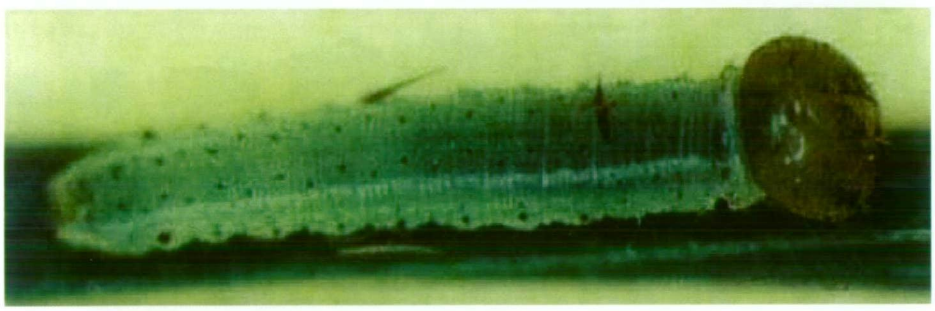


Figure 3.58
O kershawi, mature larva

(Field 2002)

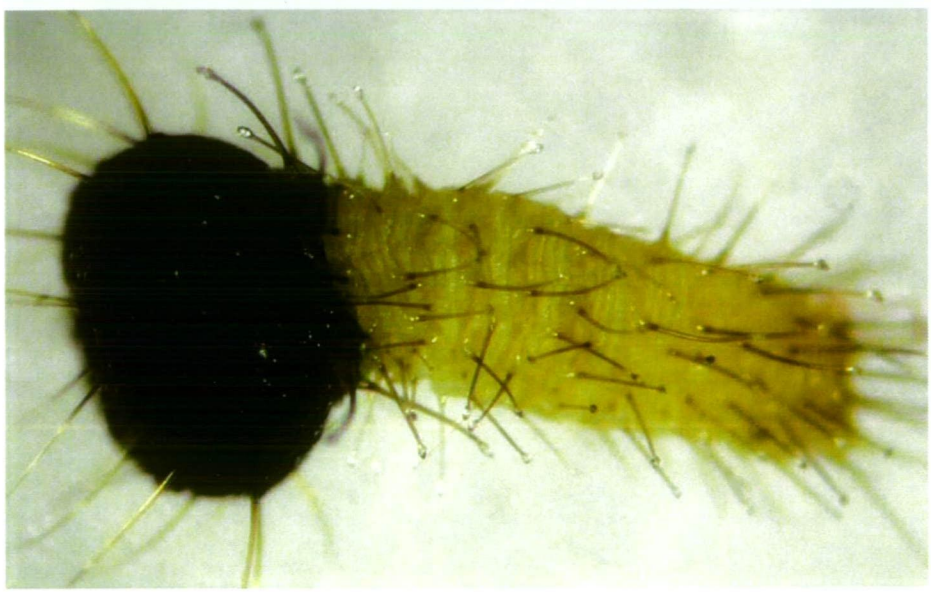


Figure 3.59
N. leprea, 1st Instar larva, dorso-lateral view.

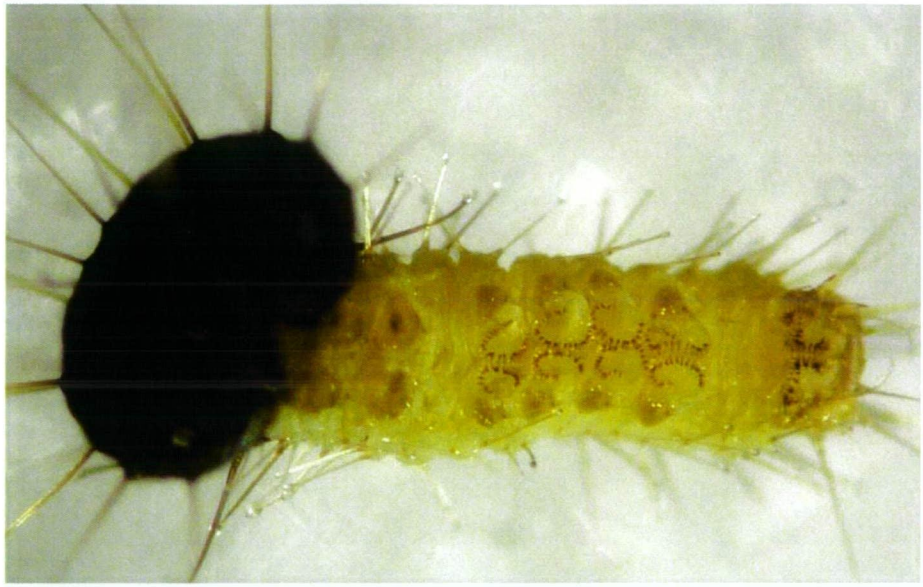


Figure 3.60
N. leprea, 1st Instar larva, ventral view.

Figure 3.61
A. hobartia, 1st Instar larva, dorso-lateral view.

Figure 3.62
A. hobartia, 1st Instar larva, ventral view.

Figure 3.63
H. cordace, 1st Instar larva, dorso-lateral view.

Figure 3.64
H. merope,
1st Instar larva,
dorso-lateral view

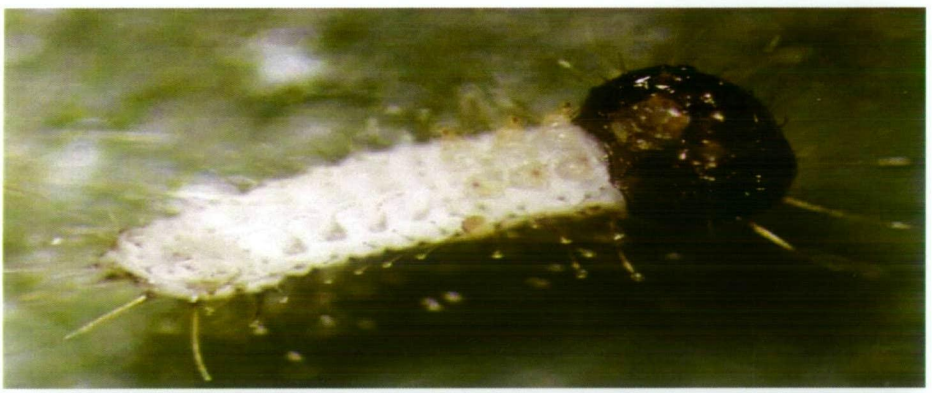


Figure 3.65
H. merope
1st Instar larva,
ventral view

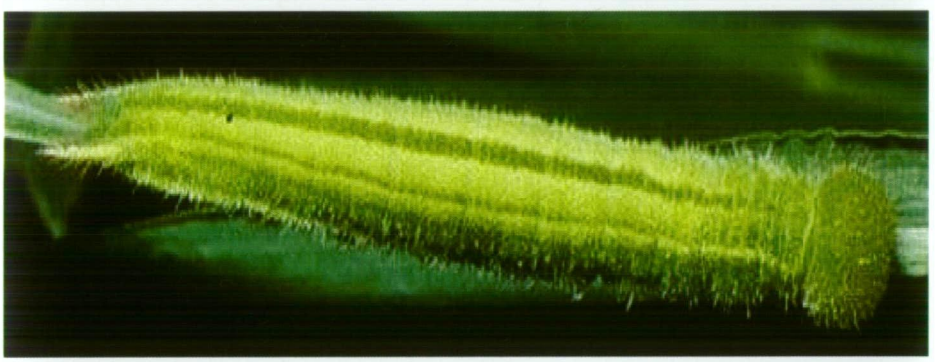


Figure 3.66
G. klugii, mature
larva, dorso-lateral
view

(Field 2002).

Figure 3.67
V. kershawi,
mature larva,
dorso-lateral view

(Field 2002).

Figure 3.68
J. villida,
mature larva,
dorso-lateral view

(Field 2002).

3.3.1 Larval food plants

The list of larval food plants presented in Table 3.3 is based on field observations augmented with information from previously published works (Waterhouse 1923; Couchman 1948, 1953, 1954; Burns 1956; Couchman 1956; McCubbin 1971; Couchman & Couchman 1978; Common & Waterhouse 1981; Prince 1988; Braby 1995a; James 1999; Braby 2000).

Table 3.3 Larval Food Plants

Species	***Main hosts***	**Minor hosts**
N. leprea	*Uncinia tenella* (Cyperaceae)	
A. hobartia	*Lolium perenne* (Poaceae) Introduced	Natural food plants have not been recorded; probably *Poa labillardieri* & *Austrodonthonia sp.*
H. cordace	*Carex appressa*	
H. merope	*Austrostipa sp.* *Imperata sp.* *Micolaena stipoides* *Poa sp.* *Themeda triandra* *Cynodon dactylon* Introduced species include *Brachypodium distachyon,* *Bromus cathartiens,* *Ehrharta erecta.*	*Agrostis sp.* *Brachypodium sp.* *Bromus sp.* *Cynodon sp.* *Ehrharta sp.* *Pennisetum sp.* rarely on *Gahnia sp.*
H. penelope	*Austrodanthonia penicillata,* *Austrodanthoniapilosa* *Themeda triandra* *Poa sp.*	*Brachypodium sp.* *Ehrharta sp.*
Geitoneura	*G. klugii* larva, in all instars, feed openly during the daytime, unlike *G. acanthi*. Although *G. klugii* larva remain fully exposed on the foliage it is difficult to detect.	
G. klugii	*Austrodanthonia sp.* *Austrostipa flavescens,* *Joycea pallida,* *Themeda triandra* (Poaceae); *Poa sp.* Introduced species include *Brachypodium distachyon,* *Ehrharta calycina,* *Vulpia sp.* (Poaceae).	*Brachypodium sp.* *Ehrharta sp.* *Vulpia sp.*
O. ptunarra	*Poa sp.*	
O. latialis	*Poa sp.*	
O. lathoniella	*Poa sp.*	*Microlaena sp.*
O. orichora	*Poa sp.*	
O. correae	*Poa sp.*	
O. kershawi	*Tetrarrhena juncea* (Poaceae)	*Poa sp.*

3.4 *Pu pal Characteristics*

3.4.1 Oreixenica ptunarra

Fresh pupae greenish grey flecked with black, on maturity exuvium (pupal shell) light transparent brown. Venter pale brown streaked with dark brown. Pair of dark brown spots on dorsolateral line and in middle of each abdominal segment on raised short ridges. Setae very short, black and blunt (Figure 3.69, Figure 3.70 & Figure 3.71). No cocoon is produced.

Anal area has longitudinal split bordered laterally by mounds with longitudinal furrows. Base of anus has deep concavity centralised in cremaster. Apex of cremaster orientated ventrally. Approximately 20 short, robust, hooked, falcate setae are crowded on apex of cremaster.

Male genital area has a short longitudinal slit at base of a small furrow.
Labrum is triangular with truncated apex transverse furrows; labium pentagonal; "mandibles" raised, rugose and large; antennae moderately broad; prothoracic legs visible; hind tibia not visible; proboscis does not reach antenna.

Prothoracic spiracles not visible, meso and meta thoracic spiracles slightly raised; thoracic spiracles inconspicuous. Abdominal spiracles A1, A2, A3, A4, A5, A6 all well developed; A7 present but under developed.

Punctures only present on abdominal segments on both dorsal and ventral sides, small randomly distributed at base of secondary setae; dorsal cremaster furrow between A7 and A8 absent.

Hind wings consolidate at A3; junction of the wings pronotum conspicuously angular.

Male pupae are 10.25mm long ±0.25mm and 4.25mm wide ±0.25mm (n=3).

Pupa lies loose at base of tussocks amongst shoots of grass resting in a fork between adjacent stems (Figure 3.72 & Figure 3.73).

Figure 3.69
O. ptunarra exuviae,
dorsal view

Figure 3.70
O. ptunarra exuviae,
ventral view

Figure 3.71
O. ptunarra exuviae,
lateral view

Figure 3.72 *O. ptunarra* pupa resting in *Poa* tussock.

Figure 3.73 *O. ptunarra* pupa resting in *Poa* tussock.

3.4.2 Satyrinae Pupae

Satyrinae pupal descriptions presented in Table 3.4 are based on field observations augmented with descriptions from previously published works (Couchman 1953; Couchman & Couchman 1978; Common & Waterhouse 1981; Braby 2000)

Table 3.4 Comparison of Satyrinae Pupae

Species	**Pupal Description**	**Attached / Unattached**
O. ptunarra	Smooth, greenish grey flecked with black, with a pair of black spots on each segment of abdomen. Lay loose in the tufts of grass. Pupa lies loose amongst shoots of grass at base of tussock, resting in a fork between adjacent stems.	Unattached
O. latialis	Smooth, pale brown with darker markings. Anterior end truncate, forewing with a white dorsal ridge. Cremaster small and downwardly curved. Abdominal segments lack prominent protuberances or lateral projections. Lay loose on the ground or amongst tussocks of grass.	Unattached
O. lathoniella	Various shades of brown. Pair of pointed lateral projections at anterior end. Abdominal segments 1 to 3 with paired dorsal projections, segments 4 to 7 each with a transverse dorsal ridge produced into a pair of lateral projections. Prominent protuberances on the abdominal segments. Suspended head downwards by cremaster, often attached to dead leaves near base of food plant.	Attached
O. orichora	Pale grey-brown, mottled with darker brown. Two short lateral spikes at anterior end. Lay loose but upright in debris at base of tussock food plant.	Unattached
O. correae	Various shades of brown, mottled with darker brown. A rounded dorsolateral process is present on abdominal segments 1 to 7. Anterior end truncate. Suspended head downwards by cremaster. Attachment of silk to substrate is very weak and frequently pupa becomes detached.	Attached
O. kershawi	Greenish brown markings. Anterior end truncate with two lateral projections. Abdominal segments 1 to 3 each with a dorsolateral process, segments 4 to 7 each with a transverse ridge produced into a dorsolateral projection. Suspended head downwards by cremaster.	Attached
N. leprea	Suspended head downwards by cremaster, on food plant.	Attached
A.. hobartia	Suspended head downwards by cremaster from stem of food plant.	Attached
H. cordace	Smooth, truncate and anterior end slightly concave, 12-14mm long. Bright green, suffused with pale yellowish –green on wings, with conspicuous black spots. Head with a lateral black spot near eye, and one to three black spots along antenna. Thorax with a slight white dorsal ridge, forewing with seven or eight black spots, three or four of them along dorsal margin; abdominal segments 1 to 7 each with a black dorsolateral sport edged posteriorly with white. Suspended head downwards by cremaster, attached to a small pad of silk spun on leaves of food plant or on adjacent objects.	Attached

H. penelope	17mm long, stout, smooth, pale brown with darker brown markings. Forewings with a series of dark brown spots along posterior margins. Cremaster short and downwardly curved. Lies loose on ground at the base of food plant, amongst leaves and debris that are usually held together by a few strands of loose silk.	Unattached
H. merope (Figure 3.74)	Smooth, grey or brown, with darker spots and markings. Forewing with a series of black spots along posterior margin. Cremaster is short and sharply pointed. Lies loose on ground beneath overhanging vegetation or debris, often in a shallow cavity lined with a few strands of silk.	Unattached
G. klugii	Pale green 13mm long, anterior end truncate. Thorax with a slightly yellow dorsal ridge. Dorsal margin of the forewing has a yellow longitudinal ridge. Abdomen with a yellow transverse ridge on segment 4. Three pairs of pale yellow dorsal spots appear on abdominal segments 1 to 3. Suspended head downwards by cremaster, attached to a pad of silk spun on food plant or sometimes on a nearby plant, stick or rock.	Attached
V. kershawi	17-18 mm long, variable in colour, grey-brown, or reddish brown with darker markings. Sometimes suffused with metallic silver or gold, and a series of four pairs of silver or golden dorsal spots. Anterior end rounded. Thorax with a prominent dorsal ridge, metathorax and abdominal segments 1 to 8 each with a small dorsolateral process and a smaller dorsal process. Hangs head downwards, attached by cremaster to either the food plant or a nearby object.	Attached
J. villida	14 - 17mm long, stout and short, variable in colour, often dull back, blotched with white or reddish yellow. Anterior end rounded, abdomen with series of small rounded dorsal processes. Suspended head downwards by cremaster from a pad of silk attached either to food plant or a nearby stone, wall or fence.	Attached

Figure 3.74 *H. merope* pupa

(Field 2002).

3.5 *General characteristics of immature stages of* O. ptunarra

3.5.1 Spermatophores

Spermatophore counts for dissected *O. ptunarra* females (n=30) revealed that only one female was found with two spermatophores in her bursar. Three were found to have no spermatophore.

3.5.2 Hatching success

The hatching success of *O. ptunarra* under laboratory condition is around 60%; the rate of egg fertilization is around 85%, with the caterpillars being visible through the transparent eggs. Hatching was observed to take around 25 minutes from when the micropyle split, until the caterpillar was completely free.

Possible reasons for the remainder not hatching include inadequate resource allocation for the larvae to fully develop (due to the variation in the batch oviposited).

On examination, it was revealed that some eggs had partially split, which may suggest inadequate strength of the larvae to fully emerge, again possibly due to inadequate resource allocation or variation in the laboratory microclimate compared to field conditions.

4 DISCUSSION

My results have contributed a considerable amount of new information about the immature stages of temperate zone southeast Australian Satyrinae especially *Oreixenica*. This study has comprehensively described the eggs of *Nesoxenica,* the Tasmanian *Heteronympha, Geitoneura,* and *Argynnina* and all the species from the genus *Oreixenica*. Secondly the larva and pupa of *O. ptunarra* were described.

4.1 *Eggs*

4.1.1 Egg morphology

All eggs upright, with slight variation in shape; *Oreixenica* eggs are globular, spherical to sub-barrel, *Heteronympha* sub-hemispherical to dome, and turbinate to sub-conical, *Geitoneura* turbinate, *Vanessa* barrel and *Junonia* dome shaped. Eggs are marked on anterior pole by hexagonal cells, some variation within cell depth, and height and thickness of cell walls. Lateral sides marked by convex hexagonal cells arranged in longitudinal rows outlined by slightly elevated aeropyles with moderately small openings, situated at cell junctions. Evidence from satyrine butterflies suggests that the external chorionic features are highly homoplasious and probably more useful at low than at high taxonomic levels within Satyrinae (Garcia-Barros & Martin 1995; Garcia-Barros & Munguira 1997). To some extent this is borne out within this study; however there are fine variation in the chorionic features between genera. The micropylar area does offer some definition between genus and species. In all species there are variations in the number of cells in the rosette, the number of rows of cells in the micropylar area and where it is not obscured, the number of openings. Arrangement and distribution of ribs also varies significantly between species. The shape, size and location of aeropyles varies to some degree between species. Eggs of *O. orichora* are further distinguished by the multiple aeropyles or multiple pores arranged along the cell walls. Multiple aeropyles appear to be reasonably uncommon within the eggs of Nymphalidae. Nevertheless the identity of multiple pores / multiple aeropyles is in doubt. Salkeld (1983) refers to them as aeropyles, however Garcia-Barros & Martin (1995) were uncertain of the homology of openings that occur along cell walls and not at cell junctions, with aeropyles.

4.1.2 Fecundity and egg size

Fecundity and adult size have been positively correlated in a number of studies (Garcia-Barros 1994; Garcia-Barros & Martin 1995; Garcia-Barros & Munguira 1997; Garcia-Barros 2000). Garcia-Barros (2000) reported significant results in more that one thousand *Papilionoidea* and *Hesperiidae* species.

In the Satyrine the correlation between egg size and adult size is also significant (Garcia-Barros 2000). Based on Garcia-Barros (2000) positive correlation between egg size and adult size of $r = 0.40$ $P < 0.0001$ *O. ptunarra* fits within the 95% confidence interval line.

Considering that large body size enhances fecundity, does it also affect egg size and survival? In the case of *O. ptunarra* the egg size is relatively large proportionate to body size when compared with other satyrine species. Males transfer nutritional resources to females during mating; a multiply-mated female *Pieris napi* (Pieridae) had higher lifetime fecundity, laid proportionally larger eggs and had longer lifespan compared to once-mated females (Kaitala & Wiklund 1994). It is possible that *O. ptunarra* females direct male-derived nutrients to their eggs.

The high variability in batch size observed across all species may have been linked to resource availability, in the form of nutrients acquired from the male ejaculate or from food availability during egg production (Oberhauser 1997). However, the main nutrient resource is the female herself and her body size is a measure of this resource.

O. ptunarra eggs are randomly dropped during flight and not clustered together. Garcia-Barros (2000) states that eggs clustered together once hatched risk increased sibling competition and host plant depletion. There may also be increased risk associated with predation in egg/larvae clustered together. The spacing of eggs by *O. ptunarra* could be a behavioural mechanism in response to poor quality host plants and also a method to help decrease the effects of stochastic events. A study on egg clustering by Courtney (1984) has suggested that egg clustering has evolved in response to increased fecundity and necessitates the need for large plants to support large numbers of larvae. Most *Poa* could not tolerate large numbers of larvae feeding on them for long periods.

O. ptunarra egg incubation periods have varied two-fold between studies (Couchman 1953; Anderson 2001b), these results suggest a high variability in the incubation period, which has shown to be related to temperature in some butterflies belonging to the Satyrinae genera (Kitching *et al.* 1999).

It is generally accepted that *O. ptunarra* is predominately a monandrous species (Anderson 2001b), however the discovery of two spermatophores in one female infers that multiple matings may sometimes occur. This finding is most likely to have been the result of two close consecutive matings contributing to a single reproductive event, rather than two separate reproductive events. Considering weather limitations on *O. ptunarra*'s flight activity (Anderson 2001b), only one successful ovarian cycle would generally be possible, resulting in a single reproductive event.

The two spermatophores found in a female may have resulted in all the offspring arising from a single spermatophore, or a combination from both, depending on the timing of the depositions. Benefits from both of these situations can be identified. Firstly, if all offspring had arisen from the first spermatophore, then the second may have still served a nutritive purpose. There is a growing body of evidence to suggest that polyandrous insects use nutrients in the male ejaculates to increase fecundity (Rutowski 1982, 1984, 1985; Rutowski & Gilchrist 1987; Rutowski *et al.* 1987; Dickinson & Rutowski 1989; Rutowski *et al.* 1989; Rutowski 1991, 1998; Wickman & Rutowski 1999; Wedell *et al.* 2002). It is however difficult to directly apply this to the case of the female in this study as the total number of eggs she laid (4) was less then most other females which had received single spermatophores. A possible explanation for this may be related to the polygynous nature of *O. ptunarra*; the two males that mated with the female, may have had reduced sperm counts and/or reduced nutritive content due to their multiple previous matings (Rutowski *et al.* 1987). Alternatively, in species such as *O. ptunarra*, which can only oviposit in suitable weather, multiple matings may jeopardize the limited time available to oviposit, result in fewer eggs laid (Anderson 2001b). In addition, Wickman & Rutowski (1999) suggest low population densities of a butterfly species may reduce the chance of multiple matings.

Secondly, if both the spermatophores were deposited closely enough together to allow for the contribution of genes from both males to the offspring, competitive and genetic benefits may arise. The greater volume of sperm may have created an environment of enhanced

competition, thus ensuring only the fittest sperm fertilize the ovum. Furthermore, genetic variability is increased with sperm being deposited from two individual males. Both situations may serve to increase the overall fitness of the female's offspring (Yasui 1998).

An even more evident and visible effect of polyandry versus monandary is sexual dimorphism. Since mating is much more costly for males than females, the males of polyandrous species are proportionally larger then females, relative to males in monandrous species (Kaitala & Wiklund 1994). Monandary emerges as a potential limiting factor for *O. ptunarra* fecundity, together with a single ovarian cycle.

O. ptunarra appears to be a protandrous species. Protandry probably evolved as a sexual selection strategy to maximise number of mating in males (Kleckner *et al.* 1995; Zonneveld 1996; Carvalho *et al.* 1998). This appears to be the case in *O. ptunarra.* Protandry has been associated with seasonal environments where overlap between generations is absent or reduced and can be facultative. Nylin *et al.* (1993) comparative studies of five different populations of *Parage aegeria* from central and south Sweden, England, Spain, and the island of Madeira found that only the three northernmost populations, where cool temperate conditions occurred exhibited protandry.

4.1.3 Egg size and latitude

Garcia-Barros (1994) demonstrated that within Satyrinae egg size increases with latitude. When the effects of latitude are removed the relationship between egg and female size becomes more evident. For example small egg size is related to long preoviposition (Garcia-Barros 1994). Garcia-Barros (2000) also determined that butterfly size increases in relation to the mean annual temperature of its range. The *O. ptunarra* habitat range can be seen as a stressful environment for the butterflies (Anderson 2001b). Compared with other *Oreixenica* species, *O. ptunarra* has the smallest wing span and is amongst largest egg size, and flies in the coldest environment.

In *Oreixenica* in general and *O. ptunarra* in particular, the smaller body size is also consistent with latitude effects. Small body size can be explained by the latitude effects seen in southern hemisphere butterflies (Barlow 1994; Hawkins & Lawton 1995). Larger taxa have an advantage over smaller taxa in use of resources when stable climates, but larger size is more of a liability in fluctuating climates.

4.2 *Larvae*

4.2.1 Larval phenology

The life cycles of the temperate zone southeast Australian Satyrinae are influenced by seasonal climates and are typically univoltine. In *Oreixenica,* especially *O. ptunarra* it is still not clear how the species spends winter, nor is it clear if the larvae feed during winter and early spring when the food plants are often covered with snow. Typical *H. merope* larvae in southern Australia develop very slowly during autumn and winter, taking 6-7 months to reach pupation (James 1999). It is suspected that *O. ptunarra* diapauses as early instar larvae, then emerge to feed during the late spring and through into the summer. This strategy is likely to be linked to the phenology of the food plants. For example, the larvae of *Oreixenica* feed on the nutritious new spring growth of *Poa* species.

The observed feeding delay in *O. ptunarra* of a few hours after hatching is consistent with other Satyrinae. James (1999) observed feeding delays of up to two hours in larvae of *H. merope merope*. No parallel was found in the literature to the observed surface grazing of *O. ptunarra*, or its progressively deeper feeding with time. This may be a result of the strengthening of its mouthparts with increased age, or due to an increased appetite resulting from growth. Feeding preference for *Poa hiemata* may be due to co-evolution of these particular *O. ptunarra* individuals with this *Poa* at their source resulting in the larvae responding best to familiar *Poa.*

In contrast to Neyland (1992) *O. ptunarra* larvae were found to be feeding in the lab during the day as well as the night. This may be a function of altered photoperiod times and temperatures. The periodic use of artificial lights may have disturbed their natural feeding patterns and the indoor environment in which the larvae were kept did not fluctuate to the extreme temperatures to which they are adapted. However, there was no obvious difference in the feeding behaviour between the larvae reared in environment cabinets programmed to mirror field conditions and those reared in the standard laboratory environment. Furthermore, consistent handling of the larvae may have further disturbed their feeding patterns. Consistent with other observations (Couchman 1953; Neyland 1992, 1993; Bell 1998; Braby 2000; Anderson 2001b; Bell 2002) mature *O. ptunarra* larvae were not observed feeding until after dusk.

4.2.2 Comparison with larval fauna

There have been a few detailed descriptions of Satyrini larvae published and almost all are limited to the tropical and neotropical fauna (Braby 1994a; Murray 2001; Freitas 2002; Murray 2003). Satyrinae larvae are characterised as being green or brown; smooth but covered with dense, usually very short, setae which may give a rough appearance; body is long and cylindrical often broader near middle; anal segment has a prominent forked posterior projection; head often has a pair of prominent dorsolateral projections or horns (Braby 2000). *O. ptunarra* larvae on the whole are consistent with other known Satyrinae larvae; i.e. anal segment has a prominent forked posterior projections, epidermis is smooth, covered with numerous secondary setae, however *O. ptunarra* larvae do not have dorsolateral projections or horns which in many Satyrinae is a reliable guide to identification of the species (Braby 2000).

4.2.3 Food plants

Food plant records are fairly comprehensive for most southeast Australian Satyrinae, and lists of known host are supplied in Braby (2000). It appears from the records, that most of these species are oligophagous with a few interesting quirks. *Oreixenica* with the exception of *O. kershawi* feed exclusively on *Poa* species. *O. kershawi* has adapted to also feed on *Tetrarrhena juncea* Wire Grass (McCubbin 1971). *A. hobartia*'s major food source is *Lolium perenne* Perennial Ryegrass, an introduced species (Couchman & Couchman 1978). Natural food plants have not been recorded for *A. hobartia* (Braby 2000), however native grasses such as *Poa labillardieri* and *Austrodonthonia* species are considered to be the native food source (Prince 1988; Braby 2000). *N. leprea* is monophagous feeding solely on *Uncinia tenella* (Cyperaceae) (Couchman 1948; Couchman & Couchman 1978). *G. klugii* is polyphagous, feeding openly during the daytime, unlike *G. acanthi* on both native: *Austrostipa flavescens, Joycea pallida, Poa labillardieri, Poa morrisii, Poa tenera, Themeda triandra;* and introduced species: *Brachypodium distachyon, Ehrharta calycina, Vulpia* species (Braby 2000). The morphology of *G. klugii* larva makes it difficult to detect even though it is fully exposed on the foliage of the grass tussock. *H. cordace* and *H. penelope* are both oligophagous species to varying extents. *H. cordace* feeds mainly on *Carex appressa* although it will feed in captivity on common grasses (Common & Waterhouse 1981). *H. penelope* feeds on *Austrodanthonia penicillata, A. pilosa Poa sp. Themeda triandra* (Braby 2000). *H. merope* is another polyphagous species feeding on a wide variety of native speceies: *Cynodon dactylon, Micolaena stipoides, Poa sp., Themeda triandra*; and introduced species: *Brachypodium distachyon, Bromus cathartiens, Ehrharta erecta* (Braby 2000).

4.3 *Pupae*

Nymphalidae pupae are normally suspended by the cremaster, although some times lie unattached on ground. In contrast to the Papilionidae, Pieridae, and Lycaenidae, it is never provided with a central silken girdle (Braby 2000). Girdled pupae, that are attached to their sites by a silken girdle around the thorax and an abdominal cremaster which is fixed to a silken pad by hooked seate are found in all Pieridae, and most Papilionidae and many Lycaenidae. In contrast, suspended pupae are attached to the substrate by the cremaster alone and occur in all Nymphalidae with the exception of Satyrinae, in which some species pupate in slight cocoons or cells. Girdled and suspended pupae face the difficulty of having to transfer their hold to the substrate from the anal prolegs of the larvae. Pupae lying free in cocoons face no problems slipping off completely the larval exuvia during moulting (Starnecker 1999).

Satyrinae pupae are either green or brown in colour and may be fairly stout, rounded and smooth or more slender and somewhat angular. They are usually suspended head downwards by the cremaster, on the food plant or sometimes on nearby vegetation or beneath logs. In three *Oreixenica* species (*O. ptunarra* , *O. latialis* and *O. orichora*) and three *Heteronympha* species (*H. merope*, *H. penelope* and *H paradelpha*) the pupa lies unattached on the ground, usually beneath debris at the base of the larval food plant (Braby 2000).

Nymphalinae pupae usually are suspended head downwards by the cremaster, often some distance away from the food plant. These pupae generally have angular projections at the anterior end, and the abdomen often has a series of dorsolateral spines or short pointed processes (Braby 2000).

Starnecker (1999) suggests that in Satyrinae pupa lying free on the ground or unattached is likely to be a secondary character; it is interesting to note that all the species which Starnecker (1999) highlighted as having unattached pupae fly in cool temperate extending into alpine environments. The *Oreixenica*; *O. ptunarra, O. latialis* and *O. orichora* are the dominant alpine species within the genus, all with unattached pupa. The association with cold environments is not universally supported within the *Heteronympha* as the ubiquitous *H. merope* also has unattached pupae.

Chapter 4

Molecular relationships of the Temperate Zone Southeast Australian Satyrinae

1 INTRODUCTION

In a study into the phylogeny of the Nymphalidae based on cladistic analysis of characters from all life stages, Freitas & Brown (2004) found that all major groups within Nymphalidae appeared as monophyletic except Biblidinae and Satyrinae which appeared as paraphyletic. Peña *et al.* (2006) in a study into the higher level phylogeny of the Satyrinae found them to be a polyphyletic grouping. Peña *et al.* (2006) emphasised the need for more extensive sampling of the genera within the tribes and subtribes of Satyrinae to better test the monophyly of the subfamily. One putative clade that was not satisfactorily resolved by Peña *et al.* (2006) consisted of genera from the subtribe Hypocystina (Miller 1968). This study explores the molecular relationships of the temperate zone southeast Australian Satyrinae generally considered to be the members of the tribe Hypocystina (Miller 1968; Brower 2000; Wahlberg *et al.* 2005b; Peña *et al.* 2006), and considers implications for the phylogeny of this group.

2 MATERIALS AND METHODS

2.1 *Taxa Examined*

The species analysed and their provenances are listed in Appendix 1. Species were chosen based on geographical range to maximise phenotypic diversity and on the availability of immature and adult morphological characters. All individuals were stored frozen at -18°C.

2.2 *Gene Fragments*

Due to its hypothesized rapid evolutionary rate Cytochrome Oxidase Subunit 1 gene (CO1), from the mitochondrial genome, has been very useful for uncovering relationships among Lepidoptera at the generic and species level; however, it has been widely used in phylogenetic studies to resolve divergences at the family, as well as the genus and species level (Brown *et al.* 1994; Sperling & Hickey 1994; Sperling *et al.* 1995; Sperling *et al.* 1999; Wahlberg & Zimmermann 2000; Nice & Shapiro 2001; Eastwood & Hughes 2003; Zakharov *et al.* 2004b; Bucheli & Wenzel 2005; Whinnett *et*

al. 2005; Chew & Watt 2006; Zhang *et al.* 2007; Wheat & Watt 2008). The CO1 gene fragment has been used to estimate divergence times up to 65 million years ago (Zakharov *et al.* 2004a).

Elongate Factor 1α (EF-1α) is a highly conserved protein-coding nuclear gene, which has traditionally been considered to be more informative for resolving deeper divergences (Mitchell *et al.* 1997), however it also appears to be useful in resolving relatively recent divergences. EF-1α has been used extensively in inter-generic studies in the Lepidoptera (Cho *et al.* 1995; Mitchell *et al.* 1997; Reed & Sperling 1999; Vane Wright *et al.* 1999; Caterino *et al.* 2001; Monteiro & Pierce 2001; Rubinoff & Sperling 2002; Wahlberg *et al.* 2005a; Braby & Pierce 2007). The *EF-1α* enzyme participates in GTP-dependent binding of tRNA's to the ribosome during translation (Danforth & Ji 1998). Cho *et al.* (1995), Mitchell *et al.* (1997) and more recently Nazari *et al* (2007) demonstrated the informative nature of EF-1α in phylogenetic inferences up to divergences of 65 million years ago.

The *Wingless* gene, from the nuclear genome has been used to investigate phylogenetic relationships at both higher and lower divergence levels within the Lepidoptera (Brower & Egan 1997; Brower & DeSalle 1998; Brower 2000; Campbell *et al.* 2000; Wahlberg *et al.* 2003b; Wahlberg *et al.* 2005a; Braby *et al.* 2006; Brower *et al.* 2006; Simonsen *et al.* 2006; Weingartner *et al.* 2006; Nazari *et al.* 2007). Primarily due to its uniform based composition, the Wingless gene appears to become saturated more slowly than mitochondrial DNA (mtDNA) (Brower & DeSalle 1998). The in-formativeness of the Wingless genes fragment has been demonstrated for divergence times up to 60 million years (Brower & DeSalle 1998).

The use of these three genes enables the comparison of phylogenies derived from different mechanisms as the evolution of RNA genes should be considered differently from that of protein-coding genes; rRNA genes are constrained by structural motifs whereas protein-coding genes are limited by frame shifts, the effects of amino acid substitution or codon translation requirements (Kjer 1995; Brower & DeSalle 1998).

2.3 *DNA Extraction*

DNA was extracted from specimens collected fresh from the field and frozen immediately at -20 °C and specimens preserved in 96% ethanol. Abdomens and other remains were stored at -20 °C as tissue vouchers and the wings were laid out in a display book, to facilitate species identification.

The DNA was extracted using a CTAB Extraction Protocol modified from Grewe *et al.* (1994) and Ausubel *et al.* (2005) as detailed in Appendix 4. Extracted DNA samples were stored at -20 °C until further use.

2.4 *Polymerase Chain Reaction (PCR)*

PCR reactions were carried out in 0.2mL microcentrifuge tubes with a total reaction volume of 50µL using a protocol adapted from Palumbi *et al.* (1996). PCR reaction reagents and their final concentrations are detailed in Table 4.2. PCR conditions are outlined in Table 4.1.

Table 4.1 PCR conditions

CO1	**EF-1α and Wingless**
1. 94°C denaturation for 3 minutes	1. 95°C denaturation for 2 minutes
2. 94°C denaturation for 30 seconds	2. 94°C denaturation for 1 minute
3. 40°C annealing for 30 seconds	3. 50°C annealing for 1 minute
4. 72°C extension for 45 seconds	4. 72°C extension for 90 seconds
5. go to 2, 35 times	5. go to 2, 35 times
6. 72°C final extension step for 5 minutes	6. 72°C final extension step for 5 minutes
7. Hold at 11°C forever.	7. Hold at 11°C forever.

Standard submarine gel electrophoresis and ethidium bromide staining confirmed PCR amplification of each template. DNA was purified prior to sequencing using *MO BIO Laboratories Inc. Ultra Clean™ PCR Clean-Up™ Kit.*

Table 4.2 PCR reagents and final concentrations

PCR Reagents	Final Concentrations
Promega 10x Buffer	
NaCl	50mM
Tris. HCl (pH9)	10mM
Triton X	0.01%
Promega $MgCl_2$	2mM
Amresco dNTP's	0.25mM
GeneWorks HCO and LCO primers	0.2ρM/mL
New England Biolab BSA	0.1mg/mL
Promega Taq Polymerase	0.01 units/μL

2.5 *CO1, EF-1α and Wingless Primers*

Sequencing was undertaken for at least two replicates of two sample localities of each species, which were located where possible from the extremes of species distribution. 900 bp of CO1, 850 bp of EF-1α and 400 bp of Wingless were sequenced for each species. The primers for CO1: HCO 2198 (F) and LCO 1490 (R) are from Folmer *et al.* (1994); EF-1α F from Reed and Sperling (1999); EF-1α R from Caterino *et al* (2001) and Wingless from Brower and Desalle (1998).

HCO 2198 (F) 5'- TAA ACT TCA GGG TGA CCA AAA AAT CA -3'
LCO 1490 (R) 5'- GGT CAA CAA ATC ATA AAG ATA TTG G -3'

EF-1α F 5'- CGG ACA CGT CGA CTC CGG -3'
EF-1α R 5'- AAC CGT TTG AGA TTT GAC CAG GG -3'

LEP Wing 1 (F) 5'- GAR TGY AAR TGY CAY GGY ATG TCT GG -3'
LEP Wing 2 (R) 5'- ACT SCG CRC ACC ART GGA ATG TRC A -3'

Sequencing reactions were prepared using a modification of the *CEQ DTCS Quick-Start Kit*, Beckman Coulter, USA and the protocol detailed in Appendix 5. Both sense and anti-sense strands were sequenced using a Beckman Coulter, USA, *CEQ 8000 Genetic Analysis System, Automated Sequencer.*

2.6 *Sequence analysis and alignment*

The editing of CO1, EF-1α, and Wingless nucleotide sequences, contig assembly, consensus sequence calculations and manual alignment of consensus sequences were performed using *Sequencher 4.5* (Gene Codes Corp., Ann Arbor, MI). Sequences were then imported into Clustal X (Higgins & Sharp 1988; Higgins *et al.* 1996; Jeanmougin *et al.* 1998; Chenna *et al.* 2003) for multiple sequence alignment. Comparisons of multiple sequence alignment programmes found that Clustal X performed well compared to other alignment programmes such as *PileUp* and *Malign* (Thompson *et al.* 1994; Thompson *et al.* 1997; Jeanmougin *et al.* 1998; Thompson *et al.* 1999; Hickson *et al.* 2000; Larkin *et al.* 2007).

2.7 *Phylogenetic analysis*

All phylogenetic analyses were performed using *PAUP*4.0 beta Win* (Swofford 1993; 2002). Unweighted parsimony analyses were preformed on each DNA dataset (heuristic search, 10000 random addition sequences, TBR swapping) and consensus trees were then constructed if necessary.

DNA sequences that code for proteins or other functional molecules usually have variable rates of nucleotide substitutions among sites due to heterogeneous selection pressures. These differences in rate variations can influence evolutionary parameters such as the transition/transversion *rate ratio* (Yang *et al.* 1994). DNA substitution mutations are of two types. Transitions are the interchanges of purines (A↔G) or of pyrimdines (C↔T), which comprise bases of similar shapes. Transversions are interchanges between purines and pyrmidine bases, which require exchange of one-ring and two-ring structures. Although there are twice as many possible transversions, because of the molecular mechanisms by which they are generated, transition mutations occur at higher frequencies than transversions. The transition/transversion *rate ratio* is simply the instantaneous rate of transitions divided by the instantaneous rate of transversions. The transition/transversion *ratio* is the probability of any transition (over a single unit of time) divided by the probability of any transversion (over a single unit of time). The transition/transversion *ratio* involves the equilibrium base frequencies, whereas the transition/transversion *rate ratio* does not (PAUP Help 2003-09). The transition/transversion *ratio* was calculated using the HKY substitution model (Takahashi & Nei 2000; Piontkivska 2004).

Likelihood values can vary considerably according to whether the rate variation is corrected in the model and also the variability of rates among sites (Yang 1995). Each data set was analysed and phylogenies created using three different optimality criteria. The first analysis uses the criterion of maximum parsimony (MP). The second analysis uses the minimum evolution (ME) criterion in conjunction with LogDet/paralinear pairwise distances. The third analysis uses the maximum likelihood (ML) criterion in conjunction with the HKY-gamma substitution model. Estimates of the ratio (the transition/transversion ratio) parameter and the gamma shape parameter are obtained using the LogDet tree. Then, these two parameters are fixed at these estimated values for the duration of the heuristic search. It was shown by Yang (1995) that as long as trees are not "too wrong" parameter estimates are stable across tree topologies.

Each phylogeny method has individual weakness and strengths according to any inconsistencies in the data that may invalidate the assumptions of the particular model used.

Maximum parsimony can be misleading if there is too much heterogeneity in substitution rates among lineages. If at least two of the terminal branches are much longer then the internal branches, homoplasious changes on these longer branches can override the signal in the internal branch; the long edges attract in the underlying true phylogeny (Felsenstein 1978; Bergsten 2005; Philippe *et al.* 2005). Long branches are thought to affect MP methods more severely, but models based on methods such as Bayesian Inference (BI) and ML are not immune to the problem (Felsenstein 1978; Siddall 1998; Bergsten 2005; Philippe *et al.* 2005).

Minimum evolution using LogDet distances can be misleading if there is too much site-to-site rate heterogeneity, or if some of the pairwise distances are undefined (PAUP Help 2003-09).

Maximum likelihood under the HKY-gamma model can be misleading if parameters that are assumed to be constant across the phylogeny (such as the transition/transversion ratio or base frequencies) actually vary among lineages in the true phylogeny (PAUP Help 2003-09).

Finally a Kishino-Hasegawa test was conducted to see whether one tree was supported significantly less by the data than another tree. Obtaining trees with similar topologies using different analytical methods is considered to provide good evidence for the robustness of common clades and to ensure that the data do not suffer significantly from parameter heterogeneity (Chen *et al.* 2003).

It has been suggested that unless there is solid evidence that the third position codon really is misleading, they should not be treated so by default (Mats 1999). In insects the saturation of variable sites in mtDNA is aggravated by rather extreme A + T richness, typically around 70% overall, and approaching 90% at the third positions of codons (Liu & Beckenbach 1992; Brower & DeSalle 1998) The third position codons were down weighted, then the data was reanalysed with three arbitrary weighting schemes (3:5:1, 2:3:1, and 2:2:1) in order to determine the effect of down weighting the third nucleotide position characters (Meyer 1994). This had no significant effect on the number of most parsimonious trees found by the analysis or on the consistency index. Bootstrap values were very similar and the trees produced by the different weighting regimes were almost identical to the unweighted tree.

Bootstrap support for individual clades in the maximum parsimony and the minimum evolution analyses were estimated by performing bootstrap analyses (10000 replicates, fast heuristic search, stepwise addition, TBR swapping, maxtrees not limited). In all trees, only bootstrap values over 50% are shown as this confidence level is sufficient as a means of testing that the hypothesized clades are, on average, least likely to be incorrect (Rodrigo 1993). The trees were rooted using the outgroup method. In this method the ingroup and outgroup are included in a simultaneous and unconstrained analysis (Nixon & Carpenter 1993; 1996).

2.8 *Age of Divergences*

In order to estimate the approximate age of divergences between taxa it was necessary to test for evolutionary rate heterogeneity among the sequences before applying a molecular clock to the data. This test was conducted for all single genes and the combined data. The optimum substitution models were first determined using the ModelTest, version 3.7 (Posada & Crandall 1998; Posada 2006). Once the appropriate likelihood model had been selected by ModelTest, a test was conducted for a molecular clock. MP consensus tree topologies for each data set were constructed and the likelihood values with and without the assumption of rate constancy were computed. The likelihood-ratio test statistic is calculated as twice the difference between the log-likelihood scores of the two models (Felsenstein 1988). The significance of the test is calculated by comparing a chi-square distribution with n-2 degrees of freedom (n=number of taxa).

Plate 4 *O. ptunarra* male, Pikes Hill March 2006

3 RESULTS

3.1 *CO1*

Alignment of the CO1 data resulted in 650 characters, of which 162 were parsimony informative. The data matrix is presented in Appendix 6 CO1, bootstrap consensus tree in Figure 4.1 and the Log/Det sequence divergence values in Appendix 7 CO1.

The rates of nucleotide substitution between genera ranged from 9.89% *O. latialis* and *H. penelope*, to 12.84% between *H. cordace* and *G. klugii*. This is similar divergence rate reported in other Nymphalidae studies e.g. Zhang *et al* (2007).

The intra-generic rate of nucleotide substitution between species ranged from 10.59% for *H. cordace* and *H. merope* to 1.13% between *O. ptunarra* and *O. latialis*. The rate of nucleotide substitution between the *Heteronympha* species is a little higher than that observed in other Lepidoptera but the divergence range between the *Oreixenica* species is similar to the divergence rate observed in other Lepidoptera (Lushai *et al.* 2003).

The largest and smallest distance was between the outgroup species and ingroup species; 8.32% between *V. kershawi* and *G. klugii* to 13.01% between *V. kershawi* and *O. lathoniella*. These rates are comparable to those reported in other studies of Lepidoptera (Lushai *et al.* 2003). The approximate matching of the distance between the outgroup and ingroup with that of the greatest inter-generic distance is consistent with saturation at high taxonomic levels or with rapid radiation at the generic level.

The average base frequencies for CO1 were A = 37.94%, C = 15.28%, G = 16.61%, and T = 30.17%. These are similar to those reported for the nymphalid subfamily Nymphalinae (Wahlberg *et al.* 2005b). There was no significant differences in base frequencies between taxa ($\chi^2 = 11.43$, df= 69 p= 1.0000).

Maximum parsimony (MP) analysis using equal weights produced seven shortest trees of length 455 (CI = 0.545, RI = 0.715). The strict consensus tree is presented in Figure A8.1. Minimum evolution (ME) analysis resulted three short trees of length 458 (CI = 0.541, RI = 0.711). The strict consensus tree is detailed in Figure A8.2. Maximum likelihood (ML) analysis resulted in one tree of length 458 (CI = 0.541,

RI = 0.711) tree detailed in Figure A8.3. The tree parameters obtained empirically by the ML analysis were as follows:

Ti/tv:		
	Expected ratio:	1.55
	Kappa	3.52
Shape parameter (alpha)		0.167
Minus log Likelihood (-In L)		2974.2

Downweighting of third position nucleotides resulted in one shortest tree of length 523 (CI = 0.581, RI = 0.746) (Figure A8.4).

Analysis of the transition/transversion *ratio* resulted in one shortest tree of length 2310 (CI = 0.501, RI = 0.738) (Figure A8.5).

The trees produced by the analysis of the CO1 sequence data are poorly resolved at deep divergences but show good resolution at some of the more recent divergences. This at first seems contradictory given the relatively conserved nature of this gene. The reasons for this topology are most likely due to multiple substitutions obscuring synapomorphies at deep divergences or the homoplasies have been diluted by the data. A similar pattern was observed by Rubinoff & Sperling (2002) in the Saturniidae genus *Hemileuca.*

All CO1 sequence analysis could be rooted with *J. villida* as a monophyletic outgroup. However many trees could not be rooted with *V. kershawi* as a monophyletic outgroup. *V. kershawi* was frequently placed as a sister to *G. klugii.*

3.2 *EF-1α*

Alignment of the EF-1α data resulted in 850 characters, of which 185 were parsimony informative, the data matrix is presented in Appendix 6 EF-1α, bootstrap consensus tree in Figure 4.2 and the Log/Det sequence divergence values in Appendix 7 EF-1α.

The rates of nucleotide substitution between genera ranged from 7.73% between *A. hobartia* and *G. klugii* to 13.00% between *H. cordace* and *O. lathoniella*. This rate is comparable to divergence rates in other Papilionoidae (Morinaka *et al.* 2002).

The intra-generic rate of nucleotide substitution between species ranged from 6.34% for *H. cordace* and *H. penelope* to 0.001% between *O. ptunarra* and *O. latialis*. This range is broader than rates observed in Heliothinae moths (Cho *et al.* 1995).

The largest and smallest distance between the outgroup species and ingroup species was 10.46% *J. villida* and *A. hobartia* to 13.52% between *V. kershawi* and *N. leprea*. This is similar to rates observed in Geometridae (Young 2006b). The approximate matching of the distance between the outgroup and ingroup with that of the greatest inter-generic distance is consistent with saturation at high taxonomic levels or with rapid radiation at the generic level.

The average base frequencies for EF-1α were A = 37.94%, C = 15.28%, G = 16.60%, and T = 30.18%. These are higher for A and T and lower for C and G to those reported for the other Papilionoidae (Zakharov *et al.* 2004a; Mallarino *et al.* 2005; Wahlberg *et al.* 2005b). There was no significant differences in base frequencies between taxa (χ^2 = 11.43, df= 69 p=1.0000).

Maximum parsimony (MP) analysis using equal weights produced two shortest trees of length 442 (CI = 0.658, RI = 0.826). The strict consensus of these trees is presented in Figure A8.6. Minimum evolution (ME) analysis resulted in nine short trees of length 443 (CI = 0.657, RI = 0.825). The strict consensus tree is detailed in Figure A8.7. Maximum likelihood (ML) analysis resulted in one tree of length 444 (CI = 0.655, RI = 0.824) tree detailed in Figure A8.8. The tree parameters obtained empirically by the ML analysis were as follows:

Ti/tv:

Expected ratio:	2.27
Kappa	4.57
Shape parameter (alpha)	0.169
Minus log Likelihood (-In L)	3391.25

Downweighting of third position nucleotides resulted in two short trees of length 566 (CI = 0.663, RI = 0.820); strict consensus tree presented in Figure A8.9.

Analysis of the transition/transversion *ratio* resulted in one shortest tree of length 1849 (CI = 0.688, RI = 0.834) (Figure A8.10).

The trees produced by the analysis of the EF-1α sequence data are well resolved at all levels detailing the Satyrinae as a monophyletic group rooted with *V. kershawi* and *J. villida* as outgroup.

3.3 *Wingless*

Alignment of the Wingless data resulted in 500 characters, of which 105 were parsimony informative, the data matrix is presented in Appendix 6 Wingless, bootstrap consensus tree in Figure 4.3 and the Log/Det sequence divergence values in Appendix 7 Wingless.

The rates of nucleotide substitution between genera ranged from 5.45% *A. hobartia* and *N. leprea* to 10.21% between *H. merope* and *O. lathoniella.* These rates are similar to those reported for other Lepidoptera studies using the Wingless gene fragment (Brower & DeSalle 1998).

The intra-generic rate of nucleotide substitution between species ranged from 4.98% *H. cordace* and *H. merope* to 2.40% between *O. ptunarra* and *O. lathoniella.* This rate is similar to divergence rates in nymphalid butterflies (Brower & DeSalle 1998).

The largest and smallest distance between the outgroup species and ingroup species was 13.33% *J. villida* and *N. leprea* to 16.86% between *V. kershawi* and *G. klugii.* These divergence rates are higher than Brower & DeSalle (1998) reported between nymphalide and *Pieris.*

The average base frequencies for Wingless were A = 21.74%, C = 28.19%, G = 31.03%, and T = 19.04%. These are similar to those reported for Nymphalinae (Wahlberg *et al.* 2005b). There was no significant differences in base frequencies between taxa ($\chi^2 = 30.17$, df = 63 p= 0.9999).

Maximum parsimony (MP) analysis using equal weights produced seven shortest trees of length 196 (CI = 0.776, RI = 0.883) strict consensus of these trees is presented in Figure A8.11. Minimum evolution (ME) analysis resulted nine short trees of length 196 (CI = 0.776, RI = 0.883). The strict consensus tree of these trees is detailed in Figure A8.12. Maximum likelihood (ML) analysis resulted in one tree of length 196 (CI = 0.776, RI = 0.883) tree detailed in Figure A8.13. The tree parameters obtained empirically by the ML analysis were as follows:

Ti/tv:

Expected ratio:	2.45
Kappa	5.03
Shape parameter (alpha)	0.20
Minus log Likelihood (-In L)	1598.58

Downweighting of third position nucleotides resulted in two short trees of length 377 (CI = 0.764, RI = 0.885). Strict consensus tree is presented in Figure A8.14.

Analysis of the transition/transversion *ratio* resulted in two short trees of length 755 (CI = 0.785, RI = 0.896); strict consensus tree presented in Figure A8.15.

It was not possible to extract a viable Wingless sequence for *H. penelope*, *O. latialis*, *O. correae*, or *O. kershawi*. The trees produced by the analysis of the Wingless sequence data are moderately well resolved detailing the Satyrinae as a monophyletic group rooted with *V. kershawi* and *J. villida* as outgroup.

3.4 *Combined Gene Fragment*

Combining data sets can give misleading results if there is heterogeneity among data sets (de Queiroz *et al.* 1995; Caterino *et al.* 2000). The Incongruence Length Difference Test (ILD) (Farris *et al.* 1994) can distinguish when the case to combine the molecular data will improve phylogenetic accuracy (Farris *et al.* 1995; Cunningham 1997; Hipp *et al.* 2004). The three datasets when combined were found to be heterogeneous by the ILD ($P = 0.01$). This may be due to the proportionally low number of informative sites in the data sets (CO1 162/650; EF-1α 185/850; Wing 105/500). There are also discrepancies between the datasets, two scenarios in which the ILD is considered to be unreliable (Cunningham 1997; Dolphin *et al.* 2000; Darlu & Lecointre 2002; Dowton & Austin 2002). Due to doubts as to the reliability of the ILD (Cunningham 1997; Dolphin *et al.* 2000; Darlu & Lecointre 2002; Dowton & Austin 2002), the data were combined for further analysis to test the effect on phylogeny reconstruction.

Alignment of the combined data resulted in 2000 characters, of which 452 were parsimony informative. The Log/Det sequence divergence values in Appendix 7 Combined and the bootstrap consensus tree in Figure 4.4.

The rates of nucleotide substitution between genera ranged from 8.25% *A. hobartia* and *H. cordace* to 11.91% between *H. cordace* and *O. latialis*.

The intra-generic rate of nucleotide substitution between species ranged from 0.50% *O. ptunarra* and *O. latialis* to 7.38% between *H. cordace* and *H. merope.*

The largest and smallest distance between the outgroup species and ingroup species was 11.38% *V. kershawi* and *H. penelope* to 13.45% between *V. kershawi* and *H. cordace.*

The average base frequencies for combined were A = 27.26%, C = 22.85%, G = 24.54%, and T = 25.35%. There was no significant differences in base frequencies between taxa ($\chi^2 = 45.55$, df = 69 p= 0.9869).

Maximum parsimony (MP) analysis using equal weights produced two shortest trees of length 1113 (CI = 0.621, RI = 0.782). The strict consensus of these trees is presented in Figure A8.16. Minimum evolution (ME) analysis resulted two short trees of length

1122 (CI = 0.616, RI = 0.778). The strict consensus tree of these trees is detailed in Figure A8.17. Maximum likelihood (ML) analysis resulted in one tree of length 1113 (CI = 0.621, RI = 0.782) tree detailed in Figure A8.18. The tree parameters obtained empirically by the ML analysis were as follows:

Ti/tv:	
Expected ratio:	1.72
Kappa	3.44
Shape parameter (alpha)	0.18
Minus log Likelihood (-In L)	8264.86

Downweighting of third position nucleotides resulted in six short trees of length 1477 (CI = 0.638, RI = 0.796). Strict consensus tree is presented in Figure A8.19.

Analysis of the transition/transversion *ratio* resulted one shortest tree of length 5002 (CI = 0.604, RI = 0.787); strict consensus tree presented in Figure A8.20.

The trees produced by the analysis of the combined sequence data are well resolved at all levels detailing the Satyrinae as a monophyletic group rooted with *V. kershawi* and *J. villida* as outgroup.

3.5 *Age of Divergences*

Recommended ModelTest (Posada & Crandall 1998) likelihood models are detailed in Table 4.3. When the two criteria choose different models the likelihood ratio test results were used. Testing for a molecular clock resulted in significant *p*-values which indicated that the clock was rejected. Thus, age of divergence should be estimated using a relaxed molecular clock model (Posada & Crandall 1998; Posada 2006).

Table 4.3 ModelTest (Posada & Crandall 1998) likelihood models

	CO1	***EF-1α****		***Wingless****		***Combined***
Recommended Model	GTR+I+G	GTR+I	**TrNef+G**	TrN+I+G	**TrNef+G**	GTR+I+G
-ln likelihood values with molecular clock	3037.57	3409.75	**3415.60**	1624.64	**1633.65**	8235.44
-ln likelihood values without molecular clock	2914.56	3364.18	**3370.17**	1592.95	**1603.71**	8179.99
LRT	246.04	91.15	**90.85**	63.43	**59.88**	110.90
df *(n taxa – 2)*	22	22		22		22
p-value*	<0.001	<0.001		<0.001		<0.001

*Likelihood ratio test results in bold.

**Significant *p*-values indicate that the molecular clock is rejected.

Fossil evidence shows that both homoneurous and heteroneurous ancestors of modern-day lepidopteran groups were present and widely distributed in Gondwana (Common & Waterhouse 1981; Braby 2000). It is suggested from the few satyrine fossils that are known, that by the Oligocene, satyrines had become well established (Murray & Prowell 2005). The earliest known satyrine, an undescribed species near the tribe Elyminiini, dates from the lower middle Eocene, 48–51 mya (Durden & Rose 1978). A fossil ancestor of *Vanessa* has been found in the *Florissant Lake Bed Shales* of Colorado dated to approximately 35 mya (Miller & Brown 1989; Emmel *et al.* 1992). This age has been used to estimate minimum divergence times (Appendix 7). Table 4.4 details approximate age of divergence for each species calculated for each gene fragment, the combined sequence and an average divergence age.

These estimates are likely to be shorter than actual ages for three reasons. First, fossil date estimation is not perfect and usually provides only an indication of the probability that species arose in some interval of time. Second, the fossil age may be younger than the actual first appearance of *Vanessa*. Finally, sequence divergence values may be underestimated due to saturation at nucleotide substitution sites.

Table 4.4 Approximate age of divergence for each species (mya).

	CO1	EF-1α	Wing	Combined	Average
A. hobartia	31.30	31.14	29.95	30.90	30.82
G. klugii	32.09	31.03	29.10	30.95	30.79
H. cordace c	30.94	31.09	29.24	30.60	30.47
H. cordace k	30.83	30.47	29.24	30.29	30.21
H. cordace l	30.78	31.00	29.10	30.47	30.34
H. merope	31.29	31.35	28.89	30.74	30.57
H. penelope	30.67	31.22		31.02	30.97
J. villida	30.78	32.16	32.31	31.75	31.75
N. leprea e	30.74	30.35	30.33	30.47	30.47
N. leprea l	30.67	30.27	30.33	30.41	30.42
O. correae	31.12	30.74		30.93	30.93
O. kershawi	30.52	30.83		30.72	30.69
O. lathoniella	30.44	30.75	29.70	30.37	30.32
O. latialis	31.07	30.57		30.81	30.82
O. orichora	31.08	30.79	29.41	30.55	30.46
O. ptunarra	30.90	30.57	29.54	30.43	30.36
O. ptunarra (NW)	30.85	30.57	29.56	30.41	30.35
V kershawi	35.00	35.00	35.00	35.00	35.00

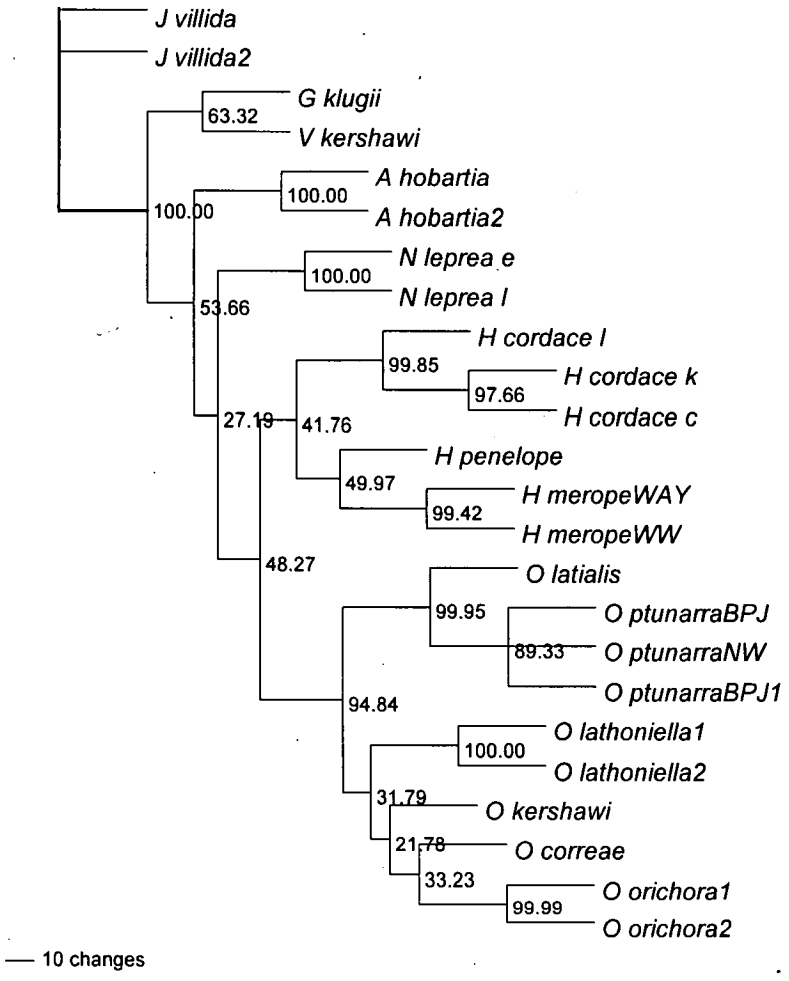


Figure 4.1 Bootstrap Consensus Tree CO1
(heuristic search, 10,000 replicates, values >50, optimality criterion = parsimony)
Percentage bootstrap values are indicated

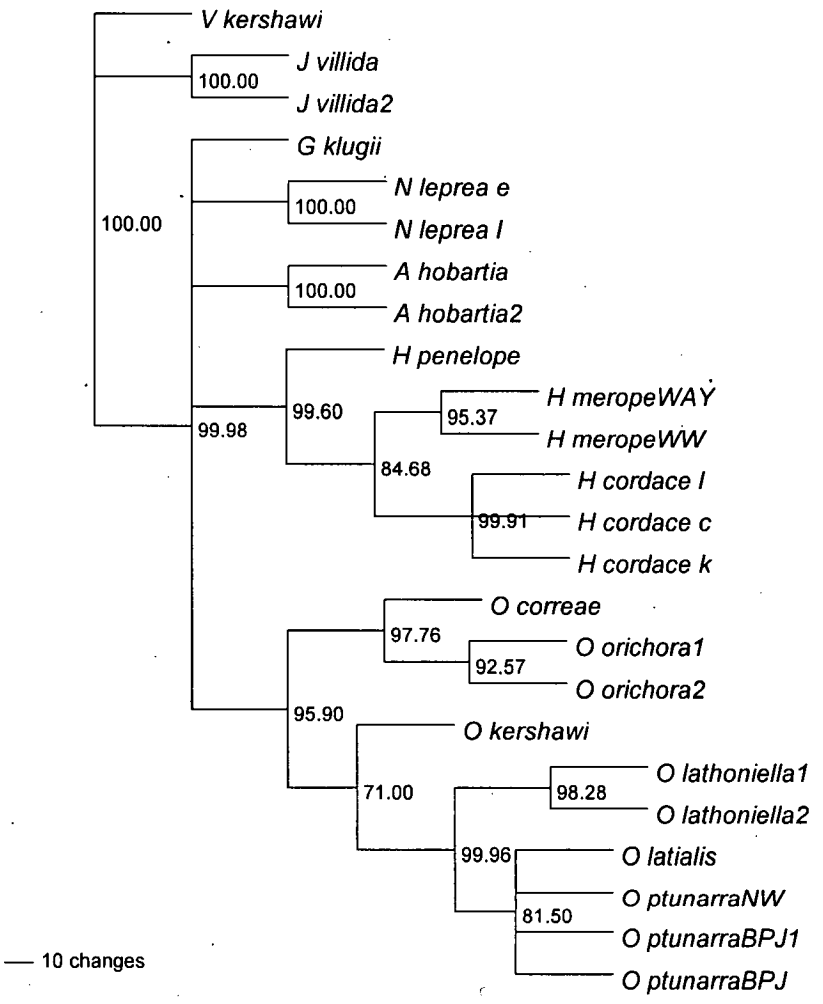


Figure 4.2 Bootstrap Consensus Tree EF-1α
(heuristic search, 10,000 replicates, values >50, optimality criterion = parsimony)
Percentage bootstrap values are indicated

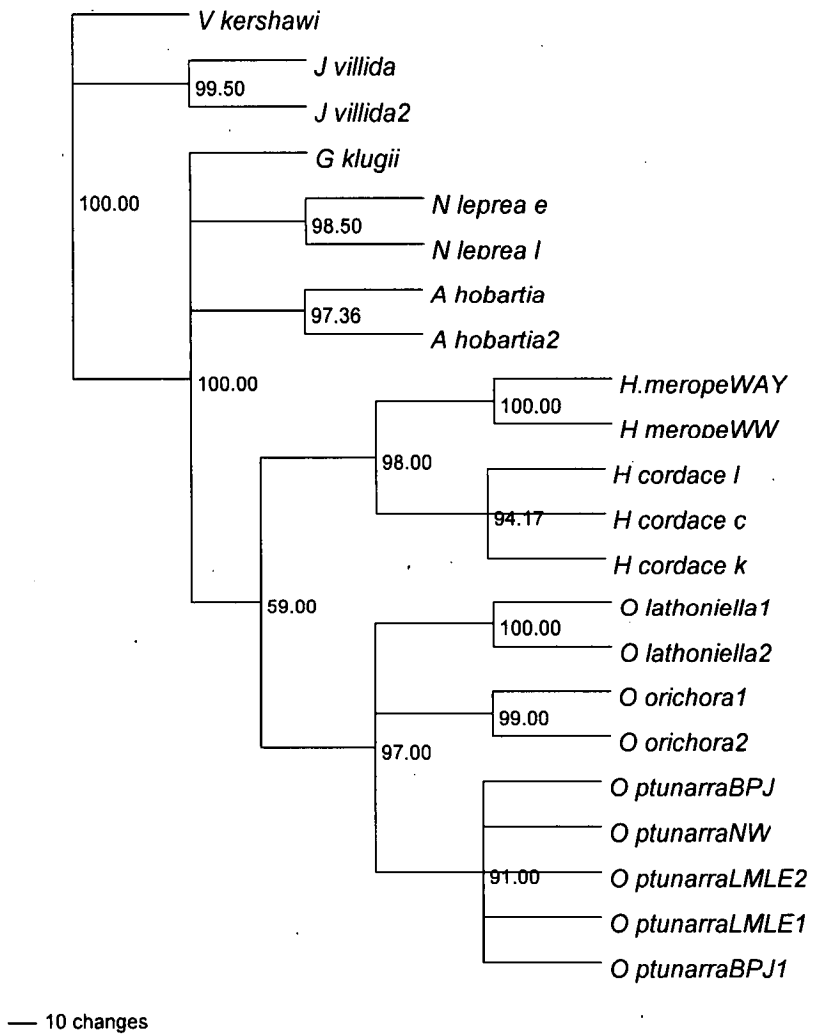


Figure 4.3 Bootstrap Consensus Tree Wingless
(heuristic search, 10,000 replicates, values >50, optimality criterion = parsimony)
Percentage bootstrap values are indicated

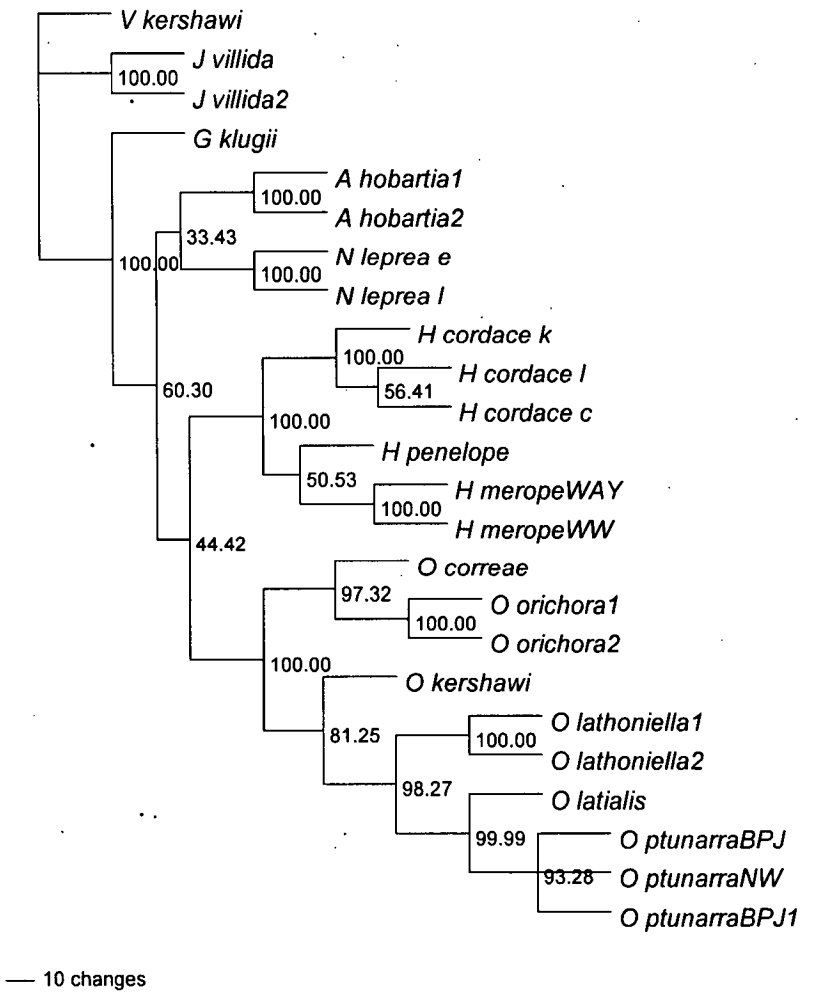


Figure 4.4 Bootstrap Consensus Combined Gene Fragments
(heuristic search, 10,000 replicates, values >50, optimality criterion = parsimony)
Percentage bootstrap values are indicated

4 DISCUSSION

This is the first comprehensive phylogenetic analysis of the relationships within the Southeast Australian Satyrinae to use molecular data. The study by Peña *et al.* (2006) only included four southern hemisphere temperate zone species: *G. klugii*, *H. merope*, *N. leprea* and *O. lathoniella.* In this study I have been able to identify clades that are well supported by three gene regions and are stable when subjected to varied character state analysis.

4.1 *CO1*

Similar phylogenetic trees were obtained from minimum evolution and maximum likelihood investigations used to analyse the CO1 sequence data, implying that the data set is robust to the various assumptions underlying these algorithms. The minimum evolution tree was the best tree obtained from the CO1 sequence data. This tree was well resolved with strong bootstrap values. The phylogenetic tree obtained from the most parsimonious analysis was not as well resolved at a basal level when compared to the ME and ML trees. The difference in the MP tree is most likely the result of homoplasious changes in the terminal branch overriding the signal in the internal (basal) braches (Long Branch attraction).

Down weighting of the third codon position resulted in a tree mirroring the ME tree with slightly different bootstrap values. Analysis transversion/transition ratio produced a phylogenetic tree which was considerably different in the basal rooting and in the *Oreixenica* clade.

All phylogenetic trees obtained from the analysis of the CO1 sequence data resulted in *V. kershawi* being included as an ingroup, generally, and unexpectedly, as a sister taxon to *G. klugii.* In previous studies into the relationships within the tribes and genera in the subfamily Nymphalinae, the tribe Nymphalini (to which *Vanessa* belongs) was found to be basal to the tribe Junoniini (Wahlberg & Nylin 2003; Wahlberg *et al.* 2005b). However, within the tribe Nymphalini the clade which contains the genus *Vanessa* has only moderate support and is not stable.

The CO1 gene has been very useful for uncovering relationships at the generic and specific level due to its hypothesized rapid evolutionary rate (Caterino & Sperling 1999; Wahlberg *et al.* 2003a). As the species chosen as outgroups for this study are relatively closely related to the ingroup species (Freitas & Brown 2004), it is possible that at deeper divergences the CO1 sequence data has been swamped by homoplasious changes, subsequently *Vanessa* has not been clearly identified as an outgroup.

In the CO1 trees the following clades and sister species relationships were supported:

- *O. latialis* is the sister to *O. ptunarra*
- The *Heteronympha* clade is sister to the *Oreixenica* clade
- *Argynnina* + *Nesoxenica* are sister to the *Heteronympha* + *Oreixenica* clade.

The strict CO1 consensus tree produced by Peña *et al.* (2006) resolved *Nesoxenica* to be a distantly related sister to *Oreixenica*; and *Geitoneura* to be a more closely related sister to *Heteronympha*. These relationships were not supported by reliable bootstrap values; all were less than 50%. The relationships resolved by my CO1 analysis all had stronger bootstrap values.

4.2 *EF-1α*

Similar trees were obtained using parsimony, distance and likelihood analysis implying that the data set is robust to the various assumptions underlying these algorithms. The maximum likelihood tree was slightly less well resolved for ancient divergences. The EF-1α gene is considered to be more informative for resolving deeper divergences than the CO1 fragment (Mitchell *et al.* 1997) subsequently all EF-1α trees resolved the satyrine to be a monophyletic in-group with *V. kershawi* and *J. villida* as basal species.

In all three analyses the placement of species in the *Oreixenica* clade is identical with slightly different bootstrap values. The recovery of identical relationships from different sources is good evidence for the reliability of this clade (Chen *et al.* 2003). Downweighting of the third position nucleotide resulted in the same basal clades as the ML tree with differences in the *Oreixenica* clade. The tree resulting from the analysis of the transition/transversion ratio had the same species placement in the *Oreixenica* clade as the tree from the third position nucleotide with considerable differences in species placement in the basal clades to every other tree.

The sister clade to *Oreixenica* in the EF-1α phylogenies is not as clear as in the CO1 and Wingless analyses as the EF-1α trees are not as well resolved; however *Nesoxenica* is consistently grouping at the sister taxon level to *Oreixenica*. This placement is consistent with the phylogeny of Peña *et al.* (2006) whose EF-1α strict consensus tree grouped *Nesoxenica* as a basal sister taxon to *Oreixenica* as they had included the dominantly tropical and subtropical genus *Hypocysta* which was placed as the sister taxon to *Oreixenica*.

In the EF-1α trees the following sister species relationships within the *Oreixenica* clade were supported:

- *O. latialis* is the sister to *O. ptunarra*
- *O. lathoniella* is the sister to the *O. ptunarra* + *O. latialis* clade
- *O. kershawi* directly derived from the ancestor to the *O. ptunarra* + *O. latialis* + *O. lathoniella* clade
- *O. correae* is sister to *O. orichora*
- *O. correae* + *O. orichora* clade is sister to all other *Oreixenica* species.

4.3 *Wingless*

Very similar trees were obtained for the three types of analysis using the wingless dataset despite the limitations of a reduced dataset. All Wingless trees resolved the satyrine to be a monophyletic in-group with *V. kershawi* and *J. villida* as basal outgroup species.

The *Heteronympha* species grouped to form a clade which is sister to the *Oreixenica* clade as consistent with my CO1 phylogenetic trees and the wingless phylogeny of Peña *et al.* (2006). As it was not possible to sequence viable wingless sequences for *O. latialis*, *O. correae*, *O. kershawi* and *H. penelope* discussing detailed sister species relationships within the wingless *Oreixenica* clade is not practicable.

Geitoneura, *Nesoxenica* and *Argynnina* formed species clades as sister genus to each other. This phylogeny is mirrored in the wingless phylogeny of Peña *et al.* (2006).

4.4 *Combined Gene Fragment*

Similar trees were obtained using parsimony, distance and likelihood analysis implying that the data set was robust to the various assumptions underlying these algorithms. The analysis of the combined data supported the relationships obtained by the single gene analyses and also helped to recover clades which were not fully resolved initially.

The phylogenetic trees produced by the analysis of the combined data supported the following clades and sister species relationships:

- Southeast Australian Satyrinae are a monophyletic group
- The *Heteronympha* clade is sister to the *Oreixenica* clade
- *O. latialis* is the sister to *O. ptunarra*
- *O. lathoniella* is the sister to the *O. ptunarra* + *O. latialis* clade
- *O. kershawi* directly derived from the ancestor to the *O. ptunarra* + *O. latialis* + *O. lathoniella* clade
- *O. correae* is the sister to *O. orichora*
- *O. correae* + *O. orichora* clade is sister to all other *Oreixenica* species.
- *H. cordace* is directly derived from the ancestor to *H. penelope* and *H. merope*
- *Argynnina* and *Nesoxenica* are sister species to the *Heteronympha* + *Oreixenica* clade
- *G. klugii* is basal within the southeast Australian Satyrinae.

4.5 *The utility of the different Gene Regions*

The gene CO1 fragments provided very useful phylogenetic information on evolutionary relationships within the southeast Australian Satyrinae and returned reasonable resolution at intermediate and recently diverged nodes, however there is some evidence of long branch corruption by homoplasy particularly in basal nodes.

The protein-coding nuclear gene fragment was valuable in corroborating the relationships obtained by the mitochondrial CO1 gene fragment. EF-1α returned good resolution at both basal and recently diverged nodes.

The phylogenetic trees produced by the Wingless gene fragment, due to the reduced data set appear not to be well resolved at recently diverged nodes; however Wingless afforded the best resolution for all divergence levels and provided the architecture for the phylogenetic trees from the combined analyses. The utility of the Wingless fragment suggests it can stand alone as a source of characters for building molecular phylogenies; however its utility is enhanced by the combination with data from other sources (Brower & DeSalle 1998).

Further molecular studies of the Satyrinae should target the Wingless gene fragment in combination with data from other sources. It appears Wingless become saturated more slowly than the CO1 and EF-1α gene fragments. In addition, the amount of useful phylogenetic information that may be obtained from a short <400 bp section of Wingless is comparable to or exceeds that of an >800 bp fragment of CO1 or EF-1α. This concurs with the findings of Brower & DeSalle (1998).

4.6 *Age of Divergence*

Investigations of the origin and times of diversification of the Satyrinae, is hindered by the scarce fossil record and uncertain higher level phylogenies (Braby *et al.* 2006; Peña & Wahlberg 2008). The associations of Lepidoptera and their foodplants may involve coevolution and therefore offer insights into the history of both (Ehrlich & Raven 1964). The evolutionary history of Satyrinae is closely tied to the evolution of Poaceae (Peña & Wahlberg 2008), which underwent a massive expansion and radiation during the Oligocene (33-26 mya) (Willis & McElwain 2002). Peña & Wahlberg (2008) dated the divergence of *Heteronympha* to be around 27 mya. I calculated the divergence date of *Heteronympha* to be around 30 mya, which ties with the radiation and expansion of the Poaceae.

Due to the constraints associated with using fossils for calibration points, divergence ages estimated from fossil are constrained to a minimum divergence age (Smith *et al.* 1992; Sanderson 1997). As a collaboration point Peña & Wahlberg (2008) used a fossil from the Late Oligocene (25 mya) placed in the extant satyrine genus *Lethe* by Nel *et al.* (1993). As a collaboration point I used the Early Oligocene (approximately 35 mya) *Vanessa* fossils described from the *Florissant Lake Bed Shales* of Colorado.

A detailed discussion of the evolutionary history of the southeast Australian Satyrinae is presented in Chapter 5.

5 CONCLUSION

The southeast Australian Satyrinae appear to be a monophyletic group based upon molecular evidence.

Chapter 5

Propositions for understanding the phylogeny and evolutionary history of temperate zone southeast Australian Satyrinae

1 Historical biogeography of Australia's Butterfly Fauna

1.1 *The Age of Butterflies*

The oldest known butterfly fossils are dated at 48 mya (Late Eocene), and belong to the family Papilionidae (Durden & Rose 1978). Nymphalidae fossils are dated from 38 mya (Late Eocene) (de Jong 2003; Braby *et al.* 2005); when Australia and South America were still connected through Antarctica. Subsequently it is possible that the diversification of the Nymphalidae and subsequently the Satyrinae did come about as a result of the breakup of Gondwana. Viloria (2003) proposed that the Hypocystina, a diverse subtribe of the Satyrinae is Gondwanan in origin. Conversely, it is possible that if a Gondwanan ancestry exists, it has been obscured by later dispersals and extinctions (de Jong 2003).

Several lines of evidence may argue for relatively recent arrival of the hypocystines from the north. For example, no Australian satyrids feed on the restiid clade (Braby 1995b; Braby 2000), despite its diversity and prevalence in the Bassian zone. Alternatively, the peculiar growth form of the restiids, featuring wiry photosynthetic stems and strongly reduced leaves may have prevented their adoption by folivorous larvae. Some other groups of Lepidoptera may have entered Australia via a similar route, e.g. xanthorhoine geometrids (Young 2003).

Zhang *et al.* (2008) in their study estimating divergence times among subfamilies in Nymphalidae estimated the divergence between the Satyrinae and its sister subfamily Charaxinae at ~53.9 mya. Peña & Wahlberg (2008) estimated the divergence of the Satyrinae subfamily at 51.7 (± 5.7) mya.

1.2 *The origins of Australia's Butterfly Fauna*

The historical biogeography of butterflies remains a topic of much debate in current lepidopteran literature, and is on the whole currently unknown (Wahlberg 2006). Advocates of both vicariance and dispersal models of butterfly divergence disagree on the order of historical events (de Jong 2003; Viloria 2003; Hall *et al.* 2004; Braby *et al.* 2005; Braby & Pierce 2007; Braby *et al.* 2007; Eastwood *et al.* 2008; Kodandaramaiah 2009).

There are two main theories advanced to explain the origin, age and evolutionary history of butterflies in the Australian region. One, all the butterflies in the Australian Region are the progeny of ancestors that dispersed relatively recently from Asia, Eurasia or Laurasia (northern dispersal hypothesis) (Ackery 1991; New 1999; de Jong 2003). Two, a component of the Australian fauna is more ancient, having descended from stocks in the southern lands of either remnant Gondwana (Madagascar, India, Australia, Antarctica, South America) or southern Gondwana (Australia, Antarctica, South America) (southern vicariance hypothesis) (Miller & Miller 1997; Kitching *et al.* 1999; Pierce *et al.* 2002; Viloria 2003; Peña *et al.* 2006). Recently, a third hypothesis has been suggested that the butterfly fauna has an origin in Gondwana, or remnant Gondwana, with dispersal from Asia via Greater India (Braby *et al.* 2005; Braby & Pierce 2007; Braby *et al.* 2007).

1.3 *Butterflies and Grasslands*

Current research suggest that butterflies are thought to be no older than approximately the mid Cretaceous ~100 mya (Braby *et al.* 2005). The oldest known fossils of angiosperms (on which the most Lepidoptera are dependent), date back to the early Cretaceous (127-138 mya) (McLoughlin 2001). Although the angiosperms must have originated before this time, the best estimates of angiosperm age range around 180 to 140 mya (Wikstrom *et al.* 2001; Sanderson *et al.* 2004; Bell *et al.* 2005). The absence of contemporary fossils thus far, may indicate that they were quite rare (de Jong 2003). Because the majority of butterflies and indeed most Lepidoptera, are highly specialized feeders of angiosperm plants as larvae, the age of butterflies cannot predate the origin of angiosperms (Wahlberg 2006).

The associations of Lepidoptera and their foodplants may involve coevolution and therefore offer insights into the history of both (Ehrlich & Raven 1964). Patterns of butterfly-plant interactions are phylogenetically conserved, with related species of butterflies feeding on related species of plants (Janz & Nylin 1998). The establishment and spread of grasslands has been dynamic in the last few million years (Stebbins 1981) including in Australia. Grasses are an important food plant for many Lepidoptera, although some large successful families have almost completely avoided them as a host e.g. the Geometridae (Young 2008). However, the evolutionary history of Satyrinae is closely tied to the evolution of Poaceae (Murray & Prowell 2005; Peña & Wahlberg 2008).

Satyrines are well known as one of the key herbivore groups which have diversified on monocots globally. The most phylogenetically basal satyrine clades are associated with tropical palms and have only a modest level of species richness, whereas the more advanced satyrines have radiated very extensively on Poaceae (Pena *et al.* 2006). Hypocystini, the major satyrine clade in Australia and New Zealand, exploit Poaceae and Cyperaceae.

In Australia, there are parallels to the satyrines in the foodplant relationships of the trapezitine hesperiid butterflies which are associated with Poaceae, Cyperaceae and *Lomandra*. There is broad overlap in the distribution of the two groups in Australia however, the hesperiid butterflies extend to more arid habitats on mainland Australia,

possibly because their larvae construct tubular silk-lined shelters from foliage which must help them resist desiccation and also perhaps because these constructions inhibit some predators (Jerman & Gauld 1988). As a clade, the trapezetines occupy the widest range of climatic conditions in Australia (Braby 2000). The most cold-adapted of Tasmania's hesperiids is the *Poa*-feeding *Anisynta dominula* (McQuillan 1994; Braby 2000). Grass-feeding Lepidoptera larvae are almost exclusively nocturnal which helps avoid exposure to diurnal grazing mammals.

Diversification among grass-feeding Lepidoptera genera in Australia is uneven. In some genera it is limited to one or a few species e.g. *Anthela* and *Pterolocera* (Anthelidae), *Persectania* (Noctuidae), *Oncopera* and *Fraus* (Hepialidae). Alternatively, in some groups the species diversification is very high (the noctuid genus *Proteuxoa*, crambids such as *Hednota*).

Oreixenica has a very strong ecological association with montane grasslands, many of which are associated with cold air drainage in valley floors. These grasslands can sustain high levels of mammalian grazing (macropods and wombats) (Kirkpatrick & Bridle 1999) but have a relatively low incidence of fire relative to similar grasslands at lower elevations. This reduced predisposition to fire results from lower standing fuel levels combined with lower temperatures and with fewer opportunities for ignition (Bridle *et al.* 2001).

2 PROPOSITIONS FOR UNDERSTANDING THE EVOLUTION OF TEMPERATE ZONE SOUTHEAST AUSTRALIAN SATYRINAE

2.1 *Larval food plant specialisation*

Larval food plant specialisation appears to be a significant driver of speciation within the temperate zone southeast Australian Satyrinae. Larval host plant adaption is a widely recognised driver of speciation within the Lepidoptera (Powell 1980; Ronquist & Nylin 1990; Janz & Nylin 1998; Powell *et al.* 1999; Janz *et al.* 2001). Although most members of the subfamily feed on Poaceae, many species have specialised on various *Poa* species. Evident within these butterflies are several examples of probable host capture among and within two Poales clades. *O. kershawi* may represent a case of capture of a novel graminid foodplant which serves to largely constrain the range of the species. Although wiregrass *Tetrarrhena* occurs in northern Tasmania the *O. kershawi* is absent. The Tasmanian endemic *Nesoxenica* is a specialist on the cyperid genus *Uncinia.*

Tussock grass is the main type of riparian vegetation on moist soils along rivers and their adjacent floodplains in Tasmania. The cool-temperate zone tussock-forming *Poa* belong to informal group "Australopoa" (Australia and New Zealand) (Gillespie & Soreng 2005) itself embedded in a near cosmopolitan clade of *Poa* exhibiting a great range of habitat associations and growth form. This group is thought to have reached Australia/New Zealand from the Americas (Soreng 1990; Doyle *et al.* 1992; Barker *et al.* 2001).

Microlaena stipoides is a widespread perennial cool-season species which is an important foodplant of several hypocystine genera. It tolerates a wide range of environments, including shade beneath eucalypts, but avoids swampy ground (Magcale-Macandog & Whalley 1991). It is common in native pastures and can coexist with introduced European grasses such as *Lolium* and *Dactylis*. *Themeda triandra* is a warm season species, widespread through the Old World (Hill 2004).

In an otherwise Poaceae feeding genus, *H cordace* has captured the cyperid *Carex* and thus extends into wetter, lower nutrient habitats particularly in western Tasmania. The genus *Tisiphone*, monophagous on the tall cyperid *Gahnia,* includes the geographic outlier *T. helena* on the Atherton Tableland, but is absent from Tasmania despite the

hostplant being common. *Dodonidia* in North Island of New Zealand is also a *Gahnia* feeder (Laidlaw 1970).

Many of the wider spread Satyrinae, which also appear to have robust populations, have adapted to feeding on introduced grassland species. For example the native food plants of *A. hobartia* have not been officially recorded as the species main host now appears to be the introduced species *Lolium perenne* (Poaceae) (Prince 1988; Braby 2000).

Plate 5 *O. ptunarra* male, sunning on *Poa labillardieri*, Pikes Hill March 2006

2.2 *Pleistocene Climate Change*

Geographical gaps in the current distribution of some butterflies raise interesting questions, where environmental modelling suggests a more continuous range. For example *Nesoxenica* is not fully coextensive with its widespread hostplant *Uncinia* in Tasmania, being absent from the northeast highlands (Couchman 1948, 1956; Common & Waterhouse 1981; Braby 2000). Similarly, *O. ptunarra* is absent from the extensive montane grasslands north of the Fingal Valley (Neyland 1992; Anderson 2001b; Bell 2002). These patterns may represent retreats from a formerly wider range or failure to recolonise after previous range contractions. Climate change in the last few million years is a likely driver of these changes.

The mid Pleistocene arid shift recorded in southern Australia was associated with colder global temperatures, and lower sea levels during glacial periods and occurred around 500,000 years ago (Pillans & Bourman 2001). In southern Australia, the Last Glacial Maximum is known to have been both drier and colder than present (Bowler *et al.* 1976). At this time sea level was up to 130 m lower than now, and much of the continental shelf was exposed (mainland Australia was joined to Tasmania, for example). Increased continentality may thus have contributed to decreased rainfall, particularly in present-day coastal areas.

O. ptunarra is largely confined to very open habitats due to its microclimatic preferences. It is intolerant of shady habitats due to its need to bask regularly. *O. ptunarra* occurs in some of the driest and coldest *Poa* grasslands in the Midlands which are home also to a number of other grass feeding endemic insects such as *Aphodius pseudotasmaniae* and *Oncopera intricata.*

The most ecologically widespread Hypocystina in the Bassian region is *Geitoneura*, a genus basal to other southern Australian genera. One species, *G. klugii*, extends from tall forest to open grassy woodland over a wide range of longitude and climatic zones. The two other species in the genus are more restricted but contained within the range of *G. klugii* (Braby 2000).

3 IMPLICATIONS FOR THE EVOLUTIONARY RELATIONSHIPS FOR AND WITHIN THE TEMPERATE ZONE SOUTHEAST AUSTRALIAN SATYRINAE

3.1 *Ge itoneura klugii as basal species*

Geitoneura klugii as the basal species within the temperate zone southeast Australian Satyrinae is very strongly supported by the molecular data (Chapter 4: Figure 4.4). Morphologically *G. klugii* is typical of the subfamily. The larvae have adapted to feeding on a wide range of both introduced and native species (Chapter 3: Table 3.2). The eggs of *G. klugii* are very unusual in the subfamily; they are most similar in morphological features to the eggs of *Pyronia bathseba* and *P. tithonus* subtribe Maniolina (Garcia-Barros & Martin 1995). Maniolina is a closely related basal subtribe to Hypocystina (Peña *et al.* 2006). The pupa of *G. klugii* is attached; the dominant state throughout the subfamily.

3.2 *Ar gynnina and Nesoxenica as sister species*

Nesoxenica and *Argynnina* as sister species is supported by the majority of the molecular data (Chapter 4: Figure 4.2 - 4). Morphologically *Nesoxeinca* is atypical of the subfamily where as *Argynnina* is fairly typical. One major point of divergence between the species is larval food plant preference. The larvae of *A. hobartia* have adapted to feeding on *Lolium perenne*, an introduced species as well as native grasses such as *Poa labillardieri* and *Austrodonthonia* species, whereas *N. leprea* has developed to feed solely on one species *Uncinia tenella* (Chapter 3: Table 3.2).

The sub-hemi-spherical eggs of *A. hobartia* are fairly typical of the temperate zone southeast Australian Satyrinae; whereas the sub-quadrate, upright eggs of *N. leprea* are quite a different, however this shape is found in other European satyrinae (Garcia-Barros & Martin 1995). The pupa of both *Nesoxenica* and *Argynnina* are attached.

3.3 *Hete ronympha as sister species to Oreixenica*

Characteristics which are not seen in other clades within the temperate zone southeast Australian Satyrinae such as distinct sexual dimorphism and unattached pupa are displayed in both the *Heteronympha* and *Oreixenica* genus. The sister species relationship of *Heteronympha* and *Oreixenica* is supported by the molecular data (Chapter 4:Figure 4.1 - 4).

Distinct sexual dimorphism is more common in tropical families such as Zygaenoidea (Yen *et al.* 2005) than temperate zone Satyrinae butterflies. *H. merope* (Chapter 2: Figure 2.45), *O. ptunarra* and *O. correae* (Chapter 2: Figure 2.8) all display distinct sexual polymorphism. Generally species that display sexual dimorphism, particularly in temperate zones have distinct differences between flight behaviour in males and females (Gilchrist & Rutowski 1986; Sibly *et al.* 1997; Emerson & Hastings 1998; Van Dyck *et al.* 1998; Berwaerts *et al.* 2006; Martinez-Lendech *et al.* 2007). This hypothesis is generally supported within the temperate zone Satyrinae. *O. ptunarra* display distinctive differences in male and female flight behaviour (Anderson & McQuillan 2003) as does *H. merope* (Braby 2000).

Unattached pupa is a characteristic that appears to have evolved recently and independently within the *Heteronympha* and *Oreixenica* clades Figure 5.1.

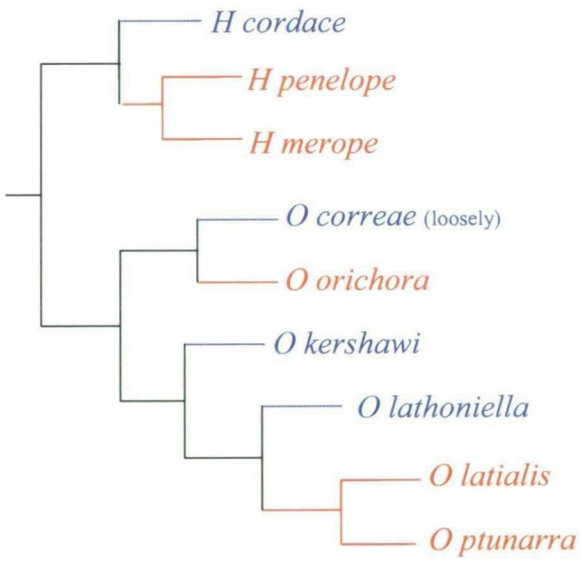


Figure 5.1 Cladogram of *Heteronympha* and *Oreixenica* clades detailing pupal state
Blue text =Attached : Red text = Unattached

The presence or absence of signa is a defining character between *Heteronympha* and *Oreixenica*; signum is absent *Oreixenica* (Chapter 2: Figure 2.31-36), and present in *Heteronympha* (Chapter 2: Figure 2.55-57).

4 HYPOTHESIS OF *OREIXENICA* SPECIATION

We can propose that *Oreixenica* populations were once much more widespread in south eastern Australia, given that climate models for a mean annual temperature depression of 5 °C predict that *Poa* grassland occupied more than twice its current extent Figure 5.2. Since the Last Glacial Maximum, there has been a steady decline in *Oreixenica* habitat Figure 5.3.

Figure 5.2 Alpine Grassland Extent at the maximum of the last glacial period

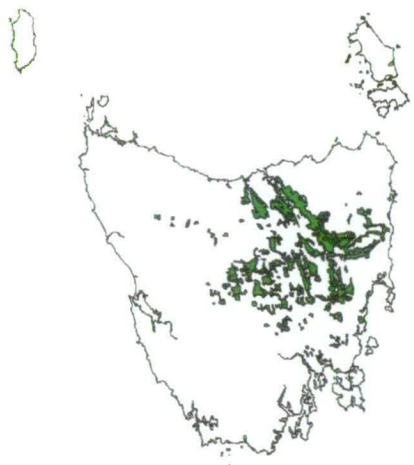


Figure 5.3 Current Extent of Tasmanian Grassland Habitat

(after Kirkpatrick *et al.* 1995)

The genus *Oreixenica* appears as the geographically restricted sister (SE Australia) to the more widespread *Heteronympha* (southern Australia). The ancestral *Oreixenica* was *Poa*-feeding, adapted to cold grasslands, and subsequent speciation was promoted by the environmental vagaries of the Pleistocene, which both diversified grassland habitats, and variously expanded and contracted their extent. The first dichotomy yielded the ancestor of *O. orichora-O. correae* and another species which subsequently gave rise to the foodplant specialist *O. kershawi* and a diversified clade of Poa-feeders. This latter clade includes the altitudinally widespread *O. lathoniella* and the ancestor of the alpine species pair *O. latialis-O. ptunarra*. This ancestor occurred on both sides of Bass Strait prior to its inundation. Subsequently, these separated populations diverged to yield the mainland *O. latialis* and the Tasmanian endemic *O. ptunarra*.

The archipelagic nature of cold grasslands has lead to the isolation of populations in several species; this is reflected in divergences in phenotype, such that they in some many cases they have been assigned subspecific names.

The lower altitudinal limits around 1000m of species such as *O. correae*, *O. orichora* and *O. latialis* has restricted the capacity of these species to extend their range. In addition, global warming is expected to further contract their range.

Cold (elevated) grasslands have existed in southern Australia since the end of the Tertiary. The ancestor to the clade *O. ptunarra / O. latialis* was most likely a wide spread open grassland species which flew during the last interglacial period. Couchman (1956) in his original description of *O. ptunarra* hypothesised that *O. ptunarra* is the most primitive form of *Oreixenica*, and most likely the basally derived species to the genus. The evidence presented here refutes this hypothesis; it is suggest that *O. ptunarra*, which is endemic to Tasmania, speciated after the inundation of Bass Strait.

Waterhouse (1923) found early instar larvae of *O. latialis* on Mt Kosciusko in December suggesting that either eggs or larvae overwinter, but not pupae. The species-pair *O. latialis-O. ptunarra* fly late summer-early autumn, the latest of all members of the genus. It is proposed that this phenology evolved to enable larvae to exploit fresh spring growth in *Poa* tussocks.

O lathoniella is most likely a close descendant of the species which specialised to give rise to the *O. ptunarra / O. latialis* clade. *O. lathoniella* is wide spread sea level to sub alpine with a long flight period January to May. Whereas *O. latialis* and *O. ptunarra* have a limited flight period late February to early April and limited altitudinal range alpine. The high degree of frost-tolerance in *Poa* enables tussock grassland to occupy extensive areas on high plateaux above the treeline, and colonise cold elevated valley bottoms.

O. kershawi appears to be a foodplant specialist on *Tetrarrhena juncea* (wiregrass) in wet forests at low to moderate elevations. Its absence from Tasmania is probably due to lack of suitable habitat. Wet forests with an understorey dominated by grasses and sedges, especially the grass *Tetrarrhena juncea* which occur in Victoria, are uncommon in Tasmania.

The ancestor to *O. correae* / *O. orichora* most likely flew in closed country. Speciation in the branch occurred due to flight period and habitat range preference.

Unfortunately, the precipitous decline in the extent of native grasslands since European settlement represents a major challenge to the future prospects of many of the species.

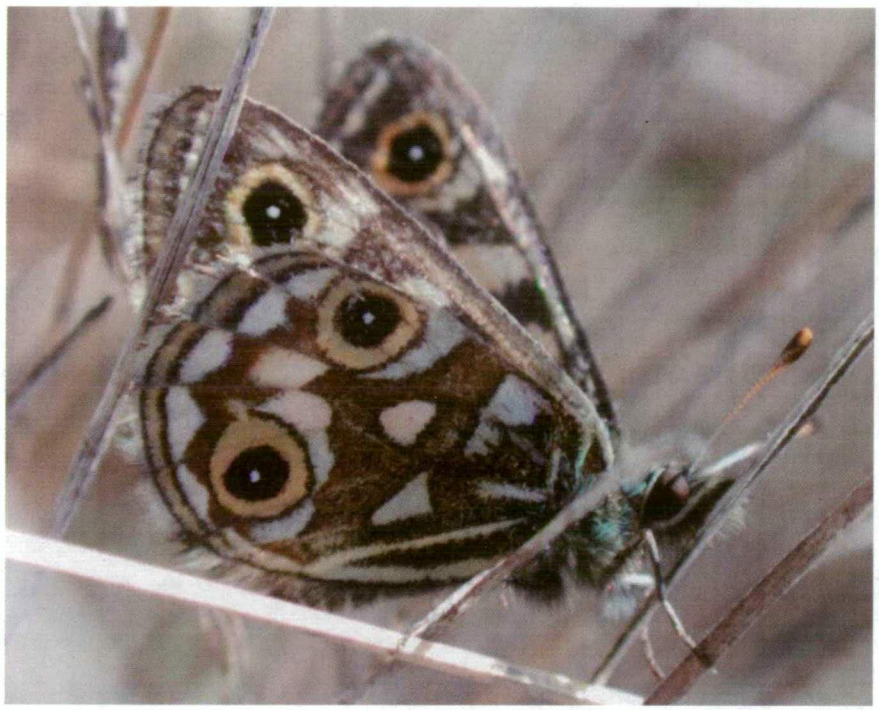


Plate 6 *O. ptunarra* male, resting on *Poa*, Pikes Hill March 2006

Chapter 6

Population management of *Oreixenica ptunarra*

1 INTRODUCTION

1.1 *Background*

O. ptunarra is an endemic Tasmanian butterfly with a fragmented and restricted distribution (Braby 2000). All known colonies are found in open habitat at altitudes above 450m that support a healthy *Poa* tussock grassland, usually in excess of 25% ground cover (Anderson 2001b). Habitats occupied by the butterfly range in structure from grassy *Eucalyptus* woodland, through grassy shrubland, to open grassland. Since European settlement a considerable reduction and modification of this habitat has occurred, particularly throughout the Midlands, a major agricultural region (Fensham & Kirkpatrick 1989; Kirkpatrick *et al.* 1995; Leonard & Kirkpatrick 2004). Unfortunately the reduction, destruction and modification *O. ptunarra* habitat of continues in some areas, particularly due to flooding of native grasslands in upper catchments for on-farm water storages.

As over 90% of the habitat of *O. ptunarra* is in private ownership, the continued survival of the species depends very heavily on sympathetic land management. A key issue in managing the species is the impact of existing and proposed land management especially in relation to *Poa* tussock grasslands which are now fragmented. Land management practices in and surrounding, *O. ptunarra* colonies the Southern Midlands will have a major bearing on the fate of the species.

Conservation genetics is the application of genetics to manage species as dynamic entities capable of dealing with environmental change. It may inform genetic management of small populations, resolution of taxonomic uncertainties, help in defining management units within species and extend understanding of a species biology (Frankham *et al.* 2002).

The deleterious effects of small population size are of major concern in conservation biology, since endangered species typically have small or declining populations. Small populations suffer usually from inbreeding and loss of genetic diversity resulting in

elevated extinction risks. Consequently, a major objective of genetic management is to minimize inbreeding and loss of genetic diversity (Frankham *et al.* 2002).

The investigation of butterfly populations has been at the forefront of conservation genetics. Leading this was the Porter & Geiger (1988) investigation into the genetic and phenotypic population structure of the *Coenonympha tullia* complex (Lepidoptera: Nymphalidae: Satyrinae) in North America. Population genetics continued to be a strong area of research throughout the nineteen-nineties leading this was Hanski's Metapopulation research group (e.g. Hanski 1999). Recent population genetic studies included the work of Agrawal (2003) integrating population genetics into community ecology; Benedick *et al.* (2007) using population genetics to study the effects of habitat fragmentation; and Schmitt and Haubrich using genetic differentiation of *Erebia euryale* to unravel the late Pleistocene history of the mountain coniferous forest biome in Europe (Schmitt & Haubrich 2008).

I would argue that *O. ptunarra* is an excellent candidate for a comprehensive genetic study of populations in a young, low contrast, fragmented landscape. Fragments are remnants of previously more continuous features, isolated by the imposition of a contrasting matrix (Watson 2002). Considerable ecological knowledge has been gathered over the last decade relating to the dynamics of individual *O. ptunarra* populations, habitat patch size, and biological characteristics (Neyland 1992; 1993; McQuillan & Ek 1997; Bell 1998; Anderson & McQuillan 2000; Anderson 2001b; Bell 2002; Anderson & McQuillan 2003). However little is known about migration patterns, population interactions or the breeding structure of *O. ptunarra.*

The range of *O. ptunarra* extends over three major Tasmanian biogeographical regions: the Centre (Northwest Plains and Central Plateau), Southern Midlands and East Coast (Orchard 1998). *O. ptunarra* range is determined by a variety of environmental factors. It is dominantly a upland species, being restricted to sites above 400m and does not extend into the lowland plains of the Midlands, where it is too dry for *Poa* to flourish (Kirkpatrick & Gilfedder 2000; Leonard & Kirkpatrick 2004). In the Northwest Plains area *O. ptunarra* is limited by the availability of suitable habitat (Neyland 1992). Although *O. ptunarra* depends on a significant cover of *Poa* tussock grassland, some apparently excellent quality *Poa* grasslands do not carry populations of the butterfly

(Neyland 1992; Bell 1998; Anderson 2001b; Bell 2002). Reasons for this are not well understood but some absences may be temporary, awaiting dispersal of colonising individuals from nearby populations.

1.2 *Aims*

The aims of this chapter are to investigate the genetic diversity of *O. ptunarra* populations, and to explore the implications for understanding the scale of movement within and between *O. ptunarra* populations. This information will give important insights to the relatedness among a cross section of populations.

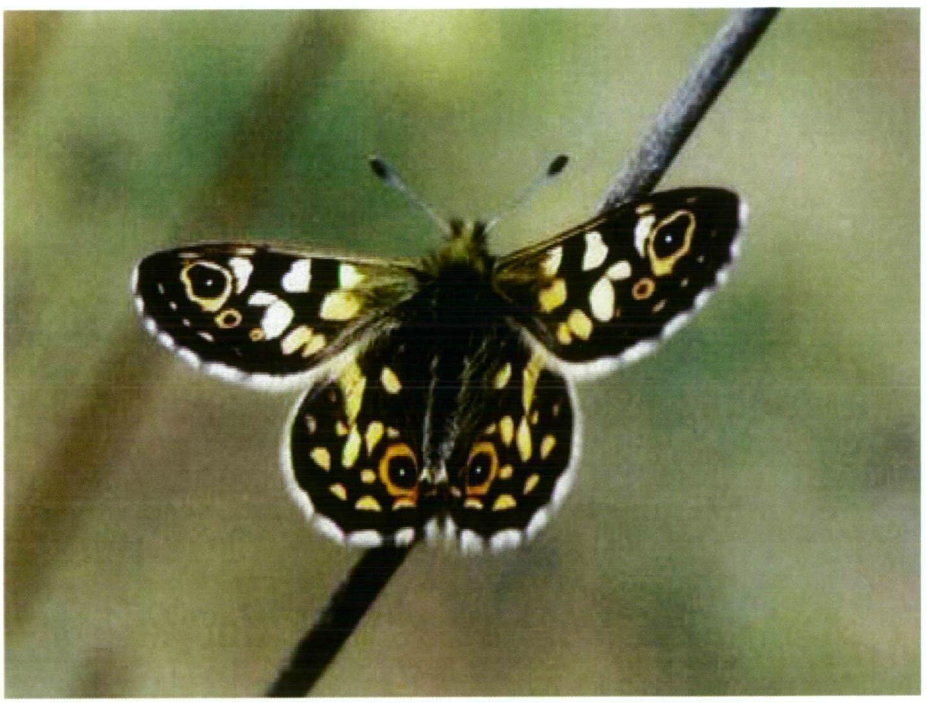


Plate 7 *O ptunarra* male, Tunbridge Tiers, 2004

2 THE GENETIC DIVERSITY OF *O. PTUNARRA* POPULATIONS

2.1 *Materials and Methods*

2.1.1 Individuals and Populations Examined

Populations were sampled along road based transects designed to adequately sample the geographical range of *O. ptunarra* habitat (detailed in field site descriptions Appendix 3). The provenance of individuals is listed in Appendix 2. All individuals were stored frozen at -18 °C until required.

2.1.2 Primers and PCR

Sequencing was undertaken from at least two individuals from each sample locality. A 750bp sequence was obtained for the *Lepidopteran Control Region (CR)* following the methods set out in Chapter 4. Vila & Bjorklund (2004) found that CR to be a more useful sequence than CO1 as it shows more variability in population genetic studies. The primers Lep 12S (F) and Met20 (R) from Taylor *et al.* (1993) were utilised and PCR conditions based on Vila & Bjorklund (2004) (Table 6.1) were implemented.

Lep 12S (F) 5'- TA GGG TAT CTA ATC CTA GGT -3'

Met20 (R) 5'- TG GGG TAT GAA CCC AGT AGC -3'

Table 6.1 PCR conditions used in population study

1. 95°C denaturation for 120 seconds
2. 94°C denaturation for 60 seconds
3. 51°C annealing for 90 seconds
4. 65°C extension for 60 seconds
5. go to 2, 35 times
6. 65°C final extension step for 7 minutes
7. Hold at 11°C forever.

2.1.3 Sequence analysis & alignment and phylogenetic analysis

Sequence analysis and alignment and appropriate phylogenetic analyses were conducted following the methods set out in Chapter 4.

2.1.4 Mantel tests

Mantel tests (Mantel 1967) were conducted to test if genetic variation and geographical distance between population localities were correlated. The method chosen was Mantel's asymptotic approximation; algorithm based on Douglas & Endler (1982).

2.2 *Results*

Alignment of the population data resulted in 750 characters, of which 129 were parsimony informative. The data matrix is presented in bootstrap consensus tree in Figure 6.1, sequences in Appendix 9 and the Log/Det sequence divergence values in Appendix 10. The average base frequencies for the population data were A = 42.20%, C = 6.99%, G = 3.77%, and T = 47.04%.

Maximum parsimony (MP) analysis using equal weights produced 38 shortest trees of length 467 (CI = 0.499, RI = 0.813). The strict consensus tree is presented in Figure 6.4 Minimum evolution (ME) analysis resulted in 27 short trees of length 498(CI = 0.468, RI = 0.788). The strict consensus tree is detailed in Figure 6.5. Maximum likelihood (ML) analysis resulted in one tree of length 458 (CI = 0.545, RI = 0.715) detailed in Figure 6.6. The tree parameters obtained empirically by the ML analysis were as follows:

Ti/Tv:	
Expected ratio:	0.8999
Kappa	4.5884
Shape parameter (alpha)	0.1981
Minus log Likelihood (-In L)	4196.4937

Analysis of the transition/transversion ratio resulted in two shortest trees of length 2736 (CI = 0.444, RI = 0.796) Figure 6.7.

Four major population groupings emerged from the phylogenetic analysis. To some degree these reflect the phenotype subspecies described by Couchman (1953; Couchman & Couchman 1978) (Figure 6.2).

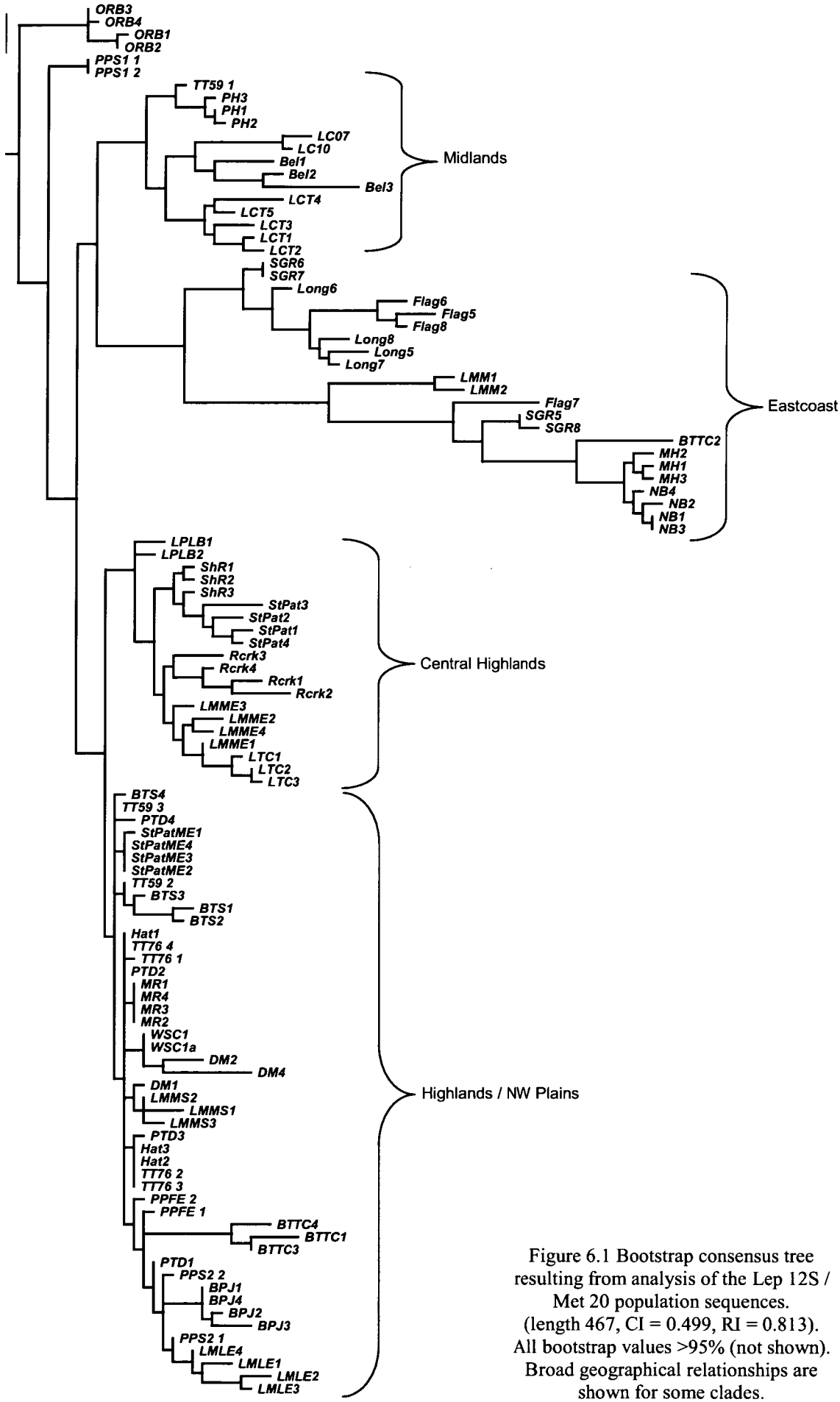


Figure 6.1 Bootstrap consensus tree resulting from analysis of the Lep 12S / Met 20 population sequences. (length 467, CI = 0.499, RI = 0.813). All bootstrap values >95% (not shown). Broad geographical relationships are shown for some clades.

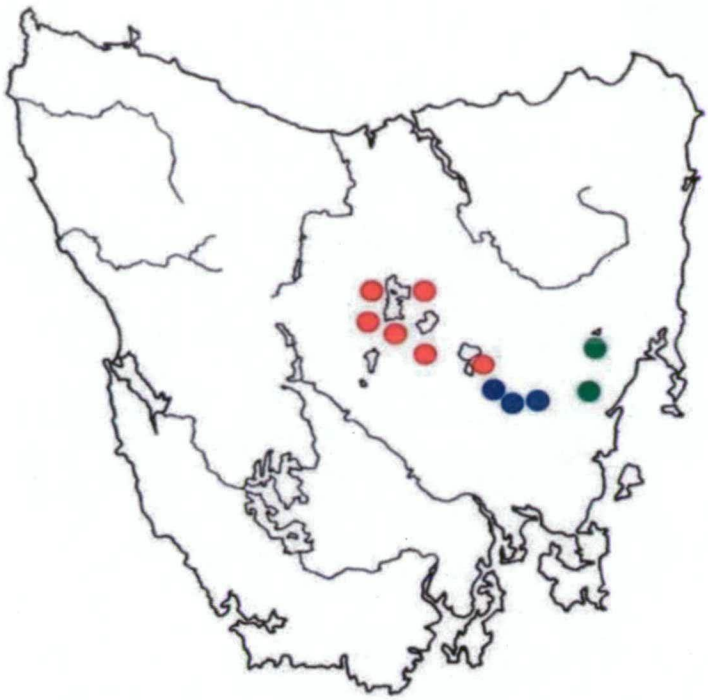


Figure 6.2 *O. ptunarra* subspecies localities (after Couchman & Couchman 1978)

- *O. p. ptunarra* occurs in the eastern part of the Central Plateau particularly around Great Lake
- *O. p. angeli* stronghold in the region around and between Lake Leake to Lake Tooms on the Eastern Tiers
- *O. p. roonina* is found in the Midlands around the Oatlands area

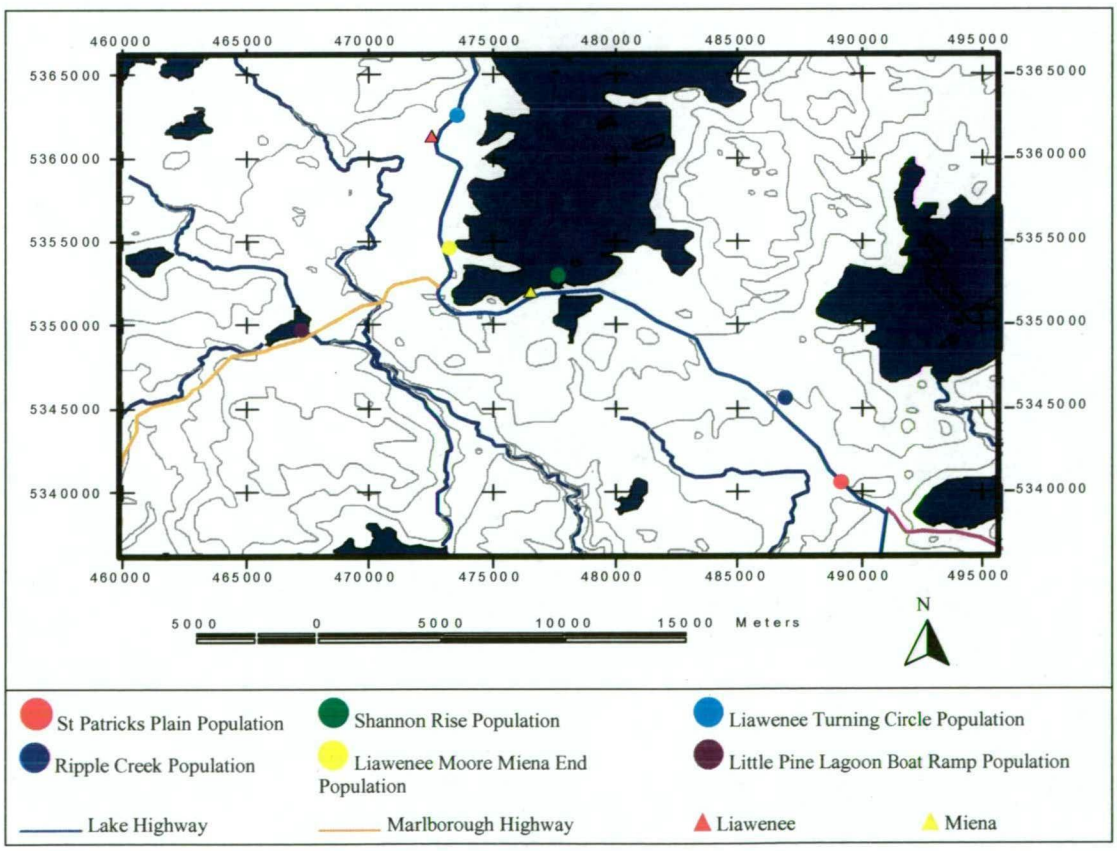


Figure 6.3 Locality of Highlands Clade Populations

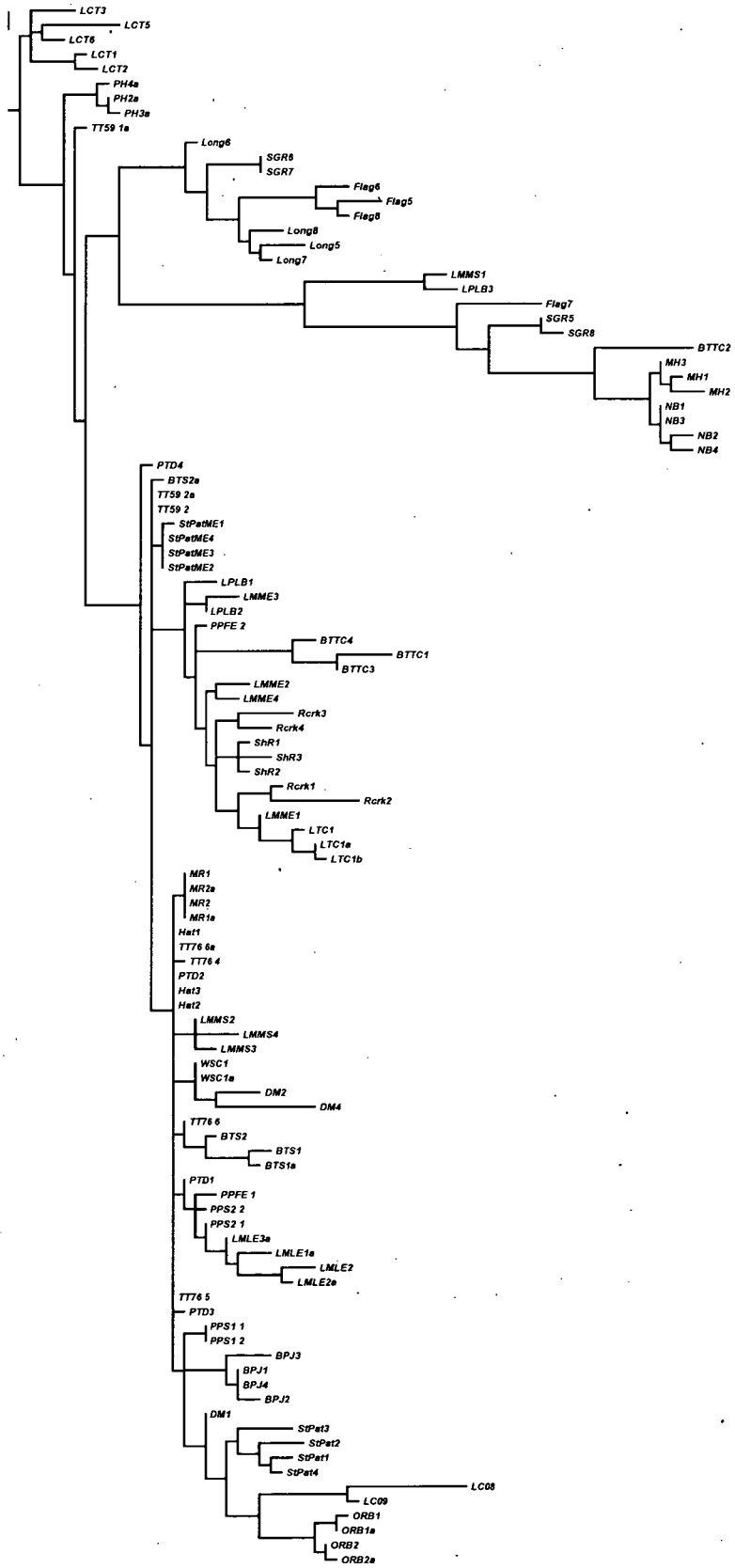


Figure 6.4 Bootstrap consensus of the most parsimonious tree (MP analysis) retrieved from analysis of the Lep 12S / Met 20 population sequences (length 467, CI = 0.499, RI = 0.813) all bootstrap values were >95% (not shown).

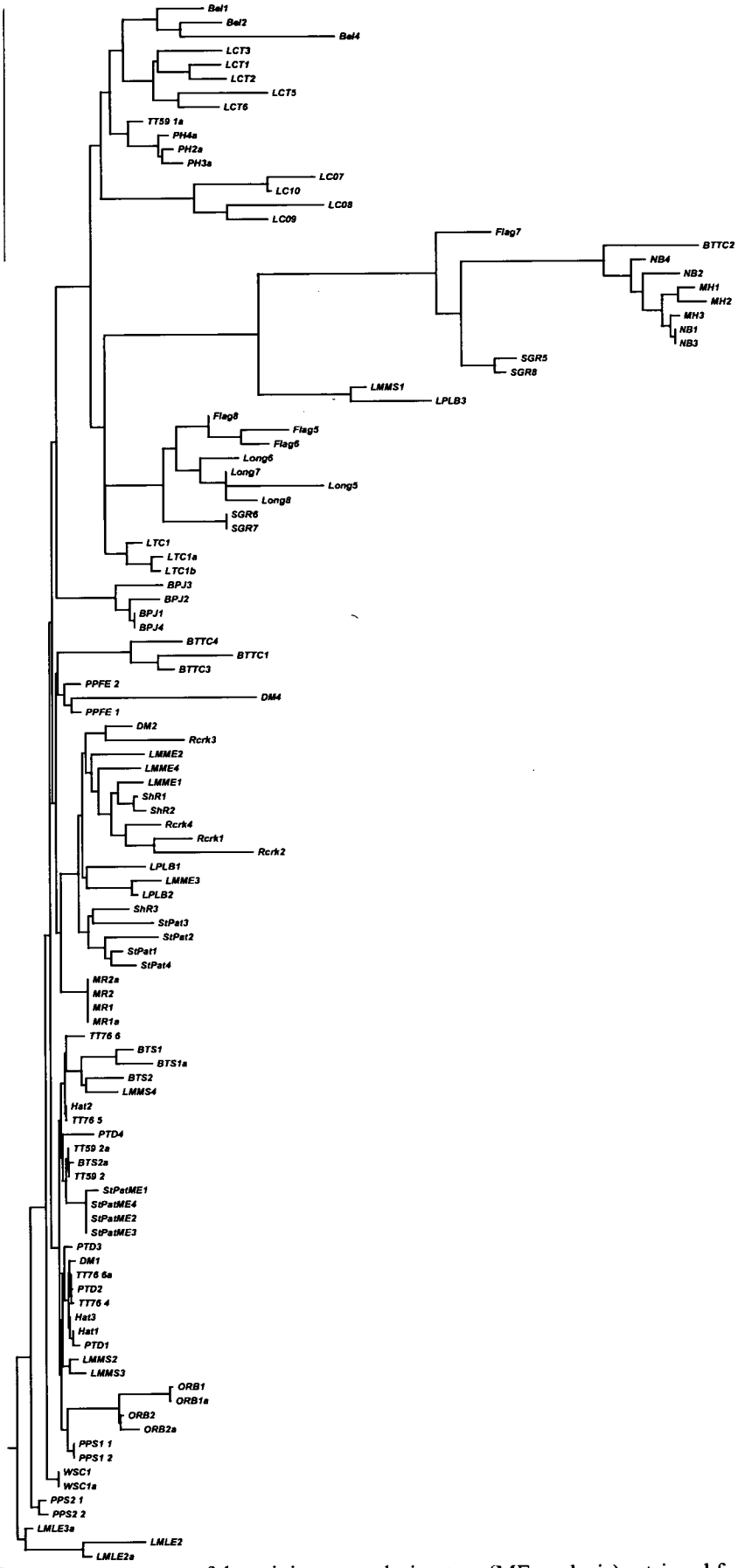


Figure 6.5 Bootstrap consensus of the minimum evolution tree (ME analysis) retrieved from analysis of the Lep 12S / Met 20 population sequences (length 498, CI = 0.468, RI = 0.788) all bootstrap values were >95% (not shown).

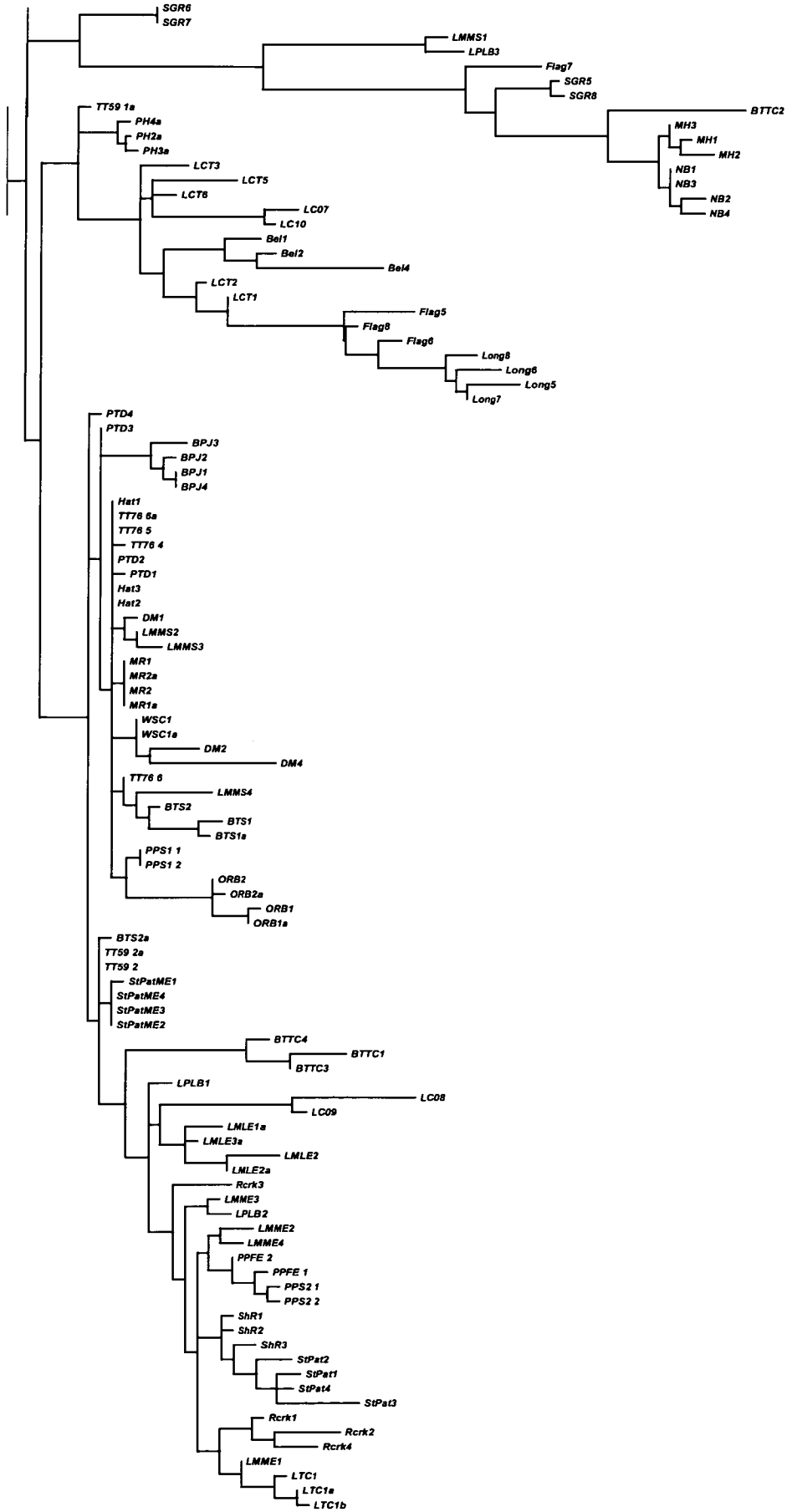


Figure 6.6 Bootstrap consensus of the minimum likelihood tree (ML analysis) retrieved from analysis of the Lep 12S / Met 20 population sequences (length 458, CI = 0.545, RI = 0.715) all bootstrap values were >95% (not shown).

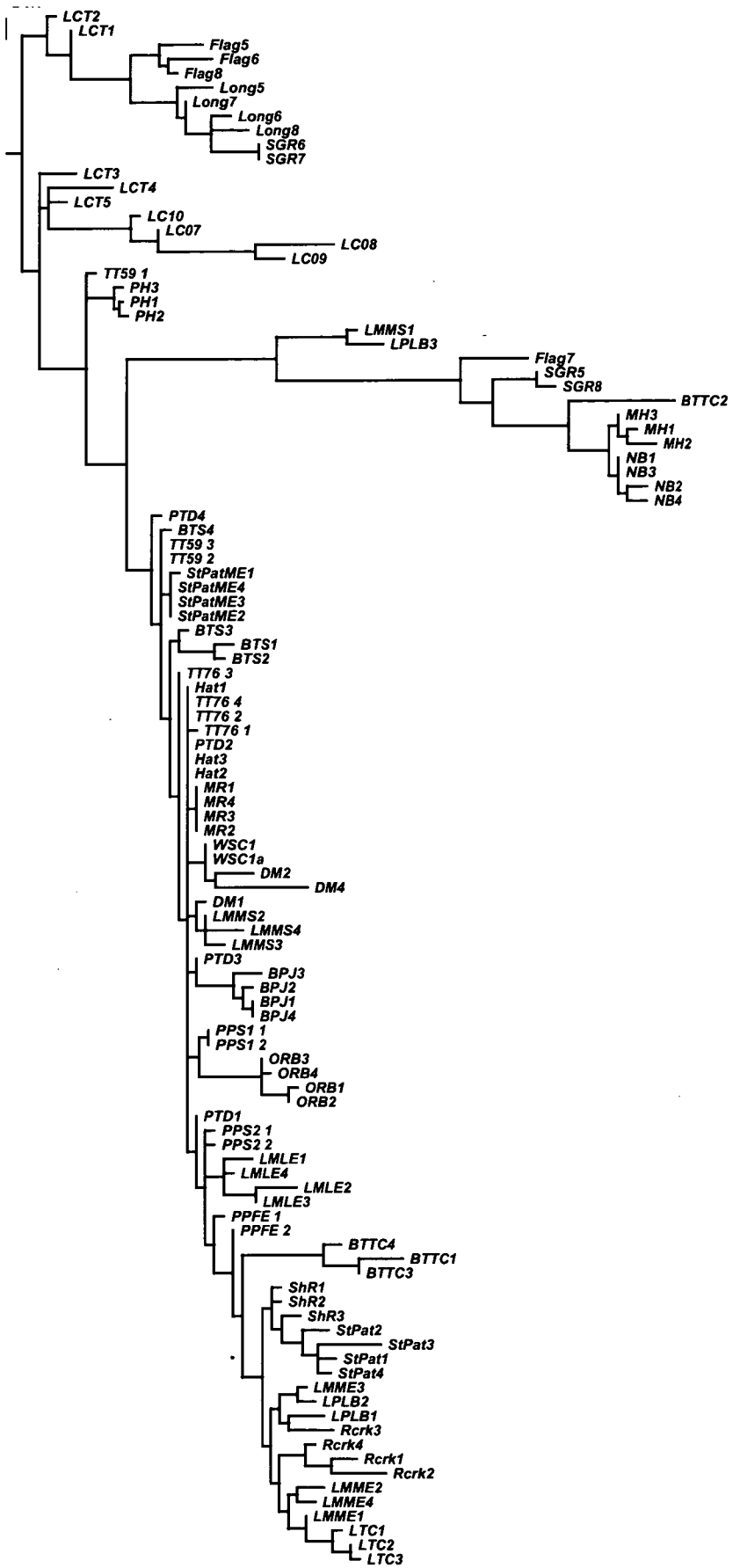


Figure 6.7 Bootstrap consensus tree resulting from analysis of the transition/transversion ratio retrieved, from the Lep 12S / Met 20 population sequences (length 2736, CI = 0.444, RI = 0.796) all bootstrap values were >95% (not shown)

2.2.1 Statistical Analysis of population genetics

The results of the overall Mantel test comparing genetic and geographical distances between populations suggest that the null hypothesis of no relationship between genetic distance and geographical distance apart is supported.

Standardised Mantel Statistic:	-0.049429 = r
Observed Z	0.2314×10^{8}
Expected Z	0.2314×10^{8}
Variance of Z	0.7899×10^{12}
Standard error of Z	0.8887×10^{6}
t = -0.7861	
p = 0.43206638	

The results of the regional Mantel test comparing genetic distances to geographic distance between populations grouped by region suggest that the null hypothesis of no relationship between genetic distance and geographical distance apart is to be rejected. A plot of the regional mantel test comparing genetic distances to geographic distance between populations grouped by region is presented in Figure 6.8. These results indicate that there is less heterogeneity within groups – population regions that expected by chance indication that there is relatedness between members of the groups.

Standardised Mantel Statistic:	0.293212 = r
Observed Z	0.1052×10^{9}
Expected Z	0.9417×10^{8}
Variance of Z	0.4771×10^{13}
Standard error of Z	0.2184×10^{7}
t = 5.0413	
p = 0.00000055	

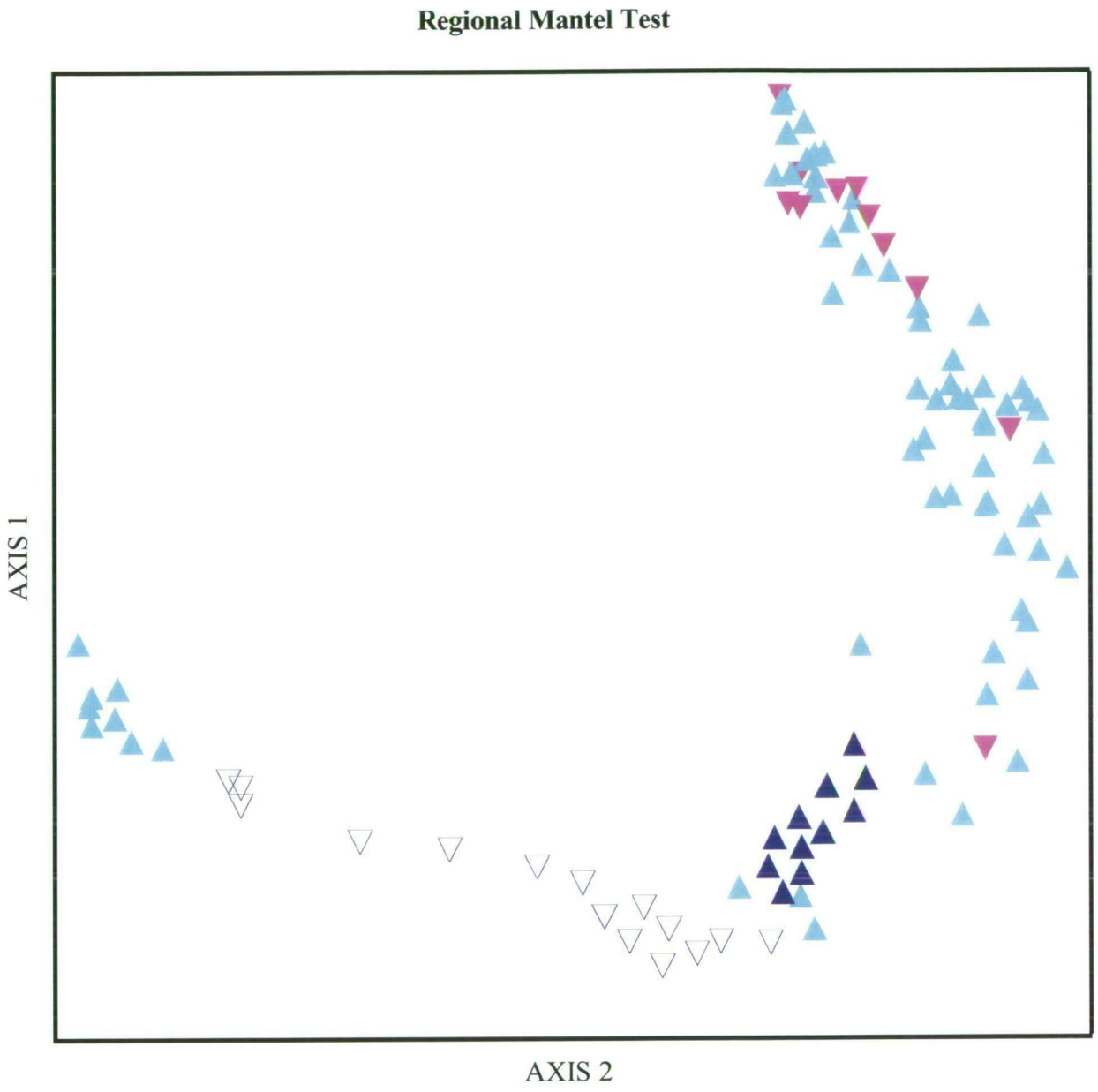


Figure 6.8 scatter plot of pair wise comparisons of Regional Mantel Test comparing genetic distances between populations grouped by region

3 DISCUSSION

This is the first analysis of the genetic relationships between various populations and subspecies within *O. ptunarra*. All previous commentaries (e.g. Couchman & Couchman 1978; Common & Waterhouse 1981; Braby 2000)on the relationships within *O. ptunarra* have been based on phenotypical evidence.

Four major population groupings have emerged from the phylogenetic analysis. To some degree these reflect the phenotype subspecies described by Couchman (1953; Couchman & Couchman 1978) (Figure 6.2 *O. ptunarra* subspecies localities (after Couchman & Couchman 1978)). Although he was not aware of the disjunct Northwest *O. ptunarra* populations when he described the subspecies of *O. ptunarra.* More recent analysis of phenotype (e.g. McQuillan & Ek 1997; e.g. Anderson & McQuillan 2000) has hypothesised that the Couchman subspecies are better understood as of clinal phenotypic variation with altitude, and have subsumed Couchman's subspecies to some degree, and recent commentators have also agreed (e.g. Braby 2000).

The habitat range of subspecies *O. p. roonina* is reflected in the Midlands clade. The Midlands populations were the first to be historically isolated and fragmented due to habitat loss and the introduction of improved pasture. Many populations recorded in the Midlands by Couchman (1953; 1954) and Couchman & Couchman (1978) are now extinct, including that at the type locality of *O. p. roonina* (Neyland 1992; Bell 1998; Threatened Species Unit 1998; Anderson 2001b; Sands & New 2002). The longer branch length in the Midlands clade arguably reflects an extended period of genetic isolation.

O. p. angeli is very clearly distinguished in the Eastcoast clade. These populations have the longest average branch length and the largest sequence divergence/less similarity to other population clades. The appearance of a BTTC (Barren Tier) individual and the very tight clade of MH (Marlborough Highway) + NB (North Bronte) at the tip of the Eastcoast clade raise interesting questions as to the origin of the Eastcoast and Midlands *O. ptunarra* populations. Individual members of populations which otherwise belong to the Highlands/NW Plains clade appear basal to the complete phylogenetic tree. This suggests that all *O. ptunarra* populations could be derived from highland populations.

This evidence is consistent with the wider hypothesis of *Oreixenica* speciation as presented in Chapter 5.

Individuals from populations that group in the Central Highlands clade fly typify *O. p. ptunarra*. Members of this clade fly in a very geographically limited area around Great Lake (Figure 6.3). The short to moderate branch lengths in this clade indicate that these populations are closely related but are becoming increasingly genetically isolated from the *O. ptunarra* populations elsewhere.

The Highlands / Northwest Plains clade is a noteworthy grouping. The short branch lengths and mixed population arrangements indicate this is a rapidly changing and evolving group. It has been assumed that *O. ptunarra* does not extend into the high altitude grasslands of the western Central Plateau (Sands & New 2002) leading to the hypothesis that the Northwest Plains *O. ptunarra* populations were a geographic isolate; however much of this area has not been thoroughly surveyed (Neyland 1992; Bell 1998). The population groupings in the Highlands/Northwest Plains clade provide evidence that *O. ptunarra* may extend throughout the grasslands of the western Central Plateau connecting the Northwest Plains populations to the Highlands populations.

Distance analysis of *O. ptunarra* population genetics also supports the existence of *O. ptunarra* subspecies. The plot of the regional Mantel test comparing genetic distances to geographic distance between populations highlights the genetic basis of the geographic regions (Figure 6.8). The three main groups: the Midlands (*O. p. roonina*), East Coast (*O. p. angeli*) and highlands (*O. p. ptunarra*) with the Northwest populations mixed in are highlighted.

In summary, *O. ptunarra* populations maintain a degree of genetic diversity and show some influence of genetically structured populations related to geography. However there is evidence from change in landuse that populations are becoming increasingly genetically isolated particularly, those in the Midlands and eastern regions of Tasmania. The fact that the described subspecies appear to be genetically supported does require some consideration in regards to future management plans of the species.

4 STRUCTURE & SPATIAL DISTRIBUTION OF *O. PTUNARRA* POPULATIONS

4.1 *Is genetic diversity reflected in the spatial distribution of populations?*

Genetic diversity is reflected in the spatial distribution of populations. Populations that are fragmented and geographically isolated are becoming increasingly genetically isolated as seen in the Eastcoast clade (Figure 6.1)

4.2 *W hat is the scale of movement within and between populations*

There is evidence of large scale spatial movement (tens of kilometres) between populations as the genetic signature of individuals appear where they are not expected such as individuals with sequences typical of Highland populations appearing in the Midlands and Eastcoast clades.

In Tasmania during the *O. ptunarra* flight period (March-April) the prevailing wind direction is from the southwest (Australian Bureau of Meteorology 2009). When disturbed, *O. ptunarra* can utilise wind currents to take evasive flight action (Anderson & McQuillan 2003). It is most likely that the Midlands and Eastcoast populations are derived from the Highlands and individuals have been recruited from the Highlands particularly to the Midlands region numerous times. This is reflected in the placement of the genotype of individuals from the Highland and intermediate populations (e.g. Lake Crescent [LC]) as sister to Midlands populations and the BTTC+MH+NB clade as sister to individuals from SGR (Stoney Gully Road) (Figure 6.1).

The very tight branching of some clades such as the Morey Road population (MR) within the Highlands / Northwest Plains clade (Figure 6.1) suggest that habitat patches which are geographically isolated have not been recruiting individuals to the population, subsequently becoming genetically isolated.

5 SUITABILITY OF HABITAT PATCHES FOR THE LONG TERM SURVIVAL OF *O. PTUNARRA*

5.1 *The sustainability of habitat patches for* O. ptunarra *survival in the Southern Midlands region of Tasmania*

Land management practices have the potential to make *O. ptunarra* not just vulnerable to extinction, but actually extinct. These practices include land clearing, overgrazing, plantation development, agricultural chemical usage and inappropriate burning regimes (Neyland 1992; Bell 1998; Threatened Species Unit 1998; Bryant & Jackson 1999; Anderson 2001b; Sands & New 2002).

The aim of this review is to investigate changing trends in land management and agricultural practices around *O. ptunarra* colonies in the Southern Midlands region of Tasmania and to discuss the potential effects on these colonies.

A series of follow up interviews were conducted with land managers in, and around, *O. ptunarra* colonies in the Southern Midlands. The results of initial interviews are presented in Anderson (2001b). These locations were chosen as they were representative of all the colonies and habitat sites in the Southern Midlands Region. Butterfly sites ranged in area from less that one hectare to over 300 hectares and included areas that had known healthy populations to areas that were known to be in decline. The managers of the sites had a range of farming experience. Initial interviews were conduced during the year 2000 and follow up interviews were conducted in 2006 (University of Tasmania Human Ethics Approval H8629).

Land managers were asked a series of open-ended questions in a one-on-one interview situation. The questions were subdivided into eight main sections: background information, property history, fire history, environment, grazing management, chemical usage, activities in paddocks adjacent to *O. ptunarra* colonies and property management practices.

The land use management regimes of several properties have experienced major changes (i.e. irrigation and grazing) in the last five years. Stock grazing of sheep is ubiquitous for all properties, however recently several properties have also facilitated cattle grazing. The increase in cattle grazing in *Poa* tussock grassland which supports *O. ptunarra* colonies is disturbing. The damage cattle cause to tussocks has been recorded during *O. ptunarra* population monitoring and there is a strong correlation

between cattle grazing and declining butterfly numbers, and in at least one case, leading to extinction of a population.

Cell grazing is becoming the dominant grazing practiced in the Southern Midlands, with several properties employing cell grazing in paddocks with *O. ptunarra* colonies. Cell grazing regimes are based upon running 5-6000 sheep in 20-hectare (50 acre) blocks for 2-3 week periods. The cells are then rested and allowed to regenerate before being grazed again (Paterson 1994). Cell grazing is designed to promote the growth of exotic pasture species over native tussock grasses (Leonard & Kirkpatrick 2004; Verrier & Kirkpatrick 2005). The long-term impact of cell grazing on *O. ptunarra* colonies needs further investigation, but is likely to be deleterious.

The aerial application of pesticides and herbicides is utilized at several properties. This practice can negatively affect *O. ptunarra* populations either by direct or secondary toxicity. Blanket sprays and aerial applications of pesticides and herbicides can be especially dangerous because they utilize large volumes of chemicals, cover considerable land areas, and are relatively indiscriminate toxins. Many non-target organisms can be affected by such chemical use (Pimentel & Edwards 1982; Edwards 1993). Even when applied with caution, pesticides and herbicides have the potential to drift and could ultimately poison adjacent butterfly populations.

The formal listing of *O. ptunarra* as a threatened species and the private tenure of most sites upon which colonies exist does complicate conservation management. Many of the land managers interviewed are distrustful of government agencies, and were generally reluctant to participate in legally binding management programs, such as covenants and management agreements. A strong belief is held that even when incentives are offered with such programs, they are generally insufficient and not worth the effort and perceived to be too costly to the managers.

In Australia there exist several different types of public-private partnership providing incentives to landowners who manage their land in an environmentally sensitive way. There are also economic incentives and information sharing incentives, whereby the government provides free technical assistance to landowners. The first type of incentive is a covenant where the landowner voluntarily enters into a legally binding agreement to protect some of the land, and this covenant is then registered on the land title and follows it even to subsequent owners. This protects the land for the long-term.

Landowners participating in this scheme receive substantial tax breaks, such as exemptions from land tax on the protected land, and may receive priority for other benefits and grants (DPIPWE 2009).

The second type of incentive is a management agreement. This is legally binding, like the covenant, but is not registered on the title and does not provide long-term protection. Again, the landowners can receive priority for funding and assistance by committing to conservation in this way. Private Reserves are another type of partnership. These are legally binding and follow the title to provide ongoing protection, and give the land a 'Reserve' status. Again, priority for funding and assistance is a key incentive here (DPIPWE 2009).

There are many purchase programs whereby the government, or NGO receiving government grants, will purchase environmentally valuable land for protection and several groups offer free labour and assistance with land care for landowners that require assistance managing for environmental issues. Lastly, there are a range of grants available for landowners who undertake environmental improvements (e.g. NETLT 2009).

Overall, these incentives are useful, but can be very confusing and time consuming to understand and implement. Landowners would already require a strong commitment to conservation to take the time and trouble. It is useful, however, to reward responsible landowners, but it is unclear whether or not these fragmented incentives will actually lead to significantly more landowners conserving their land for *O. ptunarra*.

Because so many *O. ptunarra* colonies occur on private land, land management practices that sustain the needs of the butterfly are crucial for the protection, survival, and recovery of the species. It is essential that private land managers realise the importance of species protection and successful practices of beneficial management regarding endangered species. Such goals can be obtained through education, incentives, and partnerships. It is not enough to inform landowners of the presence of an endangered species on their land, in some cases this can actually be detrimental, leading to pre-emptive land clearing. Government and organisations must take an active role to assist managers in species protection through the provision of adequate incentives to ensure the desired action, and offer possibilities to manage land through mutually beneficial practices.

5.2 *Major factors affecting the sustainability of habitat patches*

Two species of the exotic social wasp genus *Vespula* now occur in Tasmania. European or German Wasp *Vespula germanica* were first found in a Hobart suburb in 1959 and have since spread to all parts of the State. The English or Common Wasp *Vespula vulgaris* is a relative newcomer to the state, where it is believed to have arrived around 1995 and is restricted to southeast Tasmania (New 1996).

European wasps were first noted in abundance at several *O. ptunarra* monitoring sites during the 1998 flight season (Bell 2002). European wasp has been repeatedly observed taking *O. ptunarra* at several different localities (pers. obs. 1999-2006 Bell 2002).. Wasps were a significant contributing factor for the extinction of at least two *O. ptunarra* colonies, Thompsons Park and Ladies Mile Marsh (Ladies Mile Plain) (Bell 2002). Beggs & Rees (1999) recognised the potential threat social wasps pose to species such as butterflies. Their models focusing on Lepidoptera larvae show species with spring caterpillars may be able to persist, but species with larvae occurring in the peak wasp season would be eliminated.

Provided there is an adequate density of *Poa* tussock as habitat, the presence or absence of improved pasture surrounding the *O. ptunarra* colonies does not appear to directly affect the populations. However continued fragmentation of the landscape is having an impact on the long-term survival of the species. There is evidence to suggest that there may be a threshold density of around 25% *Poa* tussock cover required to support viable *O. ptunarra* populations. The availability of nectar sources increases the longevity of individuals and lengthens the flight period within individual populations (pers. obs. 1999-2006) Similarly, the availability of nectar sources was found to increase the longevity of *Lycaena hippothoe* (Lycaenidae) by three to five times; this extended survival time also distinctly increased the duration of an individuals oviposition period (Fischer & Fiedler 2001).

Recolonization by *O. ptunarra* to abandoned sites is made difficult by the fragmented nature of remaining habitat, its low fecundity, short flight season, and weak flight. The fragmentation of habitats is the key factor responsible for the decline of genetic exchange between populations (Brookes *et al.* 1997; Lewis *et al.* 1997; Van Dongen *et al.* 1998; Clarke & O'Dwyer 2000; Schmitt & Seitz 2002; Krauss *et al.* 2004). Proposed rehabilitation of sites also poses difficulty because of the necessity to use locally sourced butterflies for such attempts. Removing individuals from successful populations an risk the viability of the source population (Schmitt *et al.* 2005; De Groot *et al.* 2009). Failure to recolonise the new site is highly likely (Cassel-Lundhagen *et al.* 2009).

5.3 *Attributes for suitability*

The maintenance of native grasslands and grassy woodlands in good condition is essential for *O. ptunarra* survival. Heavy stocking for extended periods quickly reduces the quality and extent of grassland and leads to patches of bear ground facilitating weed invasion. Any activity which further fragments *O. ptunarra* habitat should be avoided. This included alteration to drainage or ground disturbance in or near colonies as this affects tussock growth.

The key requirements for *O. ptunarra* sustainability are:

- *Poa* tussock grassland of at least 1 hectare
- Threshold density of around 25% *Poa* tussock cover
- Effective wasp control
- Availability of nectar sources
- Increased connectivity of habitat patches
- Limited sheep and no cattle grazing
- The development of land management agreements with private landowners

Plate 8 *O. ptunarra* male, Liawenee Moor, 2004

Chapter 7
Concluding Comments

All the aims of this study were broadly met. The first aim was to

* Increase the pool of knowledge and understanding of the genus *Oreixenica*, and the relationship of *Oreixenica* to other temperate zone southeast Australian Satyrinae.

This study has increased the pool of knowledge and understanding of the genus *Oreixenica*, and the relationships of *Oreixenica* to other temperate zone southeast Australian Satyrinae. This study has revealed that the temperate zone southeast Australian Satyrinae are a monophyletic group based on molecular evidence. Significantly, this study revealed that the *Heteronympha* clade is sister to the *Oreixenica* clade and that *G. klugii* is basal within the southeast Australian Satyrinae. We also have a better understanding and appreciation of the evolutionary history of *Oreixenica*.

The second aim of this study was to

* Characterise the adult morphology of the five temperate zone southeast Australian Satyrinae genera and fourteen species.

The genitalia of both male and female temperate zone southeast Australian Satyrinae have been documented for the first time. The main finding of this study was that the *Oreixenica* are a supported monophyletic group within the temperate zone southeast Australian Satyrinae based on morphological evidence. The synapomorphies that support this are (1) signa is absent from the corpus bursae and (2) forewing vein 10 from subcostal arises close to end of cell with (3) the discocellular vein sharply bent. This research has lead to the availability of additional synapomorphies for many of the genera and species within this group.

The third aim of this study was to

* Describe the eggs of the temperate zone southeast Australian Satyrinae.

The eggs of all species in the study have been described in detail and photographed both as fresh specimens and with the Scanning Electron Microscope.

The fourth aim of this study was to

* Describe and document the larva and pupa of *O. ptunarra.*

The early and late instar larva and pupa of *O. ptunarra* has been documented. This study is the first time late stage *O. ptunarra* lava have be found in the field, tracked to the pupa and finally emerge as beautiful *O. ptunarra* butterflies. Understanding the whole life cycle of *O. ptunarra* is vital for developing effective conservation management strategies.

The fifth aim of this study was to

* Contribute to understanding *O. ptunarra*, and its relationship to its close relatives.

This study has contributed greatly to understanding *O. ptunarra* and the relationship of *O. ptunarra* to other *Oreixenica.* We understand the relationships within the genus *Oreixenica* and that *O. latialis* is the sister species to *O. ptunarra.*

The final aim of this study was to

* Investigate the genetic diversity of *O. ptunarra* populations which will contribute towards conservation management strategies for *O. ptunarra.*

This study has revealed some surprising results regarding genetic diversity of *O. ptunarra* populations, particularly the relationships of subspecies and various population interactions. *O. ptunarra* populations are genetically diverse and currently show limited evidence of inbreeding. However, there is evidence that populations are becoming increasingly genetically isolated, particularly in the Midlands and Eastern Regions of Tasmania. The fact that populations appear to interact within the traditional subspecies ranges is presently overlooked in current management plans. This will need to be carefully considered when future *O. ptunarra* conservation management strategies are considered.

Future research

Information from both the molecular sequences and morphological data in this study provide powerful insights into relationships within the temperate zone southeast Australian Satyrinae. The building of this information into further work resolving the relationship of Satyrinae at a global level would greatly enhance the phylogenies of Peña (2006), Wahlberg (2003b) and others.

This was the first phylogenetic analyses of *O. ptunarra* populations. The Lep12 / Met20 fragment provided very useful initial phylogenetic information. Future *O. ptunarra* phylogenetic studies should further address the question of population interaction, targeting part of the genome most proficient at resolving recent divergences.

Synapomorphies obtained in this study through the characterisation of both male and female genitalia have contributed to a better classification of some genera and species. Future research describing the genitalia of species to define synapomorphies for genera in closely related Nymphalide subfamilies would be constructive as many of the traditional characters used to define the genera and subfamilies within Nymphalidae do not hold true to all members of the group into which they are classified.

Plate 9 *O. ptunarra* male, Tunbridge Tiers, March 2004

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Appendices

Appendix 1 - Collection details for species dissected for genitalia analysis

Species	Sex	Collection Info	Dissection Code	Collector*
A. hobartia	♂	Mt Barrow Mid Slopes 15/Nov/2000	GDR2 – P	McQ
A. hobartia	♂	Mt King William Plain 02/Jan/2004	GDR2 – Q	RALA
A. hobartia	♀	Mt King William Plain 02/Jan/2004	GDR2 – R	RALA
A. hobartia	♀	Mt King William Plain 02/Jan/2004	GDR2 – S	RALA
G. klugii	♂	Darling Range, Flinders Is. 16/Mar/1982	CYD 2 – 2	McQ /Newtown
G. klugii	♀	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – F	RALA
G. klugii	♀	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – N	RALA
G. klugii	♂	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – V	RALA
G. klugii	♂	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – W	RALA
H. penelope	♀	Lake Leake 29/Mar/1949		S. Angel /Newtown
H. cordace	♂	Paradise Plains 05/Jan/2001	GDR2 – X	RALA
H. cordace	♀	Paradise Plains 05/Jan/2001	GDR2 – Y	RALA
H. merope	♀	Lindisfarne, TAS 1984	GDR2 – E	CJY /Newtown
H. merope	♂	Glenlusk 13/Jan/2002 42°29'S 147°12'E ALT~375	GDR2 – T	RALA
H. merope	♂	Waterworks 12/Jan/2005	CYD 2 – 1	RALA
H. penelope	♀	Glenlusk 13/Jan/2002 42°29'S 147°12'E ALT~375	GDR2 – K	RALA
H. penelope	♂	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – D	RALA
H. penelope	♀	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – G	RALA
J. villida	♂	Devonport, TAS. Stoney Rise Carpark 20/Mar/1992		L. Hill /Newtown
J. villida	♂	Trevallyn 1/Mar/1965		R.J. Hardy /Newtown
J. villida	♀	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – I	RALA
J. villida	♀	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – J	RALA
J. villida	♂	Glenlusk 12/Feb/2005 42°29'S 147°12'E ALT~375	GDR2 – U	RALA
N. leprea	♀	Lake St. Clair Feb/1941		J.W. Evans /Newtown
N. leprea	♂	Pelion Hut 7-8/Jan/1989 41°50'S 146°04'E ALT~900m		McQ /Newtown
N. leprea	♀	Mt Wellington Jan/1987 ALT~700m	CYD 2 – 4	McQ /Newtown

N. leprea	♂	Mt King William Plain 31/Jan/2002 42°21's 146°08'E ALT ~800m	GDR2 – L	RALA
N. leprea	♂	Mt King William Plain 31/Jan/2002 42°21's 146°08'E ALT ~800m	GDR2 – M	RALA
N. leprea	♀	Mt King William Plain 31/Jan/2002 42°21's 146°08'E ALT ~800m	GDR2 – O	RALA
O. lathoniella	♂	Lake Augusta Road 29/Feb/2000 42.610S 146.725E ALT ~1125m	OL LAR 1	RALA
O. lathoniella	♂	Lake Augusta Road 29/Feb/2000 42.610S 146.725E ALT ~1125m	OL LAR 2	RALA
O. lathoniella	♂	Steppes Sculptures 16/Mar/2000 42.106S 146.892E ~875m	OL SS 1 - 3	RALA
O. orichora	♀	5km SW Breana 23/Jan/1992 ~1070m		McQ
O. ptunarra	♀	Tunbridge Tiers Power pole 76 23/Mar/2002	'A'	RALA
O. ptunarra	♀	Tunbridge Tiers Power pole 76 23/Mar/2002	'C'	RALA
O. ptunarra	♀	Pike's Hill TAS 23/Mar/2002	'C'	RALA
O. ptunarra	♀	Pike's Hill TAS 23/Mar/2002	'D'	RALA
O. ptunarra	♀	Pike's Hill TAS 23/Mar/2002	'P'	RALA
O. ptunarra	♂	Peak Plain, TAS 3/Mar/1995 41.22S 145.45E ALT 640m	Pop H2	McQ & Ek
O. ptunarra	♂	Glovers TAS, 17/Mar/1995 42.12S 146.56E ALT 610m	Pop R2	McQ & Ek
O. ptunarra	♂	Snowy Plain, TAS 19/Mar/1995 41.54S 147.48E	Pop D4	McQ & Ek
O. ptunarra	♂	Flagstaff Marsh TAS. 19/Mar/1995 41.12S 147.51E Alt 540m	Pop F2	McQ & Ek
O. ptunarra	♂	Stony Gully Road, TAS 19/Mar/1995 41.58S 147.38E ALT 550m	Pop L1	McQ & Ek
O. ptunarra	♂	Stony Gully Road, TAS 19/Mar/1995 41.58S 147.38E ALT 550m	Pop L13	McQ & Ek
O. ptunarra	♂	Stony Gully Road, TAS 19/Mar/1995 41.58S 147.38E ALT 550m	Pop L5	McQ & Ek
O. ptunarra	♂	Mike Howe's Marsh, TAS 23/Mar/1995 42.14S 147.15E ALT 600m	Pop X2	McQ & Ek
O. ptunarra	♂	Muddy Plain Road TAS. 28/Mar/1995 42.26S 147.12E ALT 400m	Pop E1	McQ & Ek
O. ptunarra	♂	Bellvue West, TAS.29/Mar/1995 42.11S 147.24E ALT 300m	Pop B5	McQ & Ek
O. ptunarra	♂	Black Johnny's Marsh, TAS 29/Mar/1995 42.13S 147.42E ALT 320m	Pop K1	McQ & Ek
O. ptunarra	♂	Fitch's Hill TAS, 29/Mar/1995 42.18S 147.31E ALT 460m	Pop P2	McQ & Ek
O. ptunarra	♂	Vale of Belvoir, TAS 3/Apr/1995 41.31S 145.53E ALT 860m	Pop A1	McQ & Ek
O. ptunarra	♂	Vale of Belvoir, TAS 3/Apr/1995 41.31S 145.53E ALT 860m	Pop A5	McQ & Ek
O. ptunarra	♂	Vale of Belvoir, TAS 3/Apr/1995 41.31S 145.53E ALT 860m	Pop A8	McQ & Ek
O. ptunarra	♂	Hatfield Plain, TAS. 3/Apr/1995 41.30S 145.39E ALT 670m	Pop G	McQ & Ek
O. ptunarra	♂	42.09S 146.26E Nive Plain, TAS 650m 4/Apr/1995	Pop M2	McQ & Ek

O. ptunarra	♀	Dennistown Road, TAS.11/Mar/2000 42.100S 147.808E ALT ~80m		RALA
O. correae	♂	Mt Donna Buang, VIC 27/Feb/2005 37°42'S 145°40'E ~1250m	PD 5 AA151	MFB
O. correae	♀	Mt Donna Buang, VIC 27/Feb/2005 37°42'S 145°40'E ~1250m	PD 6 AA152	MFB
O. correae	♀	Mt Donna Buang, VIC 10/March/2005 37°42'S 145°40'E ~1250m	PD 13	RALA
O. correae	♂	Mt Donna Buang, VIC 10/March/2005 37°42'S 145°40'E	PD 13	RALA
O. kershawi	♀	Odd Specimen ANIC	PD 11	
O. kershawi	♂	Mt Donna Buang, VIC 27/Feb/2005 37°72'S 145°71'E ~390m	PD 7 AA156	MFB
O. kershawi	♂	Mt Donna Buang, VIC 27/Feb/2005 37°72'S 145°71'E ~390m	PD 8 AA154	MFB
O. kershawi	♀	Mt Donna Buang, VIC 10/Mar/2005 37°72'S 145°71'E ~390m	PD 12	RALA
O. kershawi	♂	Mt Donna Buang, VIC 10/Mar/2005 37°72'S 145°71'E ~390m	PD 12	RALA
O. l. latialis	♂	Prussian Ck, 1km NE of Smiggin Holes NSW ALT ~1620m 10/Mar/1973	CYD 3 – 2	ANIC
O. lathoniella	♂	Liawenee Turning Circle 17/Feb/2002 42.625S 146.735E 0 ALT ~1100m	GDR2 – B OL LTC 2	RALA
O. lathoniella	♂	Liawenee Turning Circle 17/Feb/2002 42.625S 146.735E 0 ALT ~1100m	GDR2 – C OL LTC 3	RALA
O. lathoniella	♂	Tunbridge Tiers 18/Feb/2000 42.123S 147.250E ALT ~875m	CYD 3 – 7 OL TT1	RALA
O. lathoniella	♂	Liawenee Turning Circle 29/Feb/2000 42.625S 146.735E ALT ~1100m	CYD 3 – 5 OL LTC 1	RALA
O. l. herceus	♀	Tinderry Nature Reserve NSW 1/Apr/2005 35°44'S 149°16'E ALT ~1260m	PD 3 MF8-OO-P598	MFB
O. l. herceus	♀	Tinderry Nature Reserve NSW 1/Apr/2005 35°44'S 149°16'E ALT ~1260m	PD 4 MF8-OO-P597	MFB
O. latialis	♀	Mt Hotham, VIC. 12/Mar/2005 37°00'S 147°10'E	GDR2 – A	RALA
O. latialis	♂	Mt Hotham, VIC. 12/Mar/2005 37°00'S 147°10'E	PD 1	RALA
O. latialis	♂	Lake Catani Mt Buffalo, VIC. 11/Mar/2005 36°15'S 146°39'E	PD 11	RALA
O. latialis	♀	Lake Catani, Mt Buffalo, VIC. 7/Mar/1971 36°15'S 146°39'E	CYD 2 – 5	ANIC
O. latialis	♀	Tinderry Nature Reserve NSW 1/Apr/2005 35°44'S 149°16'E ALT ~1260m	PD 1 MF8-OO-P600	MFB
O. latialis	♂	Tinderry Nature Reserve NSW 1/Apr/2005 35°44'S 149°16'E ALT ~1260m	PD 2 MF8-OO-P599	MFB
O. orichora	♀	Tallaganda N.P. NSW 6km E. Captain's Flat 19/Dec/2005 35°36'S 149°29'E ALT ~1200m	PD AA 134	MFB
O. orichora	♂	Liawenee Turning Circle 03/Jan/2002 41.625S 146.735E 1 ALT ~1060m	CYD 2 – OO LTC 3	RALA
O. orichora	♂	Lake Augusta Road, Liawenee 03/Jan/2002 41.899S 146.629E ALT ~1080m	CYD 3 – 1 LAR 1	RALA
O. orichora	♂	Canal Drive Liawenee 03/Jan/2002 41.908S 146.623E ALT ~1040m	CYD 3 – 4 OO CD1	RALA
O. orichora	♂	Liawenee Turning Circle 03/Jan/2002 41.625S 146.735E ALT ~1060m	CYD 3 – 6 OO LTC1	RALA
O. orichora	♂	Canal Drive Liawenee 03/Jan/2002 41.908S 146.623E ALT ~1040m	OO CD 3	RALA

O. orichora	♂	Canal Drive Liawenee 03/Jan/02002 41.908S 146.623E ALT ~1040m	OO LAR 2	RALA
O. orichora	♂	Liawenee Turning Circle 03/Jan/2002 41.625S 146.735E ALT ~1060m	OO LTC 2	RALA
O. orichora	♀	Canal Drive Liawenee 03/Jan/2002 41.908S 146.623E ALT ~1040m	PD 10 OO CD A	RALA
O. orichora	♀	Canal Drive Liawenee 03/Jan/2002 41.908S 146.623E ALT ~1040m	PD 9 OO CD 1	RALA
O. orichora	♂	Pine Lake 04/Jan/2002 41.758S 146.698E ALT ~1200m	CYD 3 – 3 OO PL1	RALA
O. orichora	♂	Pine Lake 04/Jan/2002 41.758S 146.698E ALT ~1200m	OO PL 2+3	RALA
O. orichora	♂	Lake Augusta Road, Liawenee 03/Jan/2001 41.899S 146.629E ALT ~1080m	CYD 2 – OO LAR 3	RALA
O. ptunarra	♀	Pike's Hill TAS 23/Mar/2002 42.373S 147.354E	PD 4	RALA
O. ptunarra	♂	Pike's Hill TAS 23/Mar/2002 42.373S 147.354E	PD 4	RALA
V. kershawi	♀	Forcett, TAS.29 Nov 1973		R.J. Hardy /Newtown
V. kershawi	♂	Devonport, TAS. Stoney Rise car park 6 Aug 1992		L. Hill /Newtown
V. kershawi	♀	Glenlusk 29/Feb/2004 42°29'S 147°12'E ALT~375	GDR2 – H	RALA
V. kershawi	♂	Newtown, TAS. 11 NOV 1952	CYD 2 – 3	W. Newport /Newtown

Collector*	
RALA	R.A.L Anderson
CJY	C.J. Young
Newtown	Held by DPIW Collection Newtown
McQ	P.B. McQuillan
ANIC	Australian National Insect Collection
MFB	M.F. Braby
McQ & Ek	P.B. McQuillan & C.J. Ek (1997)

Appendix 2 - List of specimens used in phylogenetic analysis and their province.

Specimen name	Code	Collection Details	Collection date
Argynnina hobartia	AH MtKW 1	Lyell Highway Plain opposite base of Mt King William	8/Nov/03
Argynnina hobartia	AH MtKW 2	Lyell Highway Plain opposite base of Mt King William	8/Nov/03
Argynnina hobartia	AH MtKW 3	Lyell Highway Plain opposite base of Mt King William	8/Nov/03
Argynnina hobartia	AH MtKW 4	Lyell Highway Plain opposite base of Mt King William	8/Nov/03
Geitoneura klugii	KG GLEN 1	Glenlusk	5/Jan/05
Geitoneura klugii	KG GLEN 2	Glenlusk	5/Jan/05
Heteronympha cordace	BEB Liffey 1	Plain off Lake Highway Liffey	6/Jan/03
Heteronympha cordace	BEB Liffey 2	Plain off Lake Highway Liffey	6/Jan/03
Heteronympha cordace	BEB MtKW 1	Lyell Highway Mt King William base	31/Jan/02
Heteronympha cordace	BEB MtKW 1	Lyell Highway Mt King William base	31/Jan/02
Heteronympha cordace	BEB PP 1	Paradise Plain	5/Jan/01
Heteronympha cordace	BEB PP 2	Paradise Plain	5/Jan/01
Heteronympha cordace	BEB PP 3	Paradise Plain	5/Jan/01
Heteronympha merope	CB GLEN 1 (CB7)	Glenlusk	5/Jan/05
Heteronympha merope	CB Wey 1 (CB1)	Weymouth	9/Jan/05
Heteronympha merope	CB Wey 2 (CB2)	Weymouth	9/Jan/05
Heteronympha merope	CB Wey 3 (CB6)	Weymouth	9/Jan/05
Heteronympha merope	CB WW 1 (CB3)	Water Works	12/Jan/05
Heteronympha merope	CB WW 2 (CB4)	Water Works	12/Jan/05
Heteronympha merope	CB WW 3 (CB5)	Water Works	12/Jan/05
Heteronympha penelope	SB GLEN 1	Glenlusk	5/Jan/05
Heteronympha penelope	SB GLEN 2	Glenlusk	5/Jan/05
Nesoxenica leprea	NX BBPJ 1	Big Bend Projection Bluff	3/Jan/04
Nesoxenica leprea	NX BBPJ 2	Big Bend Projection Bluff	3/Jan/04
Nesoxenica leprea	NX HTZ 1	Hartz Mt road below walkers registration	12/Feb/01
Nesoxenica leprea	NX HTZ 2	Hartz Mt road below walkers registration	12/Feb/01
Nesoxenica leprea	NX MtKW 1	Lyell Highway Mt King William base	31/Jan/02
Nesoxenica leprea	NX MtKW 2	Lyell Highway Mt King William base	31/Jan/02
Nesoxenica leprea	NX MtKW 3	Lyell Highway Mt King William base	31/Jan/02
Nesoxenica leprea	NX MtKW 3	Lyell Highway Mt King William base	31/Jan/02
Nesoxenica leprea	NX RCCP 1	Ronny Creek Car park – Dove Lake Cradle Mt	7/Jan/03
Nesoxenica leprea	NX RCCP 2	Ronny Creek Car park – Dove Lake Cradle Mt	7/Jan/03
Oreixenica corrieae	OC LmtV 1	Lake Mt Victoria	11/March/05
Oreixenica corrieae	OC LmtV 7	Lake Mt Victoria	11/March/05
Oreixenica corrieae	OC MtDBV 1	Mt Donna Buang Victoria	10/March/05
Oreixenica corrieae	OC MtDBV 2	Mt Donna Buang Victoria	10/March/05
Oreixenica corrieae	OC MtDBV 2A	Mt Donna Buang Victoria	10/March/05
Oreixenica corrieae	OC MtDBV 3	Mt Donna Buang Victoria	10/March/05
Oreixenica kershawi	OK MtDBV 1	Mt Donna Buang Victoria	10/March/05
Oreixenica kershawi	OK MtDBV 2	Mt Donna Buang Victoria	10/March/05
Oreixenica kershawi	OK MtDBV 3	Mt Donna Buang Victoria	10/March/05
Oreixenica kershawi	OK MtDBV 4	Mt Donna Buang Victoria	10/March/05
Oreixenica kershawi	OK MtDBV 5	Mt Donna Buang Victoria	10/March/05
Oreixenica kershawi	OK MtDBV 6	Mt Donna Buang Victoria	10/March/05
Oreixenica lathoniella	OL CD 1	Canal Drive Liawenee Moore	28/Feb/06
Oreixenica lathoniella	OL CD 2	Canal Drive Liawenee Moore	28/Feb/06
Oreixenica lathoniella	OL DIR 1	Dennistoun Road Interlaken	23/March/02
Oreixenica lathoniella	OL DIR 2	Dennistoun Road Interlaken	23/March/02
Oreixenica lathoniella	OL DIR 3	Dennistoun Road Interlaken	23/March/02

Specimen name	Code	Collection Details	Collection date
Oreixenica lathoniella	OL DIR 4	Dennistoun Road Interlaken	23/March/02
Oreixenica lathoniella	OL DIR 5	Dennistoun Road Interlaken	23/March/02
Oreixenica lathoniella	OL LAR 5	Lake Augusta Road Liawenee	28/Feb/06
Oreixenica lathoniella	OL LAR 6	Lake Augusta Road Liawenee	28/Feb/06
Oreixenica lathoniella	OL LAR 7	Lake Augusta Road Liawenee	28/Feb/06
Oreixenica lathoniella	OL LAR 8	Lake Augusta Road Liawenee	28/Feb/06
Oreixenica lathoniella	OL MtWel 1	Springs Mt Wellington	6/March/01
Oreixenica lathoniella	OL MtWel 1	Springs Mt Wellington	6/March/01
Oreixenica lathoniella	OL TT 1	Tunbridge Tiers	15/March/03
Oreixenica lathoniella	OL TT 2	Tunbridge Tiers	15/March/03
Oreixenica lathoniella	OL TT76	Tunbridge Tiers Power Pole 76	14/March/03
Oreixenica lathoniella	OL TT76 1	Tunbridge Tiers Power Pole 76	23/March/02
Oreixenica lathoniella	OL TT76 2	Tunbridge Tiers Power Pole 76	23/March/02
Oreixenica lathoniella	OL TT76 3	Tunbridge Tiers Power Pole 76	23/March/02
Oreixenica latialis	OLA MtBuf 1	Mt Buffalo Victoria	12/March/05
Oreixenica latialis	OLA MtBuf 2	Mt Buffalo Victoria	12/March/05
Oreixenica latialis	OLA MtBuf 3	Mt Buffalo Victoria	12/March/05
Oreixenica latialis	OLA MtHoth	Mt Hotham Victoria	13/March/05
Oreixenica orichora	OO CDFF 1	Canal Drive Flying Fox Liawenee	5/Jan/03
Oreixenica orichora	OO CDFF 2	Canal Drive Flying Fox Liawenee	5/Jan/03
Oreixenica orichora	OO CDFF 3 (OO2)	Canal Drive Flying Fox Liawenee	5/Jan/03
Oreixenica orichora	OO FHM 1	Farm House Marsh Miena	5/Jan/03
Oreixenica orichora	OO FHM 2	Farm House Marsh Miena	5/Jan/03
Oreixenica orichora	OO LAR 1	Lake Augusta Road Liawenee	5/Jan/03
Oreixenica orichora	OO LAR 2	Lake Augusta Road Liawenee	5/Jan/03
Oreixenica orichora	OO LAR 3 (OO1)	Lake Augusta Road Liawenee	5/Jan/03
Oreixenica orichora	OO ORB 1	Ouse River Bridge Miena	5/Jan/03
Oreixenica orichora	OO ORB 2	Ouse River Bridge Miena	5/Jan/03
Oreixenica orichora	OO ORB 3 (OO4)	Ouse River Bridge Miena	5/Jan/03
Oreixenica orichora	OO PLB 1	Pine Lake Base Northern End	6/Jan/03
Oreixenica orichora	OO PLB 2	Pine Lake Base Northern End	6/Jan/03
Oreixenica orichora	OO PLB 3 (OO3)	Pine Lake Base Northern End	6/Jan/03
Oreixenica orichora	OO RCCP 1	Ronny Creek Car park Dove Lake Road Cradle Mt	7/Jan/03
Oreixenica orichora	OO RCCP 2	Ronny Creek Car park Dove Lake Road Cradle Mt	7/Jan/03
Oreixenica orichora	OO RCCP 3 (OO5)	Ronny Creek Car park Dove Lake Road Cradle Mt	7/Jan/03
Oreixenica ptunarra	OP BTS 1	Barron Tier South	18/March/06
Oreixenica ptunarra	OP BTS 2	Barron Tier South	18/March/06
Oreixenica ptunarra	OP BTS 3	Barron Tier South	18/March/06
Oreixenica ptunarra	OP BTS 4	Barron Tier South	18/March/06
Oreixenica ptunarra	OP BTTC 1	Barron Tier Tods Corner	18/March/06
Oreixenica ptunarra	OP BTTC 2	Barron Tier Tods Corner	18/March/06
Oreixenica ptunarra	OP BTTC 3	Barron Tier Tods Corner	18/March/06
Oreixenica ptunarra	OP BTTC 4	Barron Tier Tods Corner	18/March/06
Oreixenica ptunarra	OP Bel 1	Bellevue Hill Anthill Ponds	25/March/05
Oreixenica ptunarra	OP Bel 2	Bellevue Hill Anthill Ponds	25/March/05
Oreixenica ptunarra	OP Bel 3	Bellevue Hill Anthill Ponds	25/March/05
Oreixenica ptunarra	OP Bel 4	Bellevue Hill Anthill Ponds	25/March/05
Oreixenica ptunarra	OP BPJ 1	Bronte Park Junction	21/March/06
Oreixenica ptunarra	OP BPJ 2	Bronte Park Junction	21/March/06
Oreixenica ptunarra	OP BPJ 3	Bronte Park Junction	21/March/06
Oreixenica ptunarra	OP BPJ 4	Bronte Park Junction	21/March/06
Oreixenica ptunarra	OP DM 1	Dairy Maids Plain NW	21/March/04
Oreixenica ptunarra	OP DM 2	Dairy Maids Plain NW	21/March/04
Oreixenica ptunarra	OP DM 3	Dairy Maids Plain NW	21/March/04
Oreixenica ptunarra	OP DM 4	Dairy Maids Plain NW	21/March/04
Oreixenica ptunarra	OP Flag 5	Flagstaff Marsh (unburnt side)	22/March/06
Oreixenica ptunarra	OP Flag 6	Flagstaff Marsh (unburnt side)	22/March/06

Specimen name	Code	Collection Details	Collection date
Oreixenica ptunarra	OP Flag 7	Flagstaff Marsh (unburnt side)	22/March/06
Oreixenica ptunarra	OP Flag 8	Flagstaff Marsh (unburnt side)	22/March/06
Oreixenica ptunarra	OP HAT 1	Hatfield Plain NW	21/March/04
Oreixenica ptunarra	OP HAT 2	Hatfield Plain NW	21/March/04
Oreixenica ptunarra	OP HAT 3	Hatfield Plain NW	21/March/04
Oreixenica ptunarra	OP HAT 4	Hatfield Plain NW	21/March/04
Oreixenica ptunarra	OP LC 1	Lake Crescent Interlaken	10/March/05
Oreixenica ptunarra	OP LC 10	Lake Crescent Interlaken	10/March/05
Oreixenica ptunarra	OP LC 2	Lake Crescent Interlaken	10/March/05
Oreixenica ptunarra	OP LC 7	Lake Crescent Interlaken	10/March/05
Oreixenica ptunarra	OP LC 8	Lake Crescent Interlaken	10/March/05
Oreixenica ptunarra	OP LC 9	Lake Crescent Interlaken	10/March/05
Oreixenica ptunarra	OP LMLE 1	Liawenee Moor Liawenee End	21/March/06
Oreixenica ptunarra	OP LMLE 2	Liawenee Moor Liawenee End	21/March/06
Oreixenica ptunarra	OP LMLE 3	Liawenee Moor Liawenee End	21/March/06
Oreixenica ptunarra	OP LMLE 4	Liawenee Moor Liawenee End	21/March/06
Oreixenica ptunarra	OP LMMS 1	Liawenee Moor Middle South	21/March/06
Oreixenica ptunarra	OP LMMS 2	Liawenee Moor Middle South	21/March/06
Oreixenica ptunarra	OP LMMS 3	Liawenee Moor Middle South	21/March/06
Oreixenica ptunarra	OP LMMS 4	Liawenee Moor Middle South	21/March/06
Oreixenica ptunarra	OP LMME 1	Liawenee Moor Miena End	21/March/06
Oreixenica ptunarra	OP LMME 2	Liawenee Moor Miena End	21/March/06
Oreixenica ptunarra	OP LMME 3	Liawenee Moor Miena End	21/March/06
Oreixenica ptunarra	OP LMME 4	Liawenee Moor Miena End	21/March/06
Oreixenica ptunarra	OP LiaweneeTC 1	Liawenee Turning Circle	29/Feb/00
Oreixenica ptunarra	OP LiaweneeTC 2	Liawenee Turning Circle	29/Feb/00
Oreixenica ptunarra	OP LiaweneeTC 3	Liawenee Turning Circle	29/Feb/00
Oreixenica ptunarra	OP LiaweneeTC 4	Liawenee Turning Circle	29/Feb/00
Oreixenica ptunarra	OP LCT 1	Little China Tier Andover	25/March/05
Oreixenica ptunarra	OP LCT 2	Little China Tier Andover	25/March/05
Oreixenica ptunarra	OP LCT 3	Little China Tier Andover	25/March/05
Oreixenica ptunarra	OP LCT 4	Little China Tier Andover	23/March/02
Oreixenica ptunarra	OP LCT 5	Little China Tier Andover	23/March/02
Oreixenica ptunarra	OP LCT 6	Little China Tier Andover	23/March/02
Oreixenica ptunarra	OP LPLB 1	Little Pine Lagoon Boat ramp	21/March/06
Oreixenica ptunarra	OP LPLB 2	Little Pine Lagoon Boat ramp	21/March/06
Oreixenica ptunarra	OP LPLB 3	Little Pine Lagoon Boat ramp	21/March/06
Oreixenica ptunarra	OP LPLB 4	Little Pine Lagoon Boat ramp	21/March/06
Oreixenica ptunarra	OP Long 5	Long Marsh	22/March/06
Oreixenica ptunarra	OP Long 6	Long Marsh	22/March/06
Oreixenica ptunarra	OP Long 7	Long Marsh	22/March/06
Oreixenica ptunarra	OP Long 8	Long Marsh	22/March/06
Oreixenica ptunarra	OP MH 1	Marlborough Highway (11km North Bronte Park)	21/March/06
Oreixenica ptunarra	OP MH 2	Marlborough Highway (11km North Bronte Park)	21/March/06
Oreixenica ptunarra	OP MH 3	Marlborough Highway (11km North Bronte Park)	21/March/06
Oreixenica ptunarra	OP MH 4	Marlborough Highway (11km North Bronte Park)	21/March/06
Oreixenica ptunarra	OP MR 1	Morey Road NW Plains	22/March/04
Oreixenica ptunarra	OP MR 2	Morey Road NW Plains	22/March/04
Oreixenica ptunarra	OP MR 3	Morey Road NW Plains	22/March/04
Oreixenica ptunarra	OP MR 4	Morey Road NW Plains	22/March/04
Oreixenica ptunarra	OP NB 1	North Bronte (5km North Bronte Park)	21/March/06
Oreixenica ptunarra	OP NB 2	North Bronte (5km North Bronte Park)	21/March/06
Oreixenica ptunarra	OP NB 3	North Bronte (5km North Bronte Park)	21/March/06
Oreixenica ptunarra	OP NB 4	North Bronte (5km North Bronte Park)	21/March/06
Oreixenica ptunarra	OP ORB 1	Ouse River Bridge Miena	21/Jan/03
Oreixenica ptunarra	OP ORB 2	Ouse River Bridge Miena	21/Jan/03
Oreixenica ptunarra	OP ORB 3	Ouse River Bridge Miena	21/Jan/03

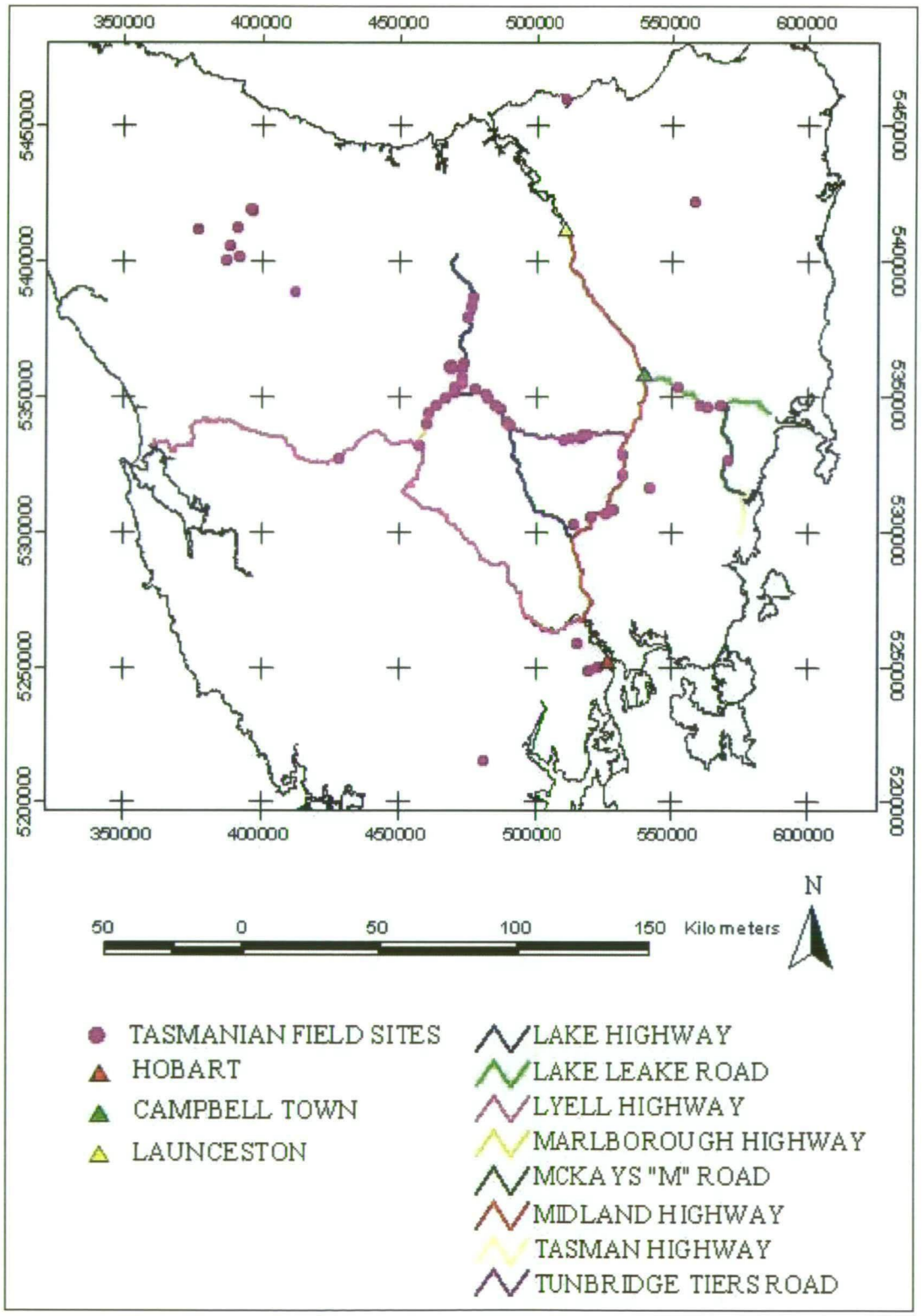
Specimen name	Code	Collection Details	Collection date
Oreixenica ptunarra	OP ORB 4	Ouse River Bridge Miena	21/Jan/03
Oreixenica ptunarra	OP PPFE 1	Peak Plain Far End NW	21/March/04
Oreixenica ptunarra	OP PPFE 2	Peak Plain Far End NW	21/March/04
Oreixenica ptunarra	OP PPFE 3	Peak Plain Far End NW	21/March/04
Oreixenica ptunarra	OP PPFE 4	Peak Plain Far End NW	21/March/04
Oreixenica ptunarra	OP PPS1 1	Peak Plain Side 1 NW	21/March/04
Oreixenica ptunarra	OP PPS1 2	Peak Plain Side 1 NW	21/March/04
Oreixenica ptunarra	OP PPS1 3	Peak Plain Side 1 NW	21/March/04
Oreixenica ptunarra	OP PPS1 4	Peak Plain Side 1 NW	21/March/04
Oreixenica ptunarra	OP PPS2 1	Peak Plain Side 2 NW	21/March/04
Oreixenica ptunarra	OP PPS2 2	Peak Plain Side 2 NW	21/March/04
Oreixenica ptunarra	OP PPS2 3	Peak Plain Side 2 NW	21/March/04
Oreixenica ptunarra	OP PPS2 4	Peak Plain Side 2 NW	21/March/04
Oreixenica ptunarra	OP PH 1	Pikes Hill	25/March/05
Oreixenica ptunarra	OP PH 2	Pikes Hill	25/March/05
Oreixenica ptunarra	OP PH 3	Pikes Hill	23/March/02
Oreixenica ptunarra	OP PH 4	Pikes Hill	23/March/02
Oreixenica ptunarra	OP PH 5	Pikes Hill	23/March/02
Oreixenica ptunarra	OP PTD 1	Pine Tier Dam Road	21/March/06
Oreixenica ptunarra	OP PTD 2	Pine Tier Dam Road	21/March/06
Oreixenica ptunarra	OP PTD 3	Pine Tier Dam Road	21/March/06
Oreixenica ptunarra	OP PTD 4	Pine Tier Dam Road	21/March/06
Oreixenica ptunarra	OP RC 1	Race Course Plain NW	20/March/04
Oreixenica ptunarra	OP RC 2	Race Course Plain NW	20/March/04
Oreixenica ptunarra	OP Rcrk 1	Ripple Creek Lake Highway	18/March/06
Oreixenica ptunarra	OP Rcrk 2	Ripple Creek Lake Highway	18/March/06
Oreixenica ptunarra	OP Rcrk 3	Ripple Creek Lake Highway	18/March/06
Oreixenica ptunarra	OP Rcrk 4	Ripple Creek Lake Highway	18/March/06
Oreixenica ptunarra	OP SH 1	Shannon River	18/March/06
Oreixenica ptunarra	OP SH 2	Shannon River	18/March/06
Oreixenica ptunarra	OP SH 3	Shannon River	18/March/06
Oreixenica ptunarra	OP SH 4	Shannon River	18/March/06
Oreixenica ptunarra	OP StPat 1	St Patrick's Plain (Church / Hall End)	10/March/05
Oreixenica ptunarra	OP StPat 2	St Patrick's Plain (Church / Hall End)	10/March/05
Oreixenica ptunarra	OP StPat 3	St Patrick's Plain (Church / Hall End)	10/March/05
Oreixenica ptunarra	OP StPat 4	St Patrick's Plain (Church / Hall End)	10/March/05
Oreixenica ptunarra	OP StPatME 1	St Patrick's Plain (Miena End)	18/March/06
Oreixenica ptunarra	OP StPatME 2	St Patrick's Plain (Miena End)	18/March/06
Oreixenica ptunarra	OP StPatME 3	St Patrick's Plain (Miena End)	18/March/06
Oreixenica ptunarra	OP StPatME 4	St Patrick's Plain (Miena End)	18/March/06
Oreixenica ptunarra	OP SHH 1	Steppes Highway Hill	10/March/05
Oreixenica ptunarra	OP SHH 2	Steppes Highway Hill	10/March/05
Oreixenica ptunarra	OP SHH 3	Steppes Highway Hill	10/March/05
Oreixenica ptunarra	OP SHH 4	Steppes Highway Hill	10/March/05
Oreixenica ptunarra	OP SGR 5	Stony Gully Road	22March/06
Oreixenica ptunarra	OP SGR 6	Stony Gully Road	22March/06
Oreixenica ptunarra	OP SGR 7	Stony Gully Road	22March/06
Oreixenica ptunarra	OP SGR 8	Stony Gully Road	22March/06
Oreixenica ptunarra	OP TT59 1	Tunbridge Tiers Power Pole 59	10/March/05
Oreixenica ptunarra	OP TT59 2	Tunbridge Tiers Power Pole 59	10/March/05
Oreixenica ptunarra	OP TT59 2	Tunbridge Tiers Power Pole 59	10/March/05
Oreixenica ptunarra	OP TT59 4	Tunbridge Tiers Power Pole 59	10/March/05
Oreixenica ptunarra	OP TT76 1	Tunbridge Tiers Power Pole 76	23/March/02
Oreixenica ptunarra	OP TT76 1a	Tunbridge Tiers Power Pole 76	14/March/03
Oreixenica ptunarra	OP TT76 2	Tunbridge Tiers Power Pole 76	23/March/02
Oreixenica ptunarra	OP TT76 2a	Tunbridge Tiers Power Pole 76	14/March/03
Oreixenica ptunarra	OP TT76 3	Tunbridge Tiers Power Pole 76	23/March/02

Specimen name	Code	Collection Details	Collection date
Oreixenica ptunarra	OP TT76 4	Tunbridge Tiers Power Pole 76	23/March/02
Oreixenica ptunarra	OP TT76 5	Tunbridge Tiers Power Pole 76	23/March/02
Oreixenica ptunarra	OP TT76 6	Tunbridge Tiers Power Pole 76	10/March/05
Oreixenica ptunarra	OP TT76 7	Tunbridge Tiers Power Pole 76	10/March/05
Oreixenica ptunarra	OP WSC 1	Weather Station Corner, Surry Hills NW	21/March/04
Oreixenica ptunarra	OP WSC 2	Weather Station Corner, Surry Hills NW	21/March/04
Oreixenica ptunarra	OP WSC 3	Weather Station Corner, Surry Hills NW	21/March/04
Oreixenica ptunarra	OP WSC 4	Weather Station Corner, Surry Hills NW	21/March/04
Junonia villida	MA GLEN 1	Glenlusk	5/Jan/05
Junonia villida	MA GLEN 2	Glenlusk	5/Jan/05
Junonia villida	MA GLEN 3	Glenlusk	5/Jan/05
Junonia villida	MA PH 1	Pikes Hill	23/March/05
Vanessa kershawi	APL MtBuff	Mt Buffalo Victoria	12/March/05
Vanessa kershawi	APL MtHoth	Mt Hotham Victoria	13/March/05

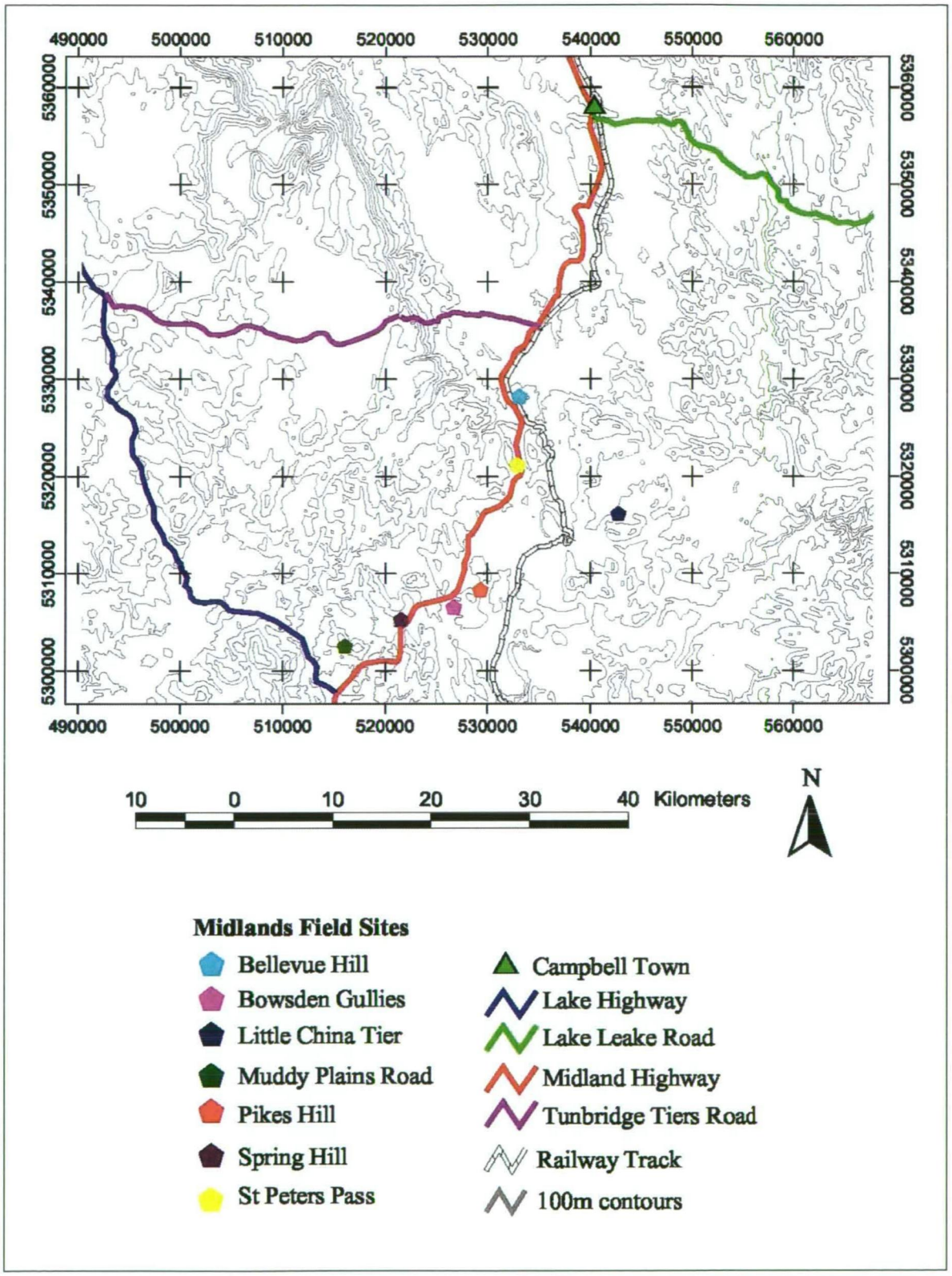
Appendix 3 - Field Site Descriptions

A3.1. Location of Tasmanian Field Sites

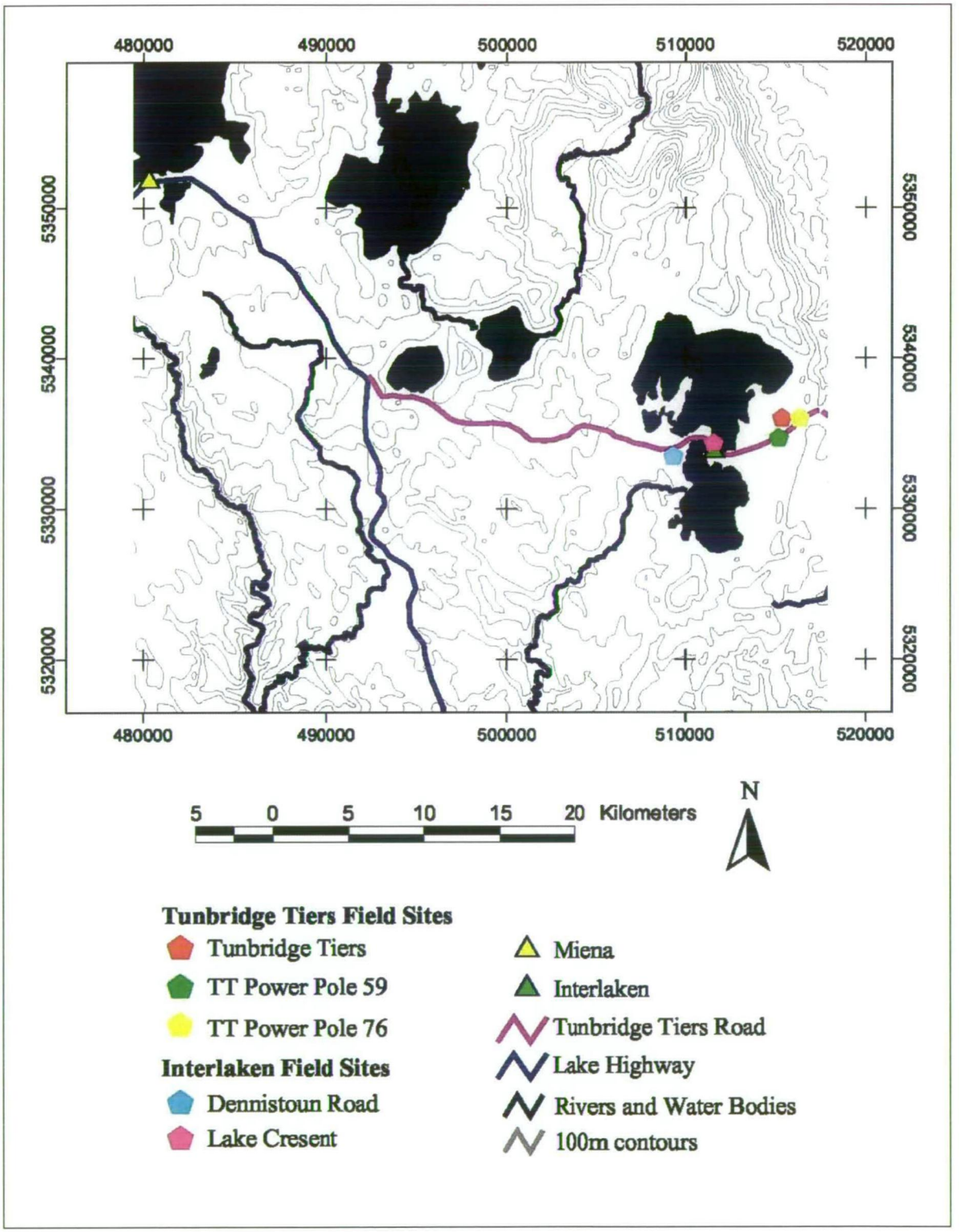
A3.1.1. Overview of Tasmanian Field Sites



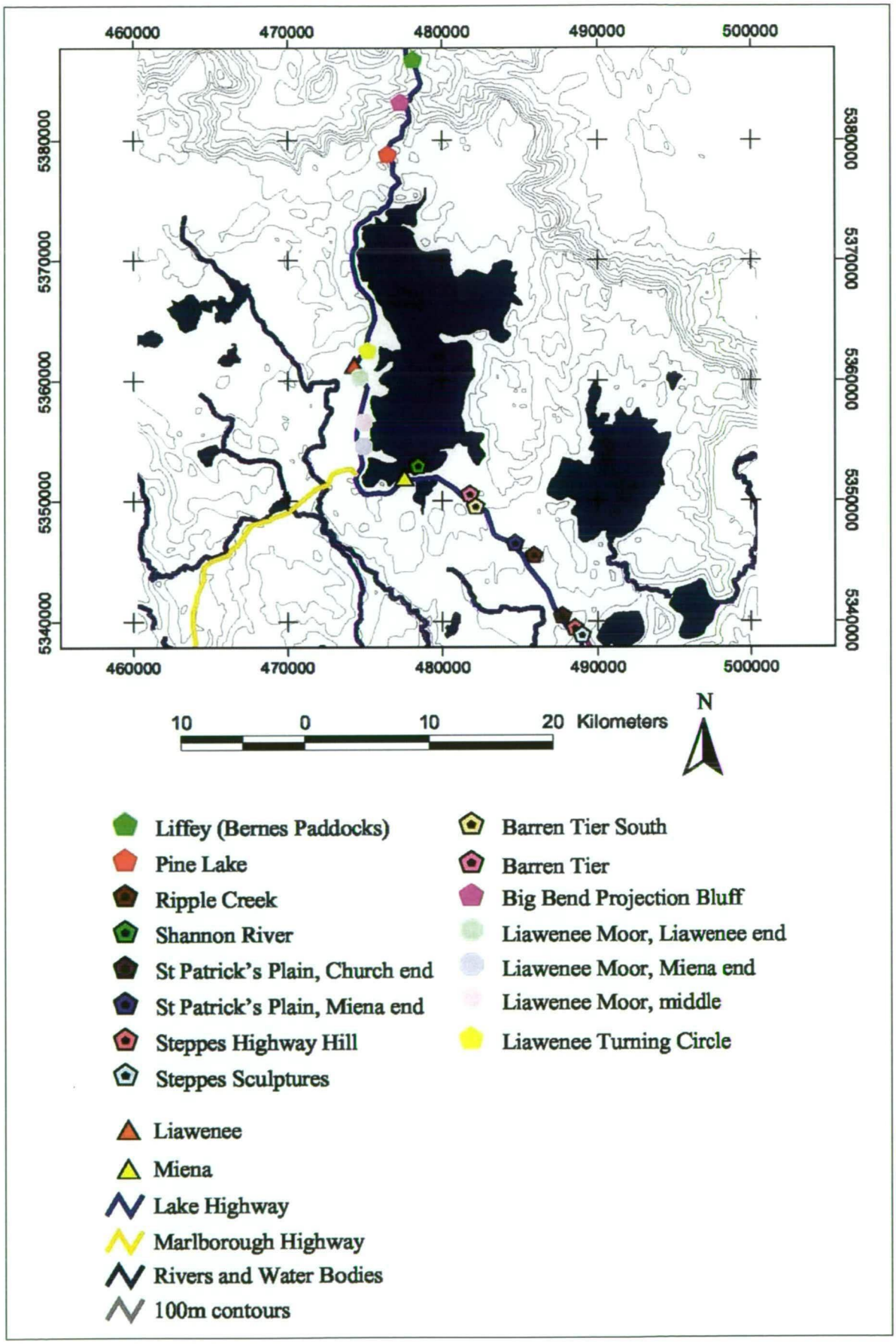
A3.1.2. Overview of Tasmanian Field Sites



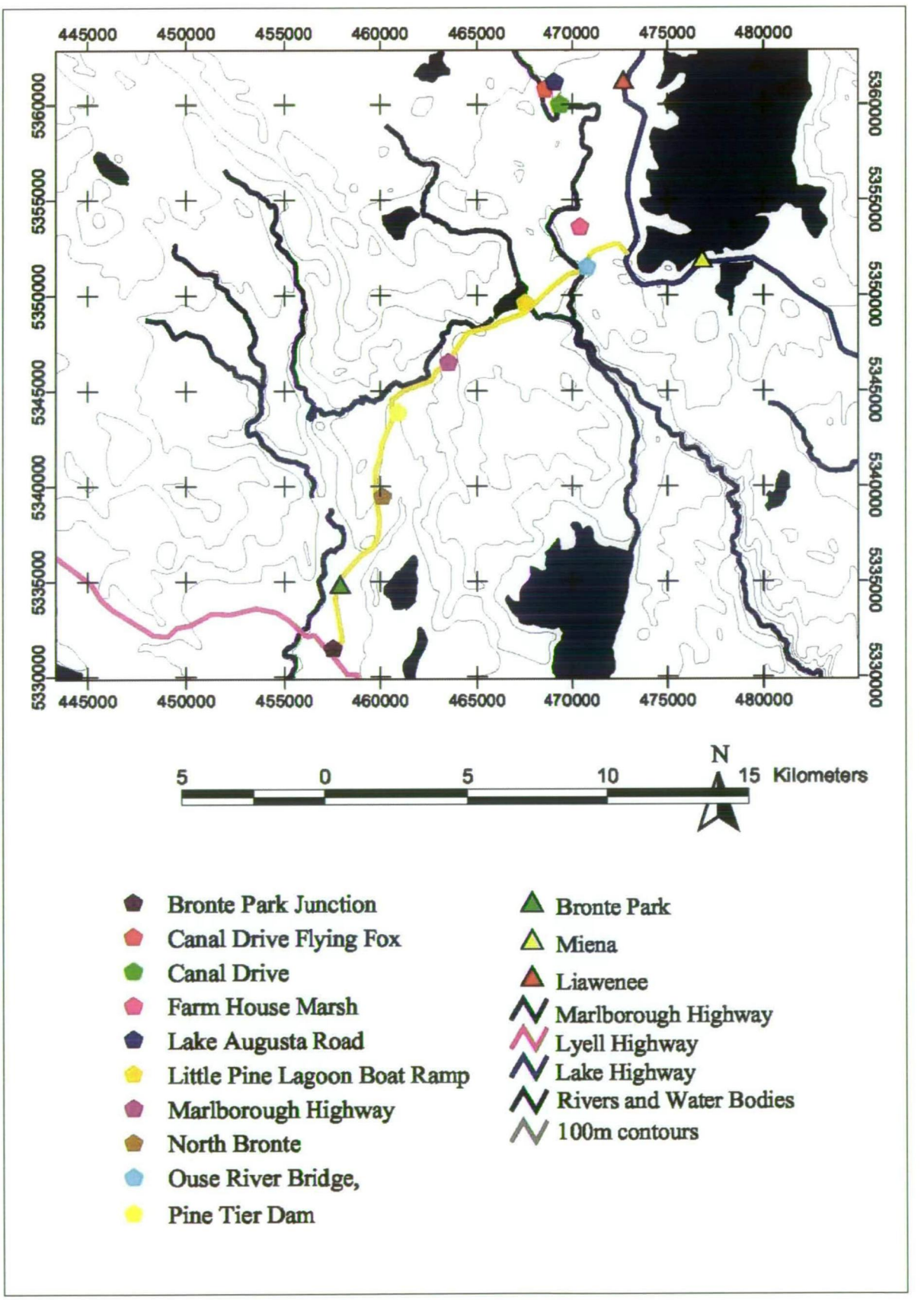
A3.1.3. Detail of Tunbridge Tiers and Interlaken Field Sites



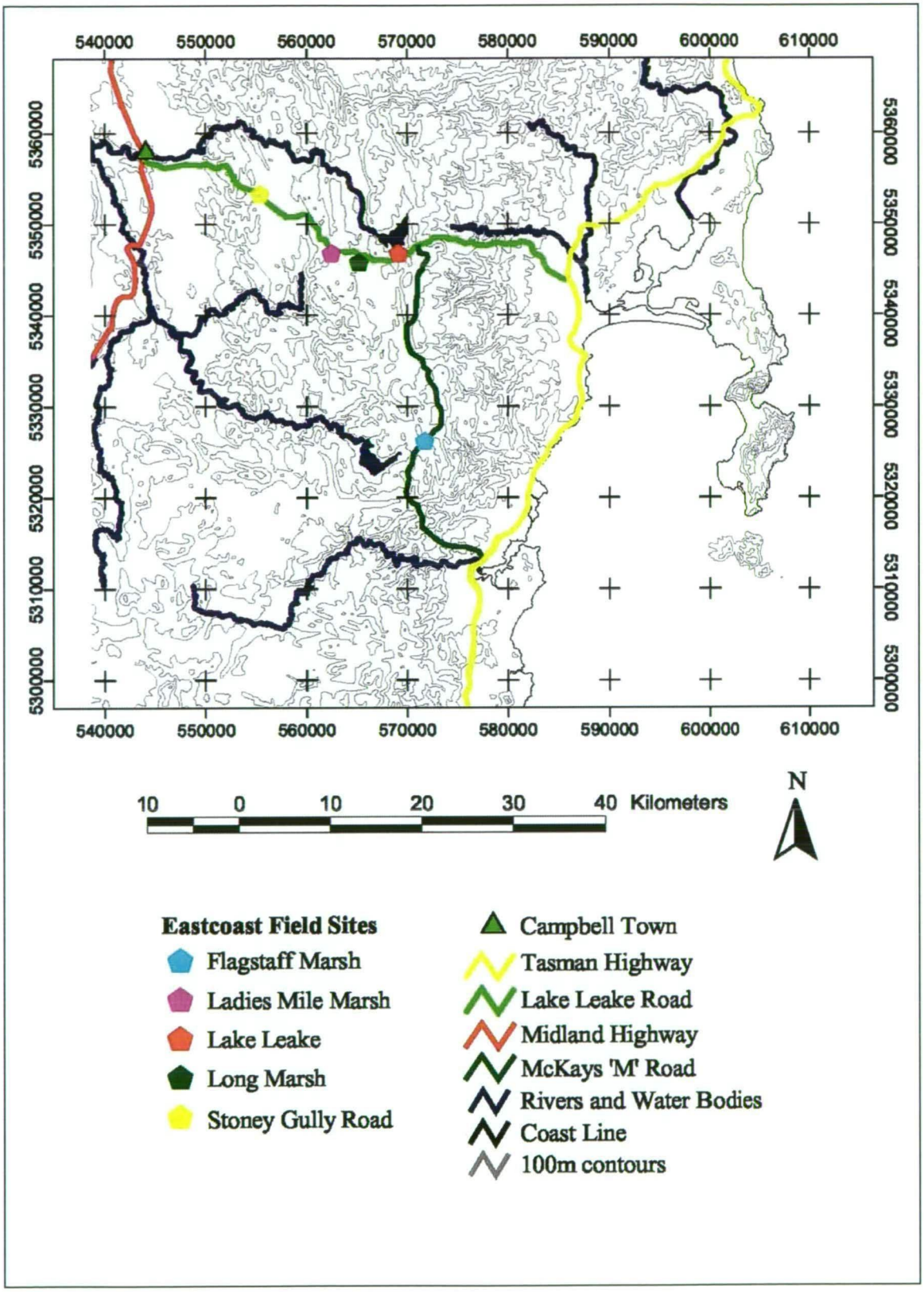
A3.1.4. Detail of Lake Highway Field Sites



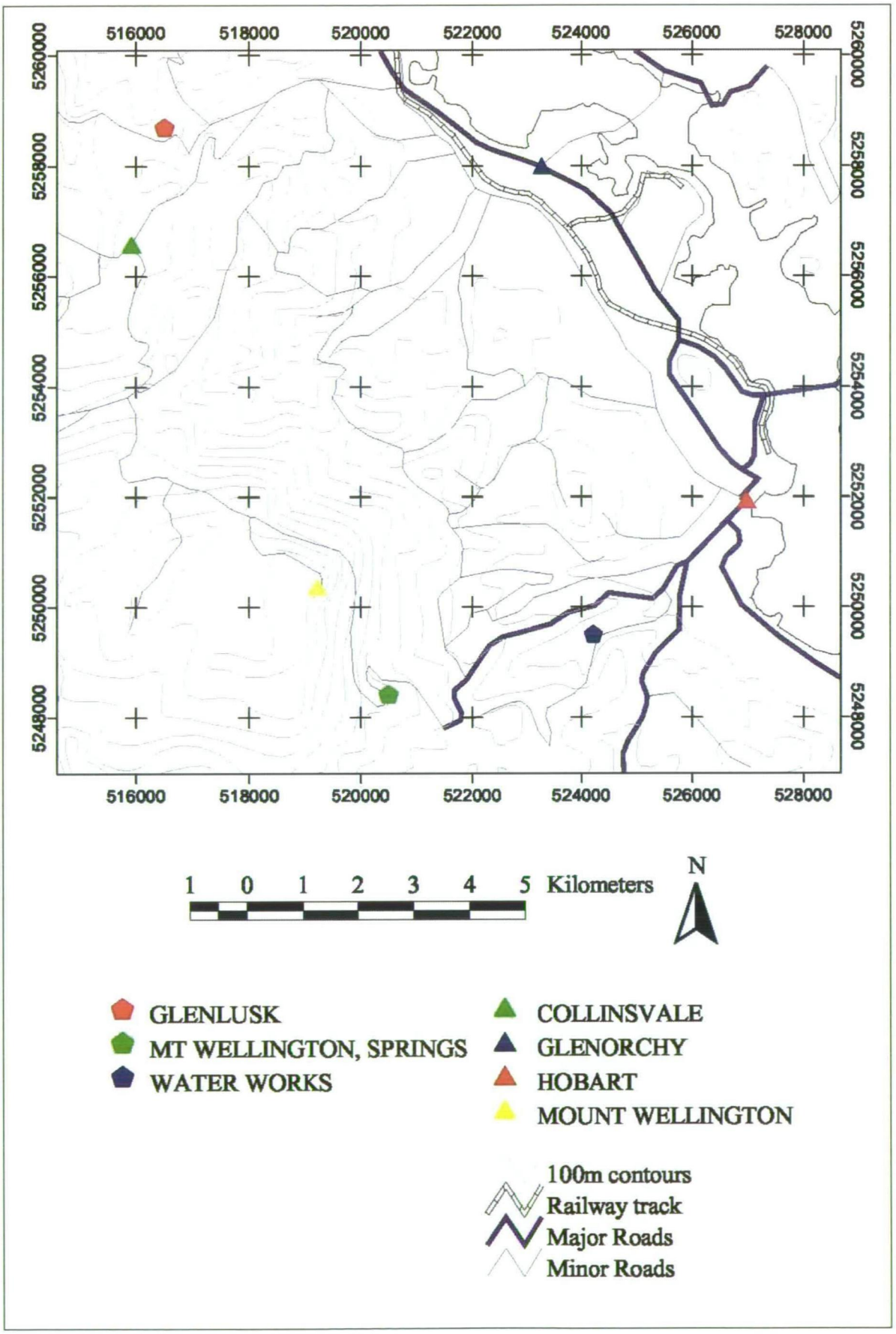
A3.1.5. Detail of Marlborough Highway Field Sites



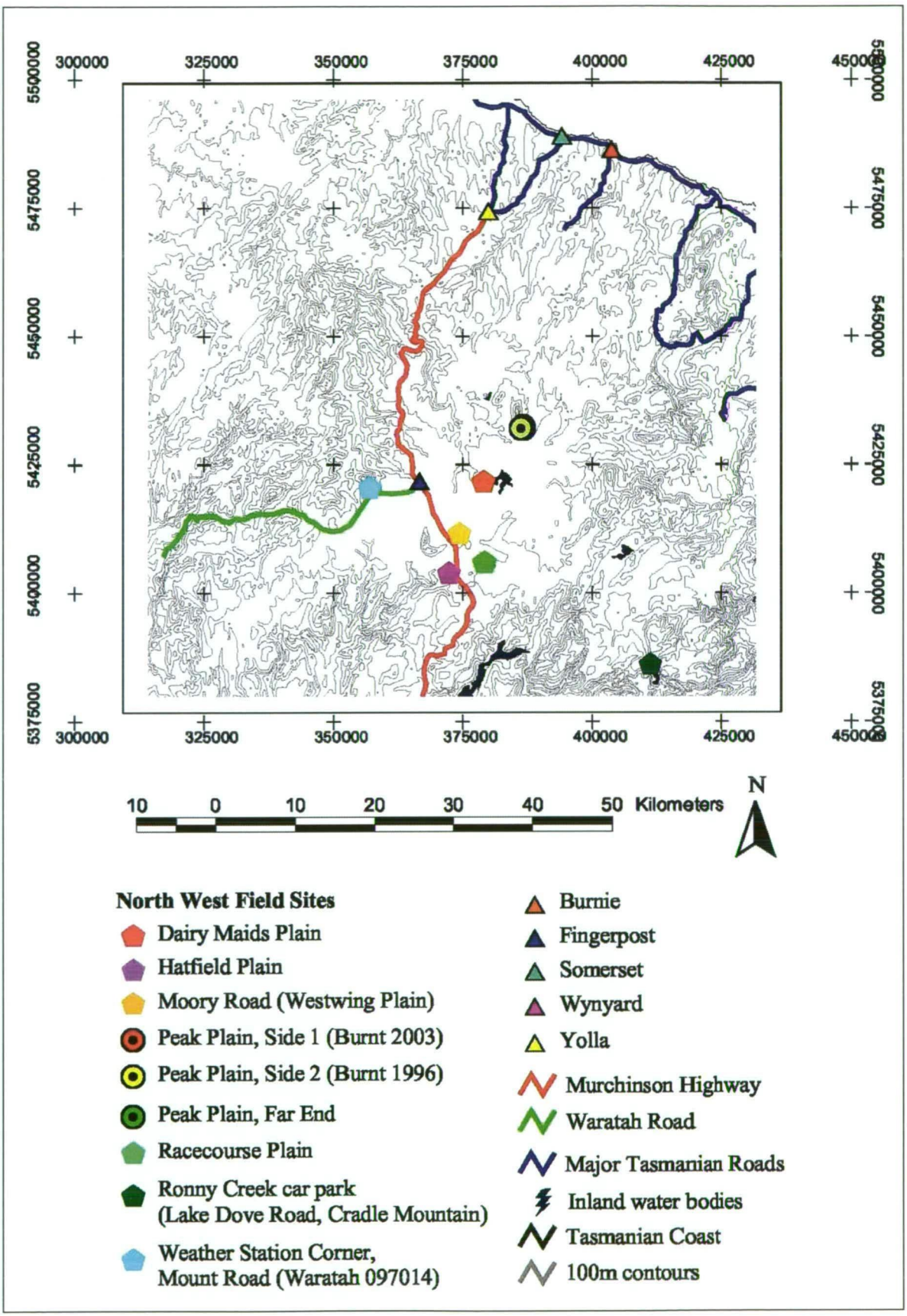
A3.1.6. Detail of Eastcoast Field Sites



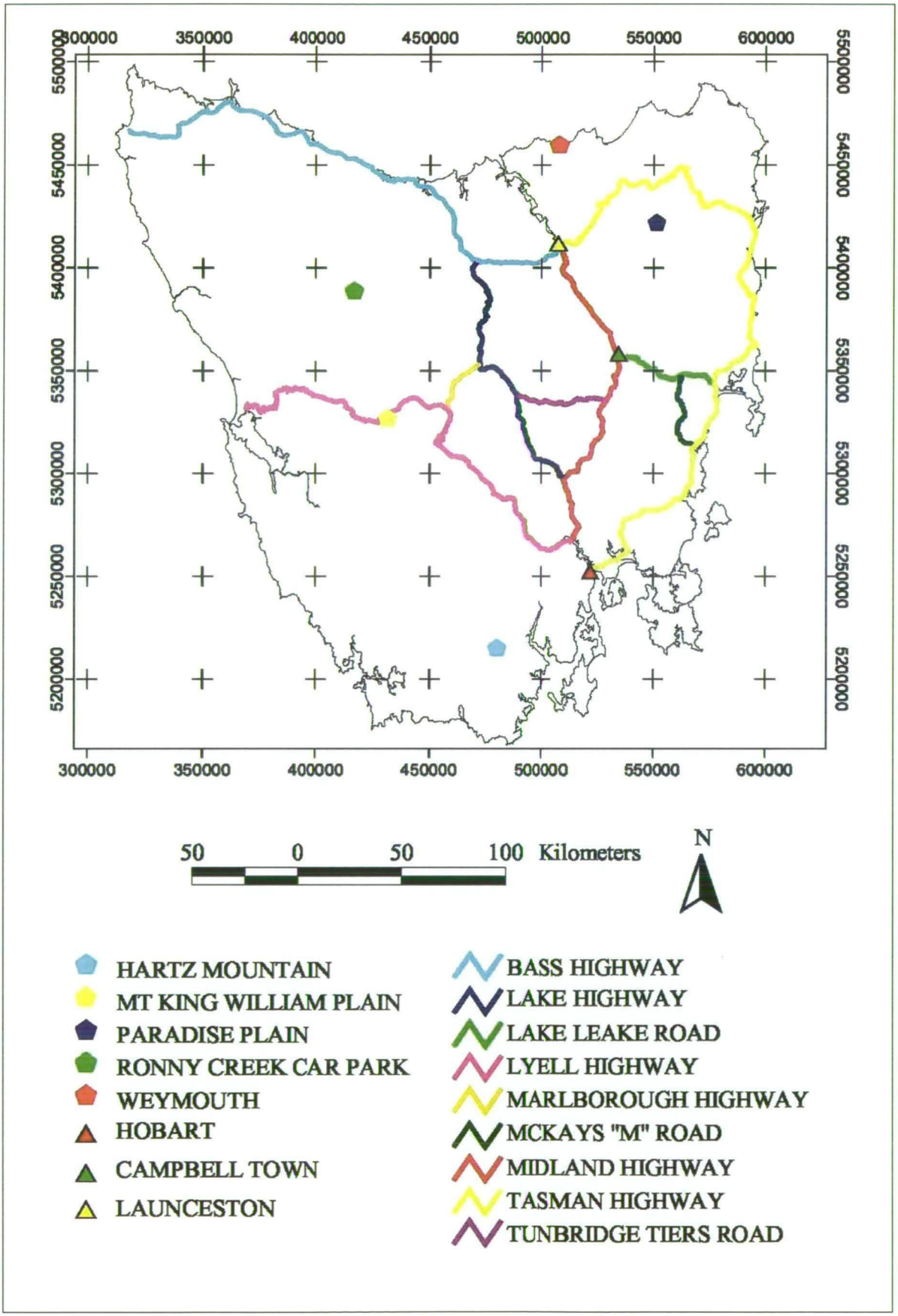
A3.1.7. Detail of Hobart Region Field Sites



A3.1.8. Detail of North West Field Sites



A3.1.9. Detail of Odd Tasmanian Field Sites



A3.2. Midlands Field Sites

A3.2.1. Bellevue Hill

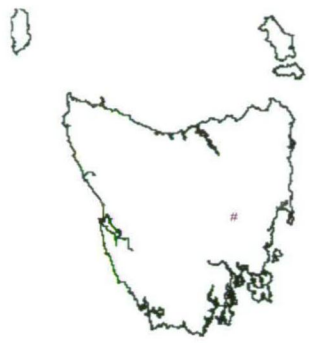
Collection ID	Bel		
UTM Zone 55 GDA 94	*easting*	*northing*	
	533200	5328200	
Elevation (metres)	370		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Vincents	5232	
Directions	Walk across the paddock from the ruins of the *Halfway Hotel* and *Antill Ponds Railway Station*. Study site is 1km from Midland Highway.		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei P. sieberiana*		
Dominant Nectar Source	*Cirsium sp* (thistles), *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Ulex europaeus* (gorse)		
Overall Habitat Quality	Satisfactory to Good		
Description	☞ Extensive area of tussock grassland with good numbers of *O. ptunarra*. Greatest numbers in areas with steep southeast aspect and high tussock cover. ☞ Westerly-facing, dry, exposed, open treeless hillside. ☞ Dominant use grazing sheep and cattle ☞ *Poa* medium sized, shows signs of being cropped. ☞ Moderate ground cover of soft herb species between the tussocks. ☞ Surround area, open grazing county with very light tree cover and improved pasture.		

Plate 10 Bellevue Hill, view to north from edge of site

Plate 11 Bellevue Hill, view to northeast from edge of site

Plate 12 Bellevue Hill, view to northwest from edge of site

A3.2.2. Bowsden Gullies – Mudwalls Road

Collection ID	BG		
UTM Zone 55 GDA 94	easting	northing	
	526500	5306500	
Elevation (metres)	450		
1:25000 TAS Map	Sheet Name	Map Sheet #	
	Stonor	5230	
Directions	500 metres along Mudwalls Rd from Midland Highway. Walk across paddock from first gate and up through gully to plateau		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	No obvious nectar sources present		
Overall Habitat Quality	Satisfactory		
Description	▱ Tussock through this area is scattered yet *O. ptunarra* are observable under good conditions. ▱ Dry, open area with very light tree cover; hillside and plateau; north-westerly aspect. ▱ Dominant use grazing sheep. ▱ *Poa* medium sized, shows signs of being cropped. ▱ *Poa* density ranges from low to high. ▱ Moderate ground cover of soft herb species between tussocks. ▱ Surrounding area wooded patches and open grazing county.		

Plate 13 Bowsden Gullies, view to east from edge of plateau

Plate 14 Bowsden Gullies, view to north from edge of plateau

A3.2.3. Little China Tier

Collection ID	LTC	
UTM Zone 55 GDA 94	*easting*	*northing*
	543200	5316100
Elevation (metres)	470	
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*
	Lemont	5431
Directions	Site is on Fitchs Road, 2.5 km from Y junction with Nala Road. Go through the gate, head up the hill, to opening in fence at top of ridge.	
Dominant butterfly species	*O. ptunarra*	
Dominant *Poa* species	*P. labillardierei*	
Dominant Nectar Source	No obvious nectar sources	
Overall Habitat Quality	Satisfactory	
Description	↗ Extensive area of tussock contiguous along hills ↗ North/south, very dry, exposed, open ridgeline ↗ Dominant use cattle and sheep grazing ↗ Tree cover varies from treeless in the south to a light covering of large trees at the northern end ↗ Overall high *Poa* density, southern end medium in size and shows signs of being cropped. Northern end very large healthy tussocks ↗ Sparse ground cover of soft herb species between the tussocks ↗ Improved pasture and cropping areas on western side; open grazing country and woodland on eastern side of site.	

Plate 15 Little China Tier, view towards southern end

Plate 16 Little China Tier, view towards northern end

Plate 17 360° views from Little China Tier Study Site

A3.2.4. Muddy Plains Road

Collection ID	MPR		
UTM Zone 55 GDA 94	*easting*	*northing*	
	515500	5302500	
Elevation (metres)	450		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Bothwell	5030	
Directions	5 km along the Muddy Plains Road from the Midland Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Cirsium sp* (thistles)		
Overall Habitat Quality	Outstanding		
Description	• Extensive tussock grassland on hillside with north-easterly aspect; dry, open and treeless, with a very high *Poa* density. • *Poa* large and healthy with a good ground cover of soft herb species between the tussocks. • Dominant use grazing sheep. • Surrounding area open treeless grazing county. • *O. ptunarra* widespread in the area, extending upslope, not quite to the ridgeline. In higher numbers to north of fence line where grazing pressure is lower. • Muddy Plains Road southern boundary of *O. ptunarra* habitat range.		

Plate 18 Muddy Plains Road, view towards the west from Muddy Plains Road

A3.2.5. Pikes Hill

A3.2.5.1. Unburnt Area

Collection ID	PH		
UTM Zone 55 GDA 94	*easting*	*northing*	
	529300	5308300	
Elevation (metres)	470		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Stonor	5230	
Directions	2.5 km along Stonor Road from Midland Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei P. sieberiana*		
Dominant Nectar Source	*Cirsium sp* (thistles), *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Acacia mearnsii* (black wattle), *Ulex europaeus* (gorse)		
Overall Habitat Quality	Satisfactory to poor		
Description	☞ *O. ptunarra* readily observed here. ☞ Extensive area of moderately hard grazed tussock. ☞ Comparatively flat paddock with rising hillside; northeast to northerly aspect. ☞ Open, treeless area, with a low density of medium to large *Poa* showing signs of being cropped by grazing. ☞ Moderate ground cover of soft herb species including clover between the tussocks. ☞ Dominant use sheep grazing. ☞ Surrounding country open, treeless grazing paddocks, mainly improved pasture and *Lomandra.*		

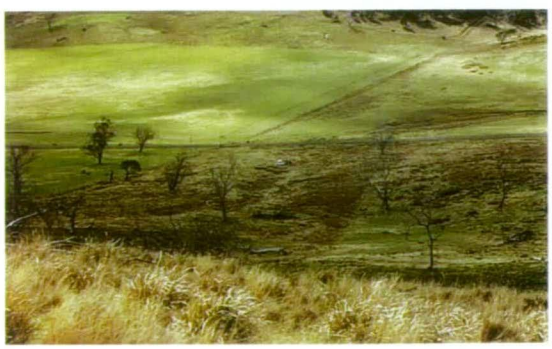
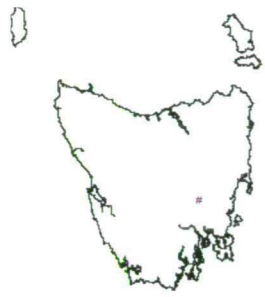


Plate 19 Pikes Hill Study Site, from top of Pikes Hill

Plate 20 Pikes Hill Study Site, Poa detail

A3.2.5.2. Burnt Area

Collection ID	PH	
UTM Zone 55 GDA 94	*easting*	*northing*
	529300	5308300
Elevation (metres)	470	
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*
	Stonor	5230
Directions	2.5 km along Stonor Road from Midland Highway, walk across the paddock through the unburnt area.	
Dominant butterfly species	*O. ptunarra*	
Dominant *Poa* species	*P. labillardierei P. sieberiana*	
Dominant Nectar Source	No obvious nectar sources	
Overall Habitat Quality	Satisfactory	
Description	☞ Open, treeless hillside northerly aspect, with a low *Poa* density ☞ *Poa* tufty and sprouting new growth. ☞ Moderate ground cover of soft herb species between the tussocks. ☞ Dominant use sheep grazing. ☞ Surrounding area open, treeless grazing country, mainly improved pasture and *Lomandra sp.*	

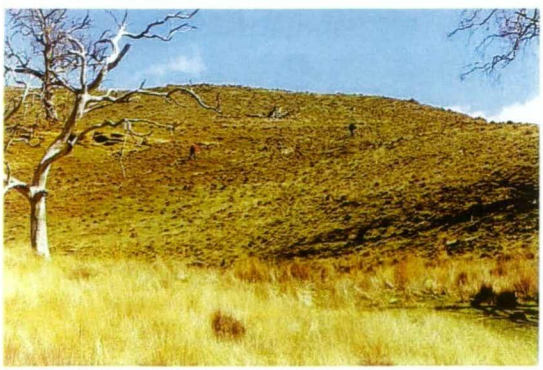


Plate 21 Pikes Hill, view towards south-west into burnt area from edge of unburnt area

Plate 22 Pikes Hill, view to the south from Stonor Road

A3.2.6. Spring Hill

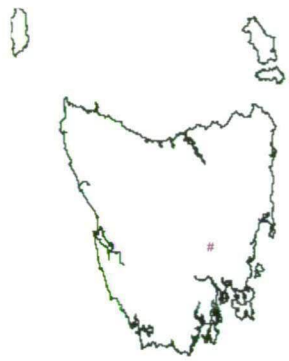
Collection ID	SpH		
UTM Zone 55 GDA 94	*easting*	*northing*	
	521200	5305200	
Elevation (metres)	500		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Stonor	5230	
Directions	Jericho side of Spring Hill Pass Midland Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Cirsium sp* (thistles) *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Satisfactory		
Description	↗ Large area of tussock grassland extending across the southern slopes on the back of Spring Hill. ↗ *O. ptunarra* common. ↗ Dry, open and treeless, with a low *Poa* density; southeast aspect. ↗ *Poa* large and tufty; generally in good condition. ↗ Lightly grazed and patchily burnt. ↗ Dominant use grazing sheep. One of the lightest stocked properties in the Midlands. ↗ Good ground cover of soft herb species between the tussocks. ↗ Surrounding area lightly wooded patches and open grazing country.		

Plate 23 Spring Hill, view east

Plate 24 Spring Hill, view west

A3.2.7. St Peters Pass

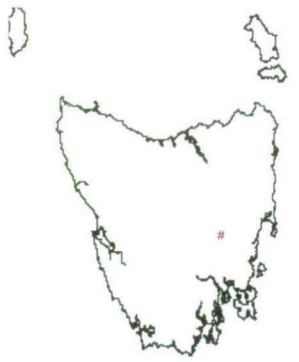
Collection ID	StPP		
UTM Zone 55 GDA 94	*easting*	*northing*	
	53300	532110	
Elevation (metres)	425		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Vincents	5232	
Directions	Opposite the St. Peters Pass Rest / Picnic Area		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei, P. sieberiana*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Poor		
Description	☞ Dry, open, treeless hillside; easterly aspect. ☞ Dominant use grazing sheep ☞ *Poa* is scrappy, small to medium in size; sparse ground cover of soft herb species between tussocks. ☞ Lightly wooded areas and open grazing county surround the site. ☞ *O. ptunarra* was not seen flying at this site.		

Plate 25 St Peters Pass, view towest from Midland Highway

A3.3. Tunbridge Tiers and Interlaken Field Sites

A3.3.1. Tunbridge Tiers

Collection ID	TT		
UTM Zone 55 GDA 94	*easting*	*northing*	
	518500	5336000	
Elevation (metres)	890		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Interlaken	5033	
Directions	6 km northeast of Interlaken on road to Tunbridge		
Dominant butterfly species	*O. lathoniella, O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Acacia dealbata* (silver wattle), *Cirsium sp* (thistles) *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Cyathodes sp.* (mountain berries), *Helichrysum sp.* (native daisies) and *Wahlenbergia stricta* (native blue bells)		
Overall Habitat Quality	Satisfactory to Good		
Description	☞ Small manually cleared area, on northeast facing slope. ☞ *Poa* medium in size and scrappy. ☞ No evidence of domestic animal grazing.		

Plate 26 Tunbridge Tiers, view to east from Tunbridge Road

A3.3.2. Tunbridge Tiers – Power Pole 59

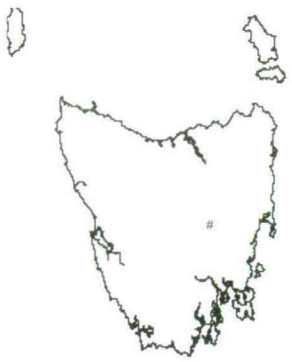
Collection ID	TT59		
UTM Zone 55 GDA 94	*easting*	*northing*	
	518300	5334700	
Elevation (metres)	860		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Interlaken	5033	
Directions	Northeast of Interlaken on road to Tunbridge area between power poles 59 and 60		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Cirsium sp* (thistles) *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Satisfactory		
Description	↗ *Eucalyptus rodwayi* grassy woodland. ↗ Roadside verge - open forest with good grass cover. ↗ *O. ptunarra* widespread in the area. ↗ *Poa* small to medium in size, well cropped by marsupial grazing. ↗ No evidence of domestic animal grazing.		

Plate 27 Tunbridge Tiers Power Pole 59, view to west from Tunbridge Tier Road

A3.3.3. Tunbridge Tiers – Power Pole 76

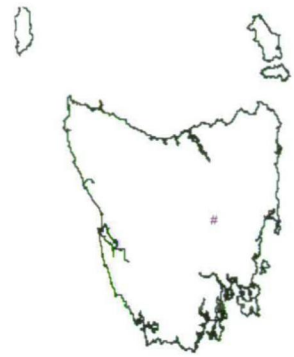
Collection ID	TT76		
UTM Zone 55 GDA 94	*easting*	*northing*	
	519700	5336000	
Elevation (metres)	885		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Interlaken	5033	
Directions	Northeast of Interlaken on road to Tunbridge area near power poles 76.		
Dominant butterfly species	*O. lathoniella, O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Cirsium sp* (thistles) *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Satisfactory		
Description	↗ *Eucalyptus rodwayi* grassy woodland. ↗ Roadside verge - open forest with good grass cover. ↗ *O. ptunarra* widespread in the area. ↗ *Poa* medium to large in size, well cropped by marsupial grazing. ↗ No evidence of domestic animal grazing.		

Plate 28 Tunbridge Tiers Power Pole 76, view to east from Tunbridge Tier Road

A3.3.4. Dennistoun Road, Interlaken

Collection ID	DIR		
UTM Zone 55 GDA 94	*easting*	*northing*	
	511300	5333500	
Elevation (metres)	815		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Interlaken	5033	
Directions	1km south of Interlaken on the Dennistoun Road. Style across fence.		
Dominant butterfly species	*O. lathoniella, O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Leontodon sp. & Hypochoeris sp.* (dandelions) and *Helichrysum sp.*, (native daisies).		
Overall Habitat Quality	Good		
Description	↗ Large, open, flat area surrounded by open woodland. ↗ Dominant use sheep and cattle grazing. ↗ *Poa* moderate density, medium in size, individual tussocks short, stocky and cropped. ↗ Sparse ground cover of grass and herb species between tussocks.		

Plate 29 Dennistoun Road, view to west from edge of site

Plate 30 Dennistoun Road, view to west from edge of site following fire

A3.3.5. Lake Crescent, Interlaken

Collection ID	LC		
UTM Zone 55 GDA 94	*easting*	*northing*	
	514000	5334400	
Elevation (metres)	810		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Interlaken	5033	
Directions	Lake Crescent conservation area west of Interlaken on link road to Lake Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Leontodon sp. & Hypochoeris sp.* (dandelions) and *Helichrysum sp.*, (native daisies)		
Overall Habitat Quality	Good		
Description	▱ Large, open, flat area surrounded by open woodland. ▱ *Poa* moderate density, medium to large in size, some individual tussocks cropped by marsupial grazing. ▱ Sparse ground cover of grass and herb species between tussocks.		

Plate 31 Lake Crescent, 180° view towards the south from east to west

Plate 32 Lake Crescent, view to southwest from road

Plate 33 Lake Crescent, view to south from road

A3.4. Lake Highway Field Sites

A3.4.1. Barren Tier (Tod's Corner Junction)

Collection ID	BTTC		
UTM Zone 55 GDA 94	*easting*	*northing*	
	482100	5350600	
Elevation (metres)	1060		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Arthurs Lake	4835	
Directions	Junction of Tods Corner Road and Lake Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. hiemata*		
Dominant Nectar Source	*Leontodon sp. & Hypochoeris sp.* (dandelions)		
Overall Habitat Quality	Good		
Description	*Richea acerosa* grassy shrubland Open, area surrounded by open woodland. Sparse *Poa* cover		

Plate 34 Barren Tier Tods Corner, view to north

A3.4.2. Barren Tier South

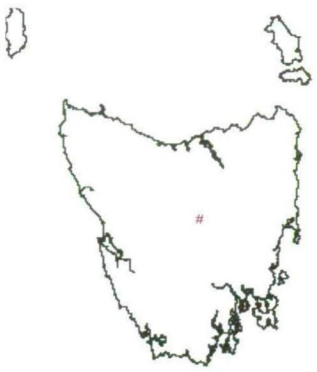
Collection ID	BTS		
UTM Zone 55 GDA 94	*easting*	*northing*	
	482500	5349600	
Elevation (metres)	1040		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Wihareja	4834	
Directions	Lake Highway ~5km north of junction to Poatina (Barren Tier Holding Paddock)		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. hiemata* and *P. labillardierei*		
Dominant Nectar Source	*Leontodon sp. & Hypochoeris sp.* (dandelions) and *Helichrysum sp.*, (native daisies)		
Overall Habitat Quality	Good		
Description	☞ Large, open, flat area surrounded by open woodland. ☞ *Poa* moderate density, medium to large in size, some individual tussocks cropped by marsupial grazing. ☞ Sparse ground cover of grass and herb species between tussocks.		

Plate 35 Barren Tier South, view to the north

A3.4.3. Big Bend Projection Bluff

Collection ID	BBPJ		
UTM Zone 55 GDA 94	*easting*	*northing*	
	476500	5383100	
Elevation (metres)	940		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Quamby Bluff	4638	
Directions	~ 20 km north of Pine Lake (Lake Highway) ~ ½ way down mountain below lookouts Entrance to site straight ahead when driving down mountain road bends to right		
Dominant butterfly species	*N. leprea*		
Description	Wet mixed sclerophyll forest *Uncinia tenella* (larval food plant) grows along track edges		

Plate 36 Big Bend Projection Bluff, view to northwest

A3.4.4. Liawenee Moor, Liawenee end

Collection ID	LMLE		
UTM Zone 55 GDA 94	*easting*	*northing*	
	473200	5360200	
Elevation (metres)	1030		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Split Rock	4636	
Directions	Liawenee village end of Liawenee Moor edge of Great Lake		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. hiemata*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Helichrysum sp.*(daisies)		
Overall Habitat Quality	Good		
Description	↗ Exposed, highland *Richea acerosa* & *Hakea macrocarpa* grassy shrubland gently sloping to the west, with few plants exceeding 0.5m in height. ↗ Dominant use grazing by sheep, cattle and rabbits. ↗ *Poa* small tussocks, moderate density. ↗ In protected areas there is a ground cover of small herbaceous species.		

Plate 37 Liawenee Moor Liawenee End, view to west from Lake Highway

Plate 38 Liawenee Moor Liawenee End, view to north from Lake Highway

Plate 39 Liawenee Moor Liawenee End, view to east from Lake Highway

A3.4.5. Liawenee Moor, middle

Collection ID	LM / LMMS		
UTM Zone 55 GDA 94	*easting*	*northing*	
	473500	5356500	
Elevation (metres)	1050		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Miena	4635	
Directions	turn-off Lake Highway, 6km north of Marlborough Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. hiemata*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Helichrysum sp.*(daisies)		
Overall Habitat Quality	Good		
Description	↗ Vast, exposed, highland *Richea acerosa* grassy shrubland; gently sloping to the west, with few plants exceeding 0.5m in height. ↗ *O. ptunarra* widespread through shrublands west of Great Lake showing a marked preference for areas dominated by grass and wind protected sites such as alongside tracks. ↗ Extensive evidence of grazing by marsupials, sheep, cattle & rabbits. ↗ *Poa* small tussocks, moderate density. ↗ In protected areas ground cover of small herbaceous species.		

Plate 40 Liawenee Moor middle, view towards the east from Lake Highway

A3.4.6. Liawenee Moor, Miena end

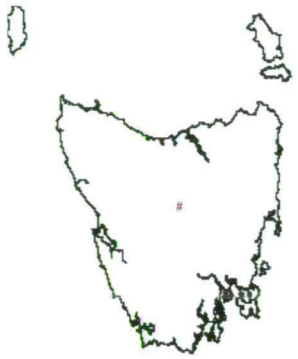
Collection ID	LMME		
UTM Zone 55 GDA 94	*easting*	*northing*	
	473500	5354500	
Elevation (metres)	1030		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Miena	4635	
Directions	Access track to left Lake Highway ~1.5km north of Marlborough Highway junction		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. hiemata*		
Dominant Nectar Source	*Hypochoeris sp. Taraxacum sp.* & *Leontodon sp.*		
Overall Habitat Quality	Good		
Description	▱ Highland *Richea acerosa* & *Hakea macrocarpa* grassy shrubland gently sloping to the west, with few plants exceeding 0.5m in height. ▱ Dominant use grazing sheep. ▱ *Poa* small tussocks, moderate density. ▱ In protected areas there is a ground cover of small herbaceous species.		

Plate 41 Liawenee Moor, Miena end, view to north across moor from access track

A3.4.7. Liawenee Turning Circle

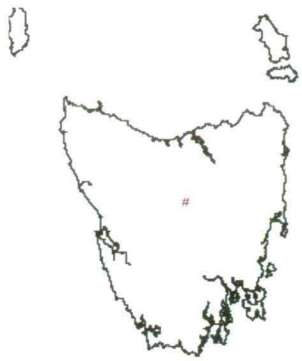
Collection ID	LTC		
UTM Zone 55 GDA 94	*easting*	*northing*	
	473800	5362500	
Elevation (metres)	1060		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Split Rock	4636	
Directions	3 km north of Liawenee, turn to the left after cattle grid		
Dominant butterfly species	*O. orichora, O. lathoniella, O. ptunarra*		
Dominant *Poa* species	*P. labillardierei P. hiemata*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions) *Helichrysum sp.* (daisies)		
Overall Habitat Quality	Excellent to Outstanding		
Description	☞ Tract of flat, open alpine woodland. ☞ *Poa*, large, healthy, with good ground cover of soft herb species between tussocks. ☞ Surrounding area is alpine woodland and moor. ☞ No evidence of domestic animal grazing; extensive evidence of marsupial grazing.		

Plate 42 Liawenee Turning Circle, view to north from Lake Highway

A3.4.8. Liffey (Bernes Paddocks), plain off Lake Highway

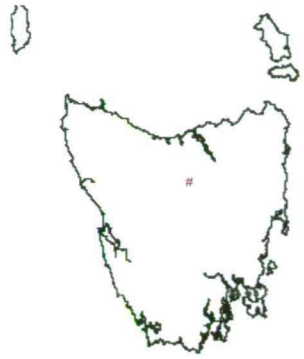
Collection ID	LIF		
UTM Zone 55 GDA 94	*easting*	*northing*	
	477500	5386700	
Elevation (metres)	860		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Quamby Bluff	4638	
Directions	Paddock adjacent to Lake Highway at warning sign for turn off to Liffey Falls and Liffey		
Dominant butterfly species	*H. cordace*		
Description	Cleared site of an old farm house Well cropped marsupial grazed lawn		

Plate 43 Liffey (Bernes Paddocks), plain off Lake Highway, view to east

A3.4.9. Pine Lake

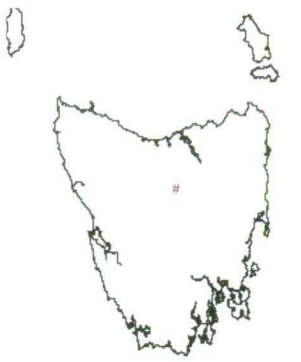
Collection ID	PL / PLB		
UTM Zone 55 GDA 94	*easting*	*northing*	
	475500	5378800	
Elevation (metres)	1200		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Breona	4637	
Directions	20 kilometres north of Liawenee on the Lake Highway		
Dominant butterfly species	*O. orichora, O. ptunarra*		
Dominant *Poa* species	*P. hiemata*		
Dominant Nectar Source	*Dracophyllum sp.* (cushion plant), *Helichrysum sp.* (native daisies) and Richea - *Pichea sprengelioidesa*		
Overall Habitat Quality	Very Good		
Description	▱ Exposed, highland moor sloping to the east, with a covering of low alpine shrubs. ▱ Significant evidence of marsupial grazing. ▱ *Poa* small in size growing in sheltered, protected areas under shrubby vegetation and in-between rocks. ▱ In other protected areas moderate ground cover of soft herb species and cushion plants (*Dracophyllum sp.*). ▱ Surrounding area alpine moor and woodland.		

Plate 44 Pine Lake, view towards east from top of ridge

A3.4.11. Ripple Creek

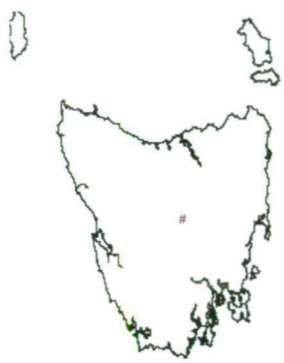
Collection ID	Rcrk		
UTM Zone 55 GDA 94	*easting*	*northing*	
	487200	5345500	
Elevation (metres)	880		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Wihareja	4834	
Directions	Ripple Creek, Lake Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Taraxacum sp.* (dandelions)		
Overall Habitat Quality	Average		
Description	*Hakea macrocarpa* grassy shrubland. *Poa* medium in size and scrappy. Dominant land use sheep grazing.		

Plate 45 Ripple Creek, view towards the southwest from Lake Highway

A3.4.12. Shannon River

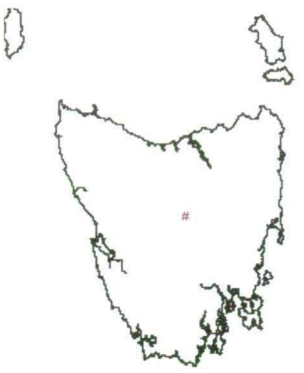
Collection ID	ShR		
UTM Zone 55 GDA 94	*easting*	*northing*	
	477900	5352900	
Elevation (metres)	1000		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Miena	8635	
Directions	Verge between Shannon Lagoon and Lake Highway, near Shannon River		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei* & *P. hiemata*		
Dominant Nectar Source	*Dracophyllum sp.* (cushion plant), *Helichrysum sp.* (native daisies) and Richea - *Pichea sprengelioidesa*		
Overall Habitat Quality	Good		
Description	Sheltered grassy herbaceous plain beside lagoon		

Plate 46 Shannon River, view towards the south

Plate 47 Shannon River, view towards south

Plate 48 Shannon River, view towards north

A3.4.13. St Patrick's Plain, Church End

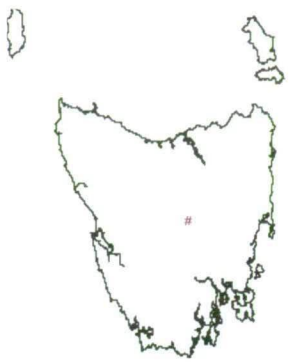
Collection ID	StPat		
UTM Zone 55 GDA 94	*easting*	*northing*	
	489500	5340500	
Elevation (metres)	920		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Wihareja	4834	
Directions	Road side verge ~50 metres north of church/hall		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Silybum marianum* (variegated thistle) & *Onopordum acanthium* (cotton thistle)		
Overall Habitat Quality	Average		
Description	*Hakea macrocarpa* grassy shrubland - roadside verge. *Poa* small to medium in size Sporadic domestic animal grazing.		

Plate 49 St Patrick's Plain Church End overview, view towards Miena End

Plate 50 St Patrick's Plain Church End detail, view towards Miena End

A3.4.14. St Patrick's Plain, Miena End

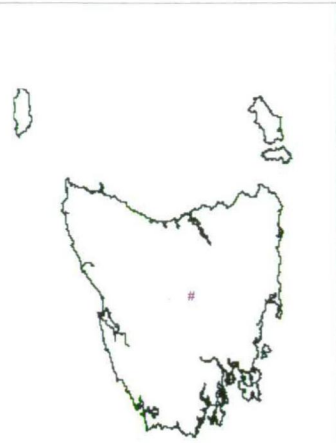
Collection ID	StPatME		
UTM Zone 55 GDA 94	*easting*	*northing*	
	489700	5346500	
Elevation (metres)	940		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Wihareja	4834	
Directions	Road side verge northern end of St Patricks Plan		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Silybum marianum* (variegated thistle) & *Onopordum acanthium* (cotton thistle)		
Overall Habitat Quality	Average		
Description	☞ Sparse *Hakea macrocarpa* grassy shrubland - roadside verge. ☞ *Poa* small to medium in size ☞ Sporadic domestic animal grazing.		

Plate 51 St Patrick's Plain Miena End, view towards the north

A3.4.15. Steppes Highway Hill

Collection ID	SHH		
UTM Zone 55 GDA 94	*easting*	*northing*	
	490500	5339500	
Elevation (metres)	880		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Steppes	4833	
Directions	Road side verge ~1km north of Steppes Homestead		
Dominant *Poa* species	*P. hiemata*		
Dominant butterfly species	*O. ptunarra*		
Dominant Nectar Source	*Silybum marianum* (variegated thistle) & *Onopordum acanthium* (cotton thistle)		
Overall Habitat Quality	Average		
Description	⬡ Thick *Hakea macrocarpa* grassy shrubland - roadside verge. ⬡ *Poa* small in size. ⬡ Sporadic domestic animal grazing. ⬡ Dominant vegetation thick hakea.		

Plate 52 Steppes Highway Hill, view to the north

A3.4.16. Steppes Sculptures

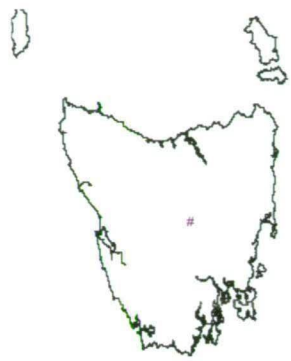
Collection ID	Step		
UTM Zone 55 GDA 94	*easting*	*northing*	
	491100	5338900	
Elevation (metres)	850		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Steppes	4833	
Directions	Steppes Sculpture Park, Lake Highway		
Dominant butterfly species	*O. lathoniella, O. ptunarra*		
Dominant *Poa* species	*P. hiemata*		
Dominant Nectar Source	*Carthamus lanatus* (saffron thistle), *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Cyathodes sp.* (mountain berries), *Helichrysum sp.* (native daisies), and *Wahlenbergia stricta* (native Bluebell)		
Overall Habitat Quality	Excellent		
Description	☞ Small, flat, enclosed area surrounded by eucalyptus forest. ☞ Dense patches of *Cyathodes sp.* within site. ☞ *Poa* healthy, small in size, froms ground cover and shows signs of marsupial grazing. ☞ Remaining ground cover between the *Poa* is herbaceous species.		

Plate 53 Steppes, view from edge of car park

A3.5. Marlborough Highway Field Sites

A3.5.1. Bronte Park Junction

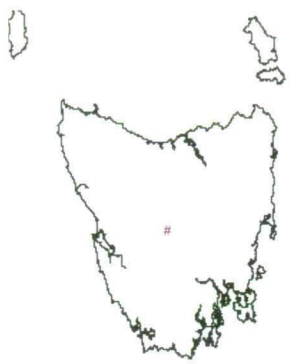
Collection ID	BPJ		
UTM Zone 55 GDA 94	*easting*	*northing*	
	457500	5331500	
Elevation	680 metres		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Bronte	4433	
Directions	Junction of the Marlborough and Lyell Highways at turn-off to Bronte Park		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Astroloma humifusum* (native cranberry)		
Overall Habitat Quality	Very Good		
Description	Area of *Hakea macrocarpa* shrublands, Tract of comparatively flat grassland, mixed with alpine shrubs. Dominant use cattle grazing. *Poa* small, healthy with a moderate density froming ground cover in clear areas. Good ground cover of other grassy and herbaceous species between tussocks. Surrounding area is alpine woodland and moor.		

Plate 54 Bronte Park Junction, view towards south-west from the corner of Lyell and Marlborough Highways

A3.5.2. Canal Drive, Liawenee Moore

Collection ID	CD		
UTM Zone 55 GDA 94	*easting*	*northing*	
	469400	5360000	
Elevation (metres)	1040		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Split Rock	4636	
Directions	From Lake Augusta Road take left-hand fork at Y junction before boundary of Central Plateau Protected Area. Follow road down to Canal. Turn off down road to Ouse River.		
Dominant butterfly species	*O. lathoniella, O. orichora, O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Helichrysum sp.* (daisies), *Cirsium sp.* (thistles) *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Excellent		
Description	☞ Extensive, undulating, tract of open *P. labillardierei* montane tussock grassland mixed with *Hakea macrocarpa* grassy shrubland and *Eucalyptus pauciflora* grassy woodlands. ☞ *Poa* large, luxuriant and healthy, very high density, with a good ground cover between tussocks. ☞ Gentle slope westerly aspect. ☞ Dominant use cattle grazing		

Plate 55 Canal Drive, view towards northwest from Canal Drive

A3.5.3. Canal Drive Flying Fox, Liawenee

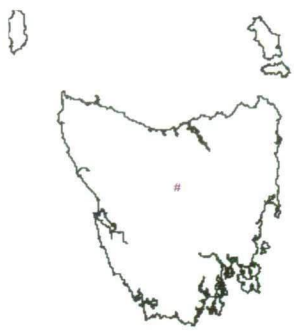
Collection ID	CDFF		
UTM Zone 55 GDA 94	*easting*	*northing*	
	468600	5360800	
Elevation (metres)	1040		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Split Rock	4636	
Directions	From Lake Augusta Road take left-hand fork at Y junction before boundary of Central Plateau Protected Area. Follow road down to canal. Follow road along canal. Turn off Canal Drive onto track heading down to the Ouse River. This site has 2 areas, the lower marsh where *H. cordace* fly and the top hakea dominated area where *Oreixenica* sp. fly		
Dominant butterfly species	*O. ptunarra, H. cordace*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Helichrysum sp.* (daisies), *Cirsium sp* (thistles) *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Excellent		
Description	☞ *P. labillardierei* montane tussock grassland mixed with *Hakea macrocarpa* grassy shrubland and *Eucalyptus pauciflora* grassy woodlands. ☞ *Poa* large, luxuriant and healthy, very high density, with a good ground cover between tussocks. ☞ Dominant use cattle grazing		

Plate 56 Canal Drive Flying Fox, Lower marsh area of site where *H. cordace* flies. View towards the north northeast

Plate 57 Canal Drive Flying Fox, lower marsh area

Plate 58 Canal Drive, top section view towards the southeast

A3.5.4. Farm House Marsh, Miena

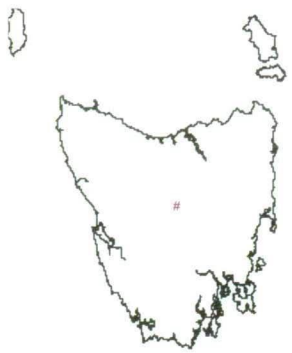
Collection ID	FHM		
UTM Zone 55 GDA 94	*easting*	*northing*	
	470400	5353600	
Elevation (metres)	1030		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Miena	4635	
Directions	Head straight ahead down track at first bend when leaving Miena on Marlborough Highway heading towards Bronte Park		
Dominant butterfly species	*O. orichora, O. ptunarra*		
Dominant *Poa* species	*P. hiemata*		
Dominant Nectar Source	*Helichrysum sp.* (daisies), *Cirsium sp* (thistles) *Taraxacum sp.* (dandelions) & *Richea sp*		
Overall Habitat Quality	Average		
Description	*Richea acerosa* grassy shrubland; slightly sheltered. Dominant use sheep and marsupial grazing		

Plate 59 Farm House Marsh, Miena, view towards the north

A3.5.5. Lake Augusta Road

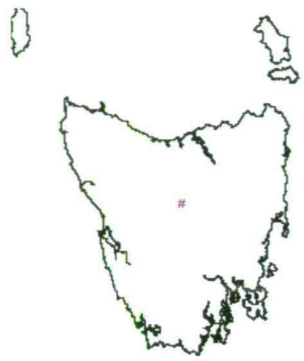
Collection ID	LAR		
UTM Zone 55 GDA 94	*easting*	*northing*	
	469100	5361200	
Elevation (metres)	1080		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Split Rock	4636	
Directions	200 m past Parks House and Botany Hut on Lake Augusta Road		
Dominant butterfly species	*O. orichora, O. lathoniella, O. ptunarra*		
Dominant *Poa* species	*P. labillardierei P. hiemata*		
Dominant Nectar Source	*Cyathodes sp.* (mountain berries), *Epacris impressa* (heath), *Helichrysum sp.* (daisies), *Leptospermum sp.* (tea tree), *Tetratheca procumbens* (lilac bells) and *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Excellent		
Description	▱ Patch of open alpine grassland surrounded by *Richea acerosa* and *Hakea macrocarpa* grassy shrubland gentle slope northerly aspect. ▱ *Poa*, medium sized and healthy forming ground cover in clear areas, ▱ No evidence of domestic animal grazing; however there is extensive evidence of marsupial grazing. ▱ Part of site regenerated following removal of buildings.		

Plate 60 Lake Augusta Road, view down onto study site from Lake Augusta Road

Plate 61 Lake Augusta Road, site detail from Lake Augusta Road

Plate 62 Lake Augusta Road, March 2006

A3.5.6. Little Pine Lagoon Boat Ramp

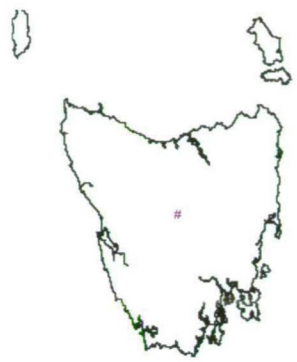
Collection ID	LPLB		
UTM Zone 55 GDA 94	*easting*	*northing*	
	467500	5349600	
Elevation (metres)	1000		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Monpeelyata	4634	
Directions	Grassland plain between Marlborough Highway and Little Pine Lagoon accessed from Little Pine Lagoon boat ramp		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Helichrysum sp.* (daisies) & *Taraxacum sp.* (dandelions)		
Overall Habitat Quality	Good		
Description	*Poa* plain along lake edge		

Plate 63 Little Pine Lagoon Boat Ramp, view towards the south

A3.5.7. Marlborough Highway

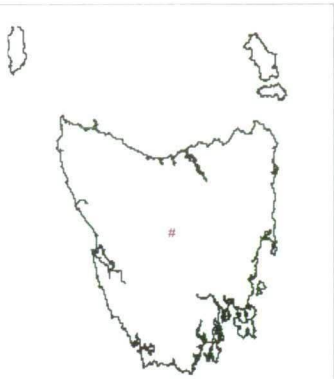
Collection ID	MH		
UTM Zone 55 GDA 94	*easting*	*northing*	
	463500	5346500	
Elevation (metres)	920		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Monpeelyata	4634	
Directions	Grassy hollow ~ 15 km north of Bronte Park on the Marlborough Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Helichrysum sp.* (daisies), *Leptospermum sp.* (tea tree), *Tetratheca procumbens* (lilac bells) and *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Good		
Description	*Eucalyptus rodwayi* grassy woodland and tussock grassland		

Plate 64 Marlborough Highway, view towards the east

A3.5.8. North Bronte

Collection ID	NB		
UTM Zone 55 GDA 94	*easting*	*northing*	
	460100	5339500	
Elevation (metres)	800		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Bronte	4433	
Directions	Grassy hollow ~ 5 km north of Bronte Park on the Marlborough Highway		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Epacris impressa* (heath), *Helichrysum sp.* (daisies), *Leptospermum sp.* (tea tree), *Tetratheca procumbens* (lilac bells) and *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Good		
Description	*Eucalyptus rodwayi* woodland and tussock grassland. Grassy hollow dominated by *P. Labillardierei*		

Plate 65 North Bronte, view towards the east

A3.5.9. Ouse River Bridge

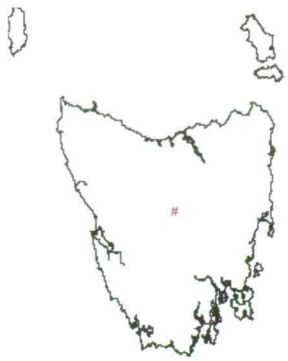
Collection ID	ORB	
UTM Zone 55 GDA 94	*easting*	*northing*
	470800	5351500
Elevation (metres)	970	
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*
	Miena	4635
Directions	Marlborough Highway ~ 5km south of Miena	
Dominant butterfly species	*O. orichora, O. ptunarra*	
Dominant *Poa* species	*P. hiemata*	
Dominant Nectar Source	*Epacris impressa* (heath), *Helichrysum sp.* (daisies), *Leptospermum sp.* (tea tree), *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)	
Overall Habitat Quality	Good	
Description	Valley of the Ouse River	

Plate 66 Ouse River Bridge, view towards the southeast from Marlborough Highway

Plate 67 Ouse River Bridge, view towards the northeast from Marlborough Highway

Plate 68 Ouse River Bridge, view towards the southeast from Marlborough Highway

A3.5.10. Pine Tier Dam

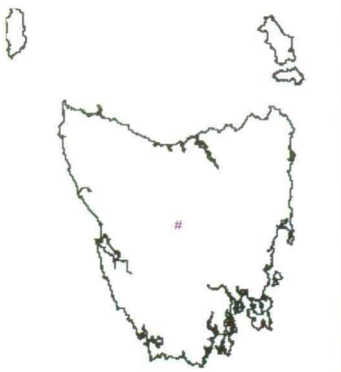
Collection ID	PTD		
UTM Zone 55 GDA 94	*easting*	*northing*	
	460900	5343900	
Elevation (metres)	760		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Monpeelyata	4634	
Directions	Corner of Pine Tier Road and Marlborough Highway ~ 10 km north of Bronte Park.		
Dominant butterfly species	*O. orichora, O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Helichrysum sp.* (daisies) & *Taraxacum sp.* (dandelions)		
Overall Habitat Quality	Good		
Description	Grassy hollow dominated by *P. Labillardierei* surrounded by dry sclerophyll forest		

Plate 69 Pine Tier Dam, view towards the north

A3.6. Eastcoast Field Sites

A3.6.1. Flagstaff Marsh

A3.6.1.1. Unburnt Area

<table>
<tr><td>Collection ID</td><td colspan="2">Flag</td><td rowspan="5">  </td></tr>
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GDA 94</td><td>easting</td><td>northing</td></tr>
<tr><td>571300</td><td>5326200</td></tr>
<tr><td>Elevation (metres)</td><td colspan="2">540</td></tr>
<tr><td rowspan="2">1:25000 TAS Map</td><td>Sheet Name</td><td>Map Sheet #</td></tr>
<tr><td>Tooms</td><td>5632</td></tr>
<tr><td>Directions</td><td colspan="3">The access track is 27 kilometres south of Lake Leake on the "M" Road. The unburnt area is on the southern side of the access track.</td></tr>
<tr><td>Dominant butterfly species</td><td colspan="3">O. ptunarra</td></tr>
<tr><td>Dominant Poa species</td><td colspan="3">P. sieberiana</td></tr>
<tr><td>Dominant Nectar Source</td><td colspan="3">Taraxacum sp., Leontodon sp. & Hypochoeris sp. (dandelions) Celmisia saxifraga (small snow daisy), Helichrysum sp. (native daisies), Leptospermum sp. (tea tree), Tetratheca sp. (lilac bells), Diplarrena moraea (white flag iris), Viola hederacea (wild violet) Wahlenbergia stricta (native bluebell)</td></tr>
<tr><td>Overall Habitat Quality</td><td colspan="3">Excellent</td></tr>
<tr><td>Description</td><td colspan="3">↗ Largest single colony of O. p angeli
↗ Unburnt site, extensive, flat area to south of access track.
↗ Poa, high density, small in size, growing under other vegetation providing dominant ground cover.
↗ Eucalyptus rodwayi - Eucalyptus ovata - Epacris lanuginose shrubby woodland.
↗ Middle strata relatively dense covering of marshland plants including Hakea sp. and Leptospermum sp. intermingled with Gahnia sp., Juncus sp. and Eucalypt sp. gradually merging into eucalypt forest on higher ground.
↗ No evidence of domestic animal grazing at Flagstaff Marsh.</td></tr>
</table>

Plate 70 Flagstaff Marsh, view south into unburnt half from access track

A3.6.1.1.2 Burnt Area

<table>
<tr><td>Collection ID</td><td colspan="2">Flag</td><td rowspan="5">  </td></tr>
<tr><td rowspan="2">UTM Zone 55
GDA 94</td><td>easting</td><td>northing</td></tr>
<tr><td>571300</td><td>5326200</td></tr>
<tr><td>Elevation (metres)</td><td colspan="2">540</td></tr>
<tr><td rowspan="2">1:25000 TAS Map</td><td>Sheet Name</td><td>Map Sheet #</td></tr>
<tr><td>Tooms</td><td>5632</td></tr>
<tr><td>Directions</td><td colspan="3">The access track is 27 kilometres south of Lake Leake on the “M” Road. The unburnt area is on the southern side of the access track.</td></tr>
<tr><td>Dominant butterfly species</td><td colspan="3">O. ptunarra</td></tr>
<tr><td>Dominant Poa species</td><td colspan="3">P. sieberiana</td></tr>
<tr><td>Dominant Nectar Source</td><td colspan="3">Taraxacum sp., Leontodon sp. & Hypochoeris sp. (dandelions) Celmisia saxifraga (small snow daisy), Helichrysum sp. (native daisies), Leptospermum sp. (tea tree)</td></tr>
<tr><td>Overall Habitat Quality</td><td colspan="3">Very Good</td></tr>
<tr><td>Description</td><td colspan="3">- Extensive, flat area to north of access track.
- Poa, small in size, moderate density growing under relatively dense covering of regrowth marshland plants including Diplarrena sp., Gahnia sp., and Juncus sp., intermingled with Hakea sp., Leptospermum sp., and Eucalypt sp..
- No evidence of domestic animal grazing at Flagstaff Marsh.</td></tr>
</table>

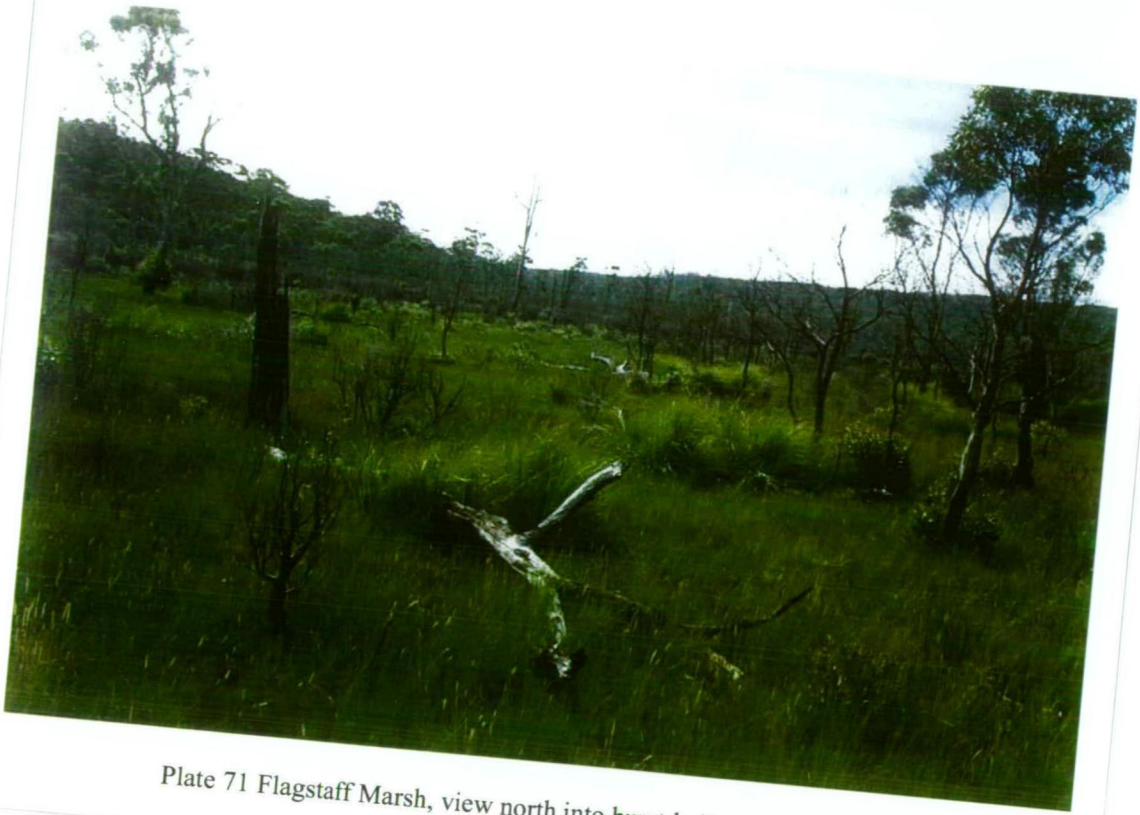


Plate 71 Flagstaff Marsh, view north into burnt half from access track

A3.6.2. Ladies Mile Marsh

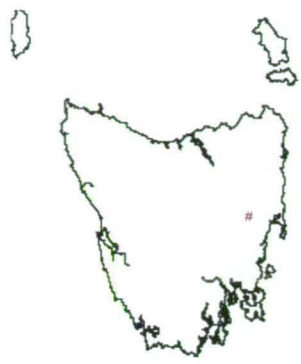
Collection ID	LMM		
UTM Zone 55 GDA 94	*easting*	*northing*	
	561100	5346800	
Elevation (metres)	605		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Leake	5634	
Directions	Lake Leake Highway, 5 km before the Lake Leake turn-off between Power Poles 245 and 246		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions) *Leptospermum sp.* (Tea Tree)		
Overall Habitat Quality	Average		
Description	↗ *Eucalyptus rodwayi* grassy woodland ↗ Possibly seasonally flooded which may restrict *O. ptunarra.* ↗ Flat, marshy area, with forest on southern border and open woodland on remaining sides. ↗ Dominant use Cattle grazing. ↗ *Poa* large in size, show signs of cropping, high *Poa* density. ↗ Good ground cover of soft herb species between tussocks. ↗ During the course of the study butterflies became extinct at this site. Suspected cause is over grazing of tussocks by cattle.		

Plate 72 Ladies Mile Marsh, view towards south

Plate 73 Cattle grazing at Ladies Mile Marsh

A3.6.3. Lake Leake

Collection ID	LL		
UTM Zone 55 GDA 94	*easting*	*northing*	
	568500	5346800	
Elevation (metres)	600		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Leake	5634	
Directions	Access from Lake Leake picnic ground and boat ramp		
Dominant butterfly species	*H. penelope, O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Average		
Description	⬡ Eucalyptus rodwayi grassy woodland ⬡ Butterflies found flying in grassy area surrounding lake		

Plate 74 Lake Leake, view towards the east

A3.6.3. Long Marsh

Collection ID	Long		
UTM Zone 55 GDA 94	*easting*	*northing*	
	564100	5345800	
Elevation (metres)	565		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Leake	5634	
Directions	~1 km along Long Marsh Road from the junction with Lake Leake Highway.		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Good		
Description	☞ Flat, marshy area, cleared from surrounding *Eucalyptus rodwayi* grassy woodland. ☞ Many primary regrowth, marshland species including *Gahnia sp., Juncus sp., Hakea sp.* and *Eucalypt sp.*. ☞ *Poa* medium to large in size however it is rank and scrappy. ☞ Light ground cover of herbaceous species between the tussocks. ☞ No evidence of domestic animal grazing.		

Plate 75 view south into Long Marsh Study Site from northern end of Long Marsh

A3.6.4. Stony Gully Road

Collection ID	SGR		
UTM Zone 55 GDA 94	*easting*	*northing*	
	533500	5353400	
Elevation (metres)	550		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Campbell Town	5435	
Directions	~15 km along Lake Leake Highway from Campbell Town, 100m past Power Pole 130. Wires cross the road, site downhill and around bend.		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardierei*		
Dominant Nectar Source	*Diplarrena moraea* (white flag iris) *Eucalyptus viminalis* (white gum) *Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions)		
Overall Habitat Quality	Very Good		
Description	↗ *Poa labillardierei* lowland tussock grassland ↗ Flat, narrow, marshy area running east west, with forest on the southern side and open woodland on northern border. ↗ Dominant use cattle grazing ↗ *Poa* moderate density, large in size, healthy and luxuriant. ↗ Moderate ground cover of soft herb species including clover between the tussocks. ↗ Strong *O. ptunarra* colony on a lightly grazed area of tussock grassland. ↗ This site is the northern end of a more extensive colony which is cut by the Lake Leake Highway.		

Plate 76 Stony Gully Road, view towards the east

Plate 77 Stony Gully Road, view towards the south

A3.6.7. Hobart Region Field Sites

A3.7.1. Glenlusk

Collection ID	GLEN	
UTM Zone 55 GDA 94	*easting*	*northing*
	516500	5258700
Elevation (metres)	380	
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*
	Collinsvale	5025
Directions	318 Glenlusk Road	
Dominant butterfly species	*H. merope, H. penelope, G klugii, J. villida, V. kershawi*	
Description	Semi rural family property, native and introduced plants.	

Plate 78 Glenlusk, view towards the north

A3.7.2. Mt Wellington, Old Springs Hotel

Collection ID	MtWel		
UTM Zone 55 GDA 94	*easting*	*northing*	
	520500	5248400	
Elevation (metres)	690		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Taroona	5224	
Directions	Site of the old Springs Hotel; grassland area at top of one way loop road which circles to the left from the main Springs area.		
Dominant butterfly species	*O. lathoniella*		
Description	Open marsupial grazed grassland area.		

Plate 79 Springs Hotel site, Mt Wellington, view towards the southeast

A3.7.3. Water Works

Collection ID	WW		
UTM Zone 55 GDA 94	*easting*	*northing*	
	524200	5249500	
Elevation (metres)	160		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Taroona	5224	
Directions	Grassland area 100m above gate to Waterworks Picnic area. Waterworks side of the Ridgeway Road.		
Dominant butterfly species	*H. merope*		
Description	Open grassland area surrounded by mixed eucalyptus woodland.		

Plate 80 Waterworks, view towards the south

A3.8. Northwest Field Sites

A3.8.1. Dairy Maids Plain, NW

Collection ID	DM	
UTM Zone 55 GDA 94	*easting*	*northing*
	391600	5412000
Elevation (metres)	650	
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*
	Guilford	3841
Dominant butterfly species	*O. ptunarra*	
Dominant *Poa* species	*P. gunnii*	
Dominant Nectar Source	*Hakea microcarpa*	
Overall Habitat Quality	Good	
Description	*Hakea macrocarpa* grassy shrubland and *P. gunnii* montane tussock grassland Grassy plain amidst closed *E. delegatensis* forest	

Plate 81 Dairy Maids Plain, view towards the east

A3.8.2. Hatfield Plain, NW

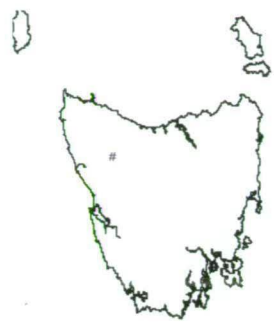
Collection ID	HAT		
UTM Zone 55 GDA 94	*easting*	*northing*	
	387300	5400400	
Elevation (metres)	680		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Pearse	3840	
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardieri*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Helichrysum sp.* (native daisies) & *Wahlenbergia stricta* (native blue bells)		
Overall Habitat Quality	Excellent		
Description	↗ *P. labillardieri* montane tussock grassland and *Hakea macrocarpa* grassy shrubland ↗ *L. filiforme* and *P. gunnii* occurs with *P. labillardieri* ↗ Large plain carrying huge population of butterflies		

Plate 82 Hatfield Plain, view towards the south

Plate 83 Hatfield Plain, view towards the east

Plate 84 Hatfield Plain, view towards the north

A3.8.3. Morey Road (Westwing Plain), NW

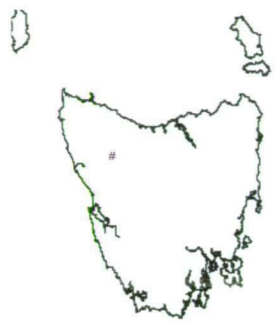
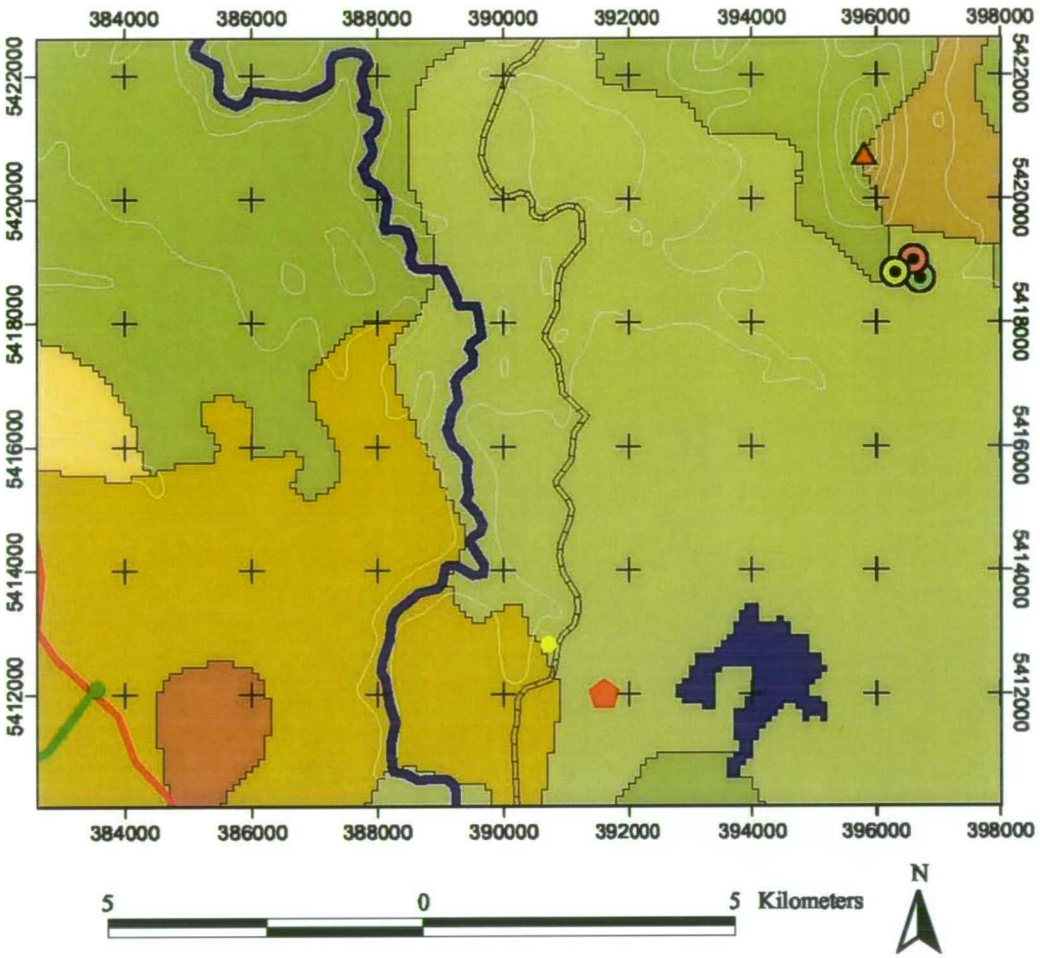
Collection ID	MR		
UTM Zone 55 GDA 94	*easting*	*northing*	
	387300	5473400	
Elevation (metres)	675		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Pearse	3840	
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. gunnii*		
Dominant Nectar Source	*Helichrysum sp.* (native daisies)		
Overall Habitat Quality	Good		
Description	*P. gunnii* montane tussock grassland Extensive grassy plain with minimal weed invasion		

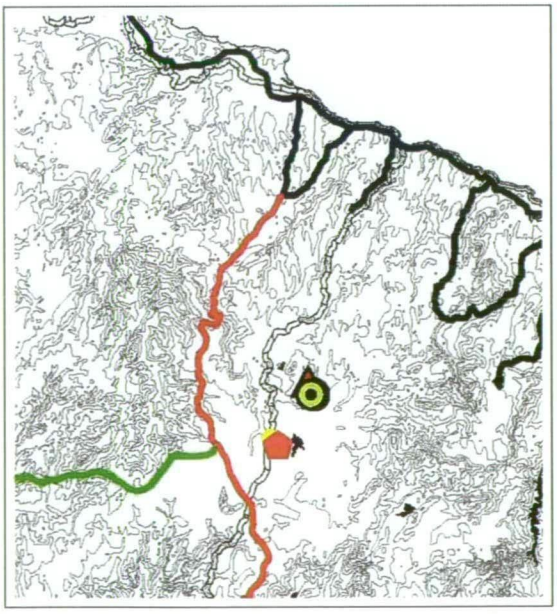
Plate 85 Morey Road, view towards the east

A3.8.4. Peak Plain

A3.8.4.1. Detail of Peak Plain Location details



- Peak Plain, Far End
- Peak Plain, Side 1 (Burnt 2003)
- Peak Plain, Side 2 (Burnt 1996)
- Guildford
- Dairy Maids Plain
- St. Valentines Peak
- Railway
- Murchinson Highway
- Waratah Road
- Hellyer River
- Buttongrass moor
- Cleared
- Eucalyptus delegatensis forest
- Eucalyptus obliqua tall forest
- High Woodland
- Rainforest
- Wet scrub
- Inland waters



A3.8.4.2. Peak Plain, Side 1

Collection ID	PPS1		
UTM Zone 55 GDA 94	*easting*	*northing*	
	396600	5419000	
Elevation (metres)	630		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Gulford	3841	
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. gunnii*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Helichrysum sp.* (daisies) & *Wahlenbergia stricta* (native blue bells)		
Overall Habitat Quality	Good		
Description	Peak Plain (Side 1 Burnt 2003) *P. gunnii* montane tussock grassland with *Hakea microcarpa* grassy shrubland		

Plate 86 Peak Plain, Side 1, view towards the west

A3.8.4.3. Peak Plain, Side 2

Collection ID	PPS2		
UTM Zone 55 GDA 94	*easting*	*northing*	
	396300	5418800	
Elevation (metres)	640		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Gulford	3841	
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. gunnii*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Helichrysum sp.* (daisies) & *Wahlenbergia stricta* (native blue bells)		
Overall Habitat Quality	Good		
Description	Peak Plain (Side 2 Burnt 1996) *P. gunnii* montane tussock grassland with *Hakea microcarpa* grassy shrubland		

Plate 87 Peak Plain, Side 2, view towards the north

A3.8.4.4. Peak Plain, Far End

Collection ID	PPFE	
UTM Zone 55 GDA 94	*easting*	*northing*
	396700	5418700
Elevation (metres)	650	
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*
	Gulford	3841
Dominant butterfly species	*O. ptunarra*	
Dominant *Poa* species	*P. gunnii*	
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Helichrysum sp.* (daisies) & *Wahlenbergia stricta* (native blue bells)	
Overall Habitat Quality	Good	
Description	Remnant grassland separated from main Peak Plain area *P. gunnii* montane tussock grassland with *Hakea microcarpa* grassy shrubland	

Plate 88 Peak Plain, Far End, view towards the west

A3.8.5. Race Course Plain

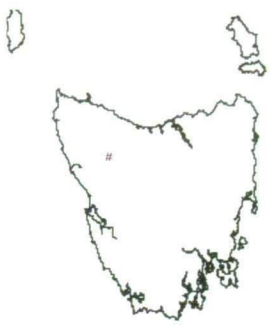
Collection ID	RC		
UTM Zone 55 GDA 94	*easting*	*northing*	
	391700	5401750	
Elevation (metres)	700		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Pearse	3840	
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. labillardieri* and *P. gunnii*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Helichrysum sp.* (daisies) & *Wahlenbergia stricta* (native blue bells)		
Overall Habitat Quality	Good		
Description	☞ *P. labillardieri / P. gunnii* montane tussock grassland with *Hakea microcarpa* grassy shrubland ☞ Surrounded by *N. Curringhamii* ranforest and *E. delegatensis* woodland. ☞ Part of the site was burnt 1996/1997		

Plate 89 Racecourse Plain, view towards the east

A3.8.6. Weather Station Corner

Collection ID	WSC		
UTM Zone 55 GDA 94	*easting*	*northing*	
	377200	5411300	
Elevation (metres)	610		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Waratah	3641	
Directions	Waratah (097014) Weather Station at corner of Mount Road		
Dominant butterfly species	*O. ptunarra*		
Dominant *Poa* species	*P. gunnii*		
Dominant Nectar Source	*Taraxacum sp., Leontodon sp. & Hypochoeris sp* (dandelions), *Helichrysum sp.* (daisies)		
Overall Habitat Quality	Good		
Description	*P. gunnii* montane tussock grassland Extensive plain, mosaic of grassland, shrubland and woodland		

Plate 90 Weather Station Corner, view towards the east

A3.9.1. Odd Tasmanian Field Sites

A3.9.1.1. Hartz Mountain

Collection ID	Htz		
UTM Zone 55 GDA 94	*easting*	*northing*	
	481200	5215100	
Elevation (metres)	860		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Waterloo	4821	
Directions	Road edges below Waratah Lookout ~7.5km along Hartz Road from junction with Arve Road.		
Dominant butterfly species	*N. leprea*		
Description	Wet mixed sclerophyll forest *Uncinia tenella* grows along track edges		

Plate 91 Hartz, view towards the northeast

A3.9.1.2. Mt King William

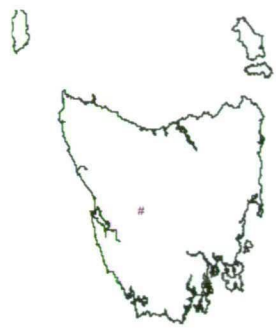
Collection ID	MtKW		
UTM Zone 55 GDA 94	*easting*	*northing*	
	428800	5326800	
Elevation (metres)	800		
1:100 000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Nive	8113	
Directions	Lyell Highway~12 km south of Derwent Bridge, base of Mt King William, start of walking track.		
Dominant butterfly species	*H. cordace, N. leprea, A. hobartia*		
Description	Grassy plain surrounded by wet sclerophyll forest		

Plate 92 Mt King William, view towards the west

A3.9.1.3. Paradise Plain

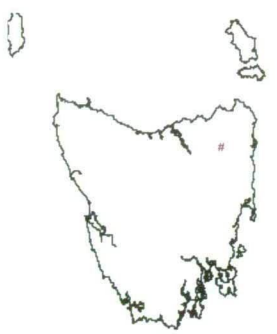
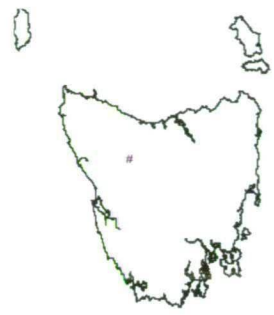
Collection ID	PP		
UTM Zone 55 GDA 94	*easting*	*northing*	
	559000	5421800	
Elevation (metres)	800		
1:100 000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Forester	8415	
Directions	Newitts Creek, Ben Ridge Road off Mathinna Plains Road		
Dominant butterfly species	*H. cordace*		
Description	Grassy plain surrounded by mixed forest.		

Plate 93 Paradise Plain, views towards the north

A3.9.1.4. Ronny Creek Car Park – Lake Dove Cradle Mountain

<table>
<tr><td>Collection ID</td><td colspan="2">RCCP</td><td rowspan="5">  </td></tr>
<tr><td rowspan="2">UTM Zone 55
GDA 94</td><td>easting</td><td>northing</td></tr>
<tr><td>412600</td><td>5388800</td></tr>
<tr><td>Elevation (metres)</td><td colspan="2">870</td></tr>
<tr><td rowspan="2">1:25000 TAS Map</td><td>Sheet Name</td><td>Map Sheet #</td></tr>
<tr><td>Cradle</td><td>4038</td></tr>
<tr><td>Directions</td><td colspan="3">Ronny Creek Car Park – Lake Dove Road, Cradle Mountain</td></tr>
<tr><td>Dominant butterfly species</td><td colspan="3">O. orichora, O. ptunarra</td></tr>
<tr><td>Dominant Poa species</td><td colspan="3">P. gunnii</td></tr>
<tr><td>Dominant Nectar Source</td><td colspan="3">Cyathodes sp. (mountain berries), Helichrysum sp. (native daisies), and Wahlenbergia stricta (native Bluebell), Richea scoria</td></tr>
<tr><td>Overall Habitat Quality</td><td colspan="3">Good</td></tr>
<tr><td>Description</td><td colspan="3">↗ Poa gunnii montane tussock grassland
↗ Only butterfly site within a National park</td></tr>
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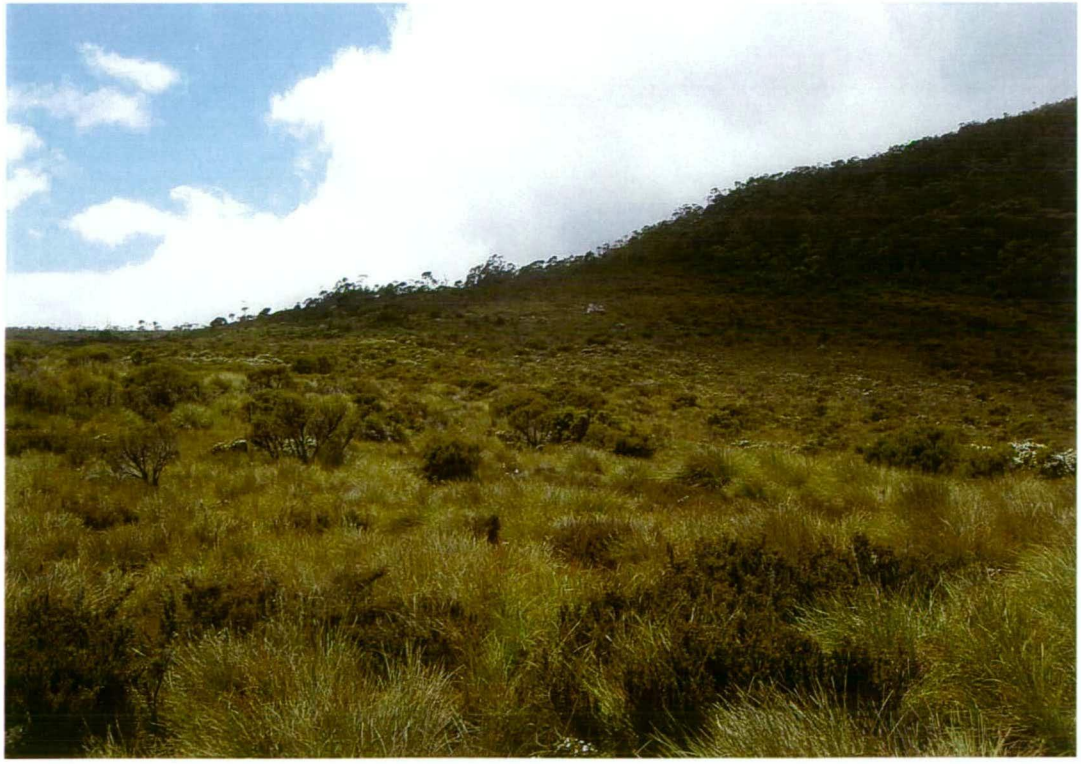


Plate 94 Ronny Creek Car Park, views towards the southeast

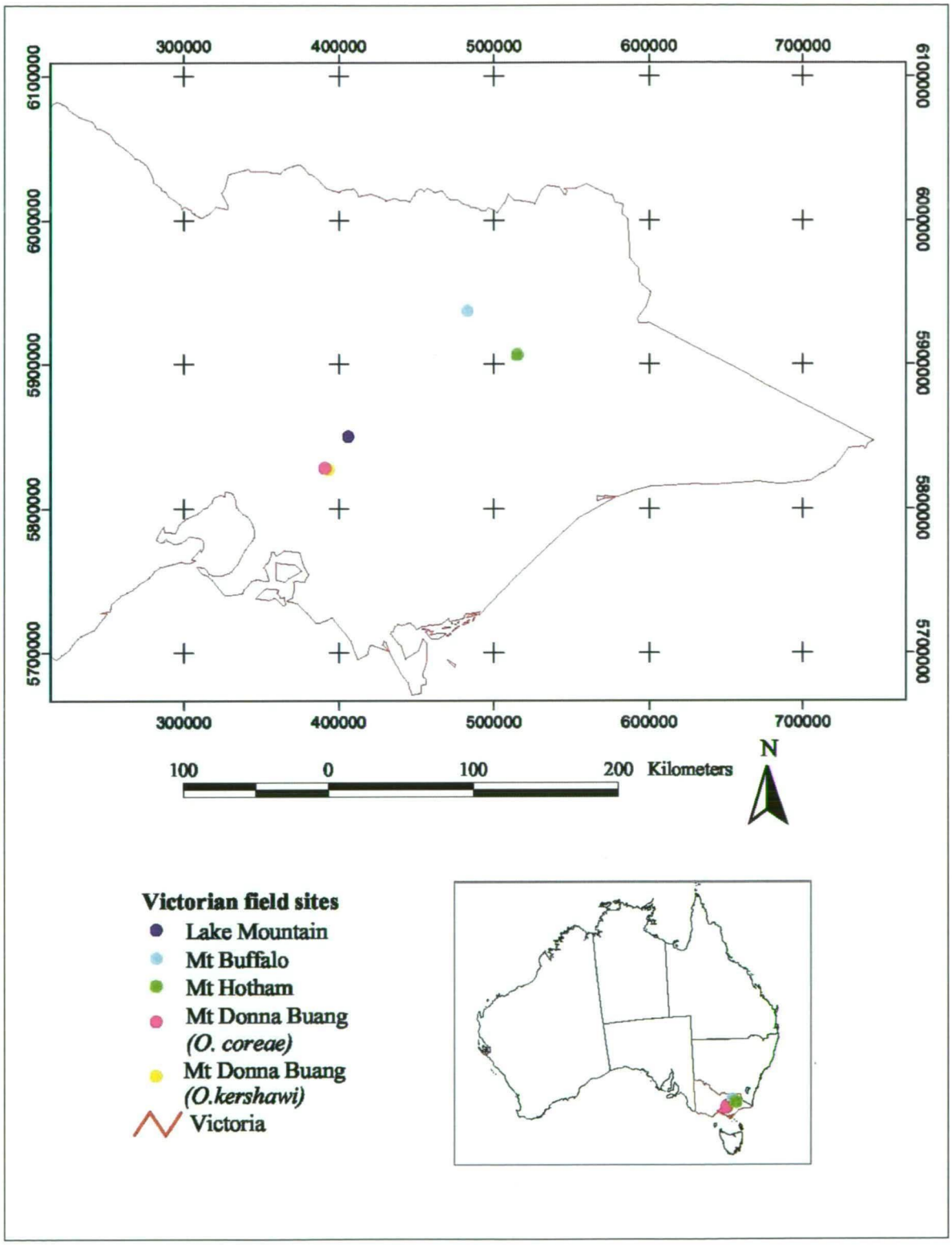
A3.9.1.5. Weymouth

Collection ID	Wey		
UTM Zone 55 GDA 94	*easting*	*northing*	
	512100	5459700	
Elevation (metres)	10		
1:25000 TAS Map	*Sheet Name*	*Map Sheet #*	
	Weymouth	5045	
Directions	Weymouth northeast Tasmania		
Dominant butterfly species	*H. merope*		
Description	Sheltered sunny grassy patches surrounded by *Leptospermum sp.*		

Plate 95 Weymouth, views towards northeast

A3.10.1. Victorian Field Sites

A3.10.1. Detail of Victorian Field Sites



A3.10.2. Lake Mountain

Collection ID	LmtV	
UTM Zone 55 GDA 94	*easting*	*northing*
	400420	5847600
Elevation (metres)	1320	
Directions	Lake Mountain Road, Snowy Hill Shelter	
Dominant butterfly species	*O. cordace*	
Description	Open grassy plain	

Plate 96 Lake Mountain , view of flight area

A3.10.3. Mt Buffalo, Lake Catani, Victoria

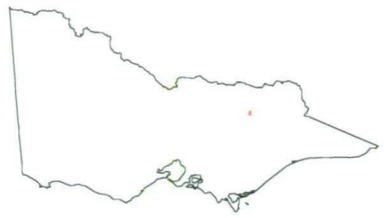
Collection ID	MtB / MtBuf	
UTM Zone 55 GDA 94	*easting*	*northing*
	482500	5934570
Elevation (metres)	1350	
Directions	Lake Catani picnic area and herbaceous grassy plain surrounding lake	
Dominant butterfly species	*O. latialis, V. kershawi*	
Description	Open grassy plain	

Plate 97 Mt Buffalo, Lake Catani, view towards the east

A3.10.4. Mt Donna Buang, Victoria

A3.10.4.1. Oreixenica kershawi site

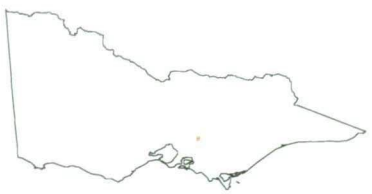
Collection ID	MtDB (MtDB site 1)		
UTM Zone 55 GDA 94	*easting*	*northing*	
	386733	5824465	
Elevation (metres)	390		
Directions	6km from Warburton on road to Mount Donna Buang		
Dominant butterfly species	*O. kershawi*		
Description	Wet sclerophyll mixed forest.		

Plate 98 Mt Donna Buang, view over flight area

A3.10.4.2. Oreixenica correae site

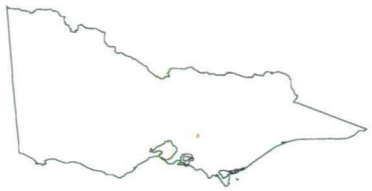
Collection ID	MtDB (MtDB site 2 / 2A)		
UTM Zone 55 GDA 94	*easting*	*northing*	
	383674	5825752	
Elevation (metres)	1260		
Directions	Top of Mt Donna Buang Road – far side of car park		
Dominant butterfly species	*O. correae*		
Description	Open woodland (grassy) extensive ragwort, clover and other introduced weed species.		

Plate 99 Mt Donna Buang, view towards north

A3.10.5. Mt Hotham, Victoria

Collection ID	MtH / MtHoth	
UTM Zone 55 GDA 94	*easting*	*northing*
	516550	5904030
Elevation (metres)	1600	
Directions	~ 10 km south of Mt Hotham village	
Dominant butterfly species	*O. latialis, V. kershawi*	
Description	lightly wooded frost hollow	

Plate 100 Mt Hotham, view into site from road

Appendix 4 - CTAB Extraction Protocol modified from Grewe et al. (1994)

1. Add 200µL of CTAB buffer to 100mg of tissue, then grind.
2. Add 300µL of CTAB buffer continue grinding until al tissue has been homogenised
3. Add 5µL of 20mg/mL proteinaseK and vortex briefly.
4. Incubate at 65°C for at least 1 hour. Vortex occasionally and re-grind the tissue if necessary.
5. Extract the homogenate with 500µL of chloroform-isoamyl alcohol (24:1), shake for 1 minute and centrifuge at 1300 rpm for 20 minutes.
6. Remove the upper aqueous layer taking care not to disturb the interface separating the organic (chloroform) layer. Add the aqueous layer to a new tube containing 600µL of phenol/chloroform-isoamyl alcohol (25:24:1). Mix well for at least 1 minute and centrifuge at 1300 rpm for 10 minutes. Repeat this step until the upper aqueous layer is totally clear (generally two extractions)
7. Remove the upper aqueous layer; add it to a new tube containing 600µL of chloroform-isoamyl alcohol and mix well. Centrifuge at 1300 rpm for 30 seconds.
8. Transfer the upper aqueous layer to a new tube labelled for storage containing 900µL (approximately 1.5 volumes) of cold (-20°C) isopropanol. Invert the tube gently 10 times; a white stringy pellet should form.
9. Allow the DNA to precipitate at -20°C overnight. Centrifuge at 1300 rpm for 20 minutes.
10. Remove the supernatant and add 180µL of cold 70% ethanol. Invert the tube gently and centrifuge at 1300 rpm for 10 minutes.
11. Dry the DNA pellet under vacuum for 30 minutes.
12. Re-suspend the DNA pellet in 100 of distilled H_2O. Allow the DNA pellet to re hydrate for several hours at 4°C.

2x CTAB Buffer:

50mL 1.0M Tris-HCl pH 8.0 [0.10M final]

20mL 0.5M EDTA [0.02M final] (ethylenediaminetetraacetic acid)

40g NaCl [1.40M final] (sodium chloride)

10g CTAB (hexadecyltrimethylammonium bromide)

distilled H_2O to 500mL

Appendix 5 - CEQ Dye Terminator Cycle Sequencing with Quick Start Kit

1. Preparation of the DNA Sequencing reaction:

Sequencing reactions were prepared in 0.2ml thin-wall tube or microplate well. All reagents were kept on ice while preparing the sequencing reactions and were added in the order listed below.

dH_2O (to adjust to total volume to 20μL)	0-9.5μL
DNA Template* (see template Preparation)	0.5-10.0μL
Customer supplied or -47 Sequencing Primer (1.6 ρmol/μL or 1.6 μM)	0.65μL
DTCS Quick Start Master Mix	2.0μL
Total	10μL

**Use 0.5μL for pUC18 control template*

NOTE: Mix reaction components thoroughly. Consolidate the liquid in the bottom of the tube or well by briefly centrifuging before thermal cycling.

2. Thermal Cycling program:

96°C 20 seconds

50°C 20 seconds

60°C 4 minutes

for 30 cycles followed by holding at 4°C.

3. Ethanol Precipitation:

a. Prepare a labelled, sterile 0.5mL microfuge tube for each sample.

b. Prepare fresh Stop Solution/Glycogen mixture (per sequencing reaction):

2.00μL of 3.0M Ch_3COONa (pH 5.2) [sodium acetate]

2.00μL of 100mM Na_2EDTA (pH 8.0) [EDTA disodium salt]

0.25μL of 20mg/mL glycogen [supplied with the kit]

To each of the labelled tubes add 4.25μL of the Stop Solution/Glycogen mixture.

c. Transfer the sequencing reaction to the appropriately labelled 0.5mL microfuge tube and mix thoroughly.

d. Add 60µL cold 95% (v/v) ethanol/dH_2O from -20°C freezer and mix thoroughly. Immediately centrifuge at 14 000 rpm at 4°C for 15 minutes. Carefully remove the supernatant with a micropipette (the pellet should be visible).
Note: For multiple samples, always add the cold ethanol/dH_2O immediately before centrifugation.

e. Rinse the pellet 2 times with 200 µL 70% (v/v) ethanol / dH_2O from -20°C freezer. For each rinse, centrifuge immediately at 14 000 rpm at 4°C for a minimum of 2 minutes. After centrifugation carefully remove all of the supernatant with a micropipette.

f. Vacuum dry for 15 minutes (or until dry)

g. Resuspend the sample in 28µL of the Sample Loading Solution (provided with the kit)

4. Sample preparation for loading into the CEQ:

a. Transfer the resuspended samples to the appropriate wells of the CEQ sample plate.

b. Overlay each of the resuspended samples with one drop of light mineral oil (provided in the kit or Sigma Cat #M 5904).

c. Load the sample plate into the CEQ and start the desired method.

Appendix 6 - Genus Sequences

CO1

A_hobartia	ATAGGATCTCCTCCCCCCTGCAGGATCGAAAAAAAGAGGTATTTAAATTT
A_hobartia2	ATAGGATCTCCTCCCCCCTGCAGGATCGAAAAAAAGAGGTATTTAAATTT
G_klugii	ATTGGATCTCCTCCTCCCTGCTGGATCGAAAAAATGATGTATTAATATTT
H_cordace_1	ATAGGATCTCCTCCACCTTGCAGGATCAAAAAAAAGAAGTATTTAAATTT
H_cordace_k	ATAGGATCTCCTCCACCTGGCAGGATCAAAAAAAAGAAGTATTTAAATTT
H_cordace_c	ATAGGATCTCCTCCACCTGGCAGGATCAAAAAAAAGAAGTATTTAAATTT
H_meropeWAY	ATGGGATCTCCTCCTCCTGGCGGGGTCAAAAAAAAGAAGTGTTTAAATTT
H_meropeWW	ATGGGATCTCCTCCTCCGGGCTGGGTCAAAAAAAAGAAGTGTTTAAATTT
H_penelope	ATAGGATCTCCTCCTCCTTGCGGGGTCAAAAAAAAGAAGTGTTTAAGTTT
J_villida	ATGGGATCTCCTCCACCTAGCCGGATCACAAAAATGAAGTATTAATATTT
J_villida2	ATGGGATCTCCTCCACCTAGCCGGATCACAAAAATGAAGTATTAATATTT
N_leprea_e	ATAGGATCTCCCCCCCCCCGCAGGATCAAAAAAAAGAAGTGTTTAAATTT
N_leprea_l	ATAGGATCTCCCCCTCCCAGCAGGATCCAAAAAAAGAAGTGTTTAAATTT
O_correae	ATAGGATCTCCTCCCCCTGGCGGGATCAAAAAAATGAAGTATTTAAATTT
O_kershawi	ATAGGATCTCCTCCTCCCCGCAGGATCAAAAAAATGAAGTATTTAAATTT
O_lathoniella1	ATAGGATCTCCTCCCCCAGGCTGGGTCAAAAAAATGAAGTATTTAAATTT
O_lathoniella2	ATAGGATCTCCTCCCCCAGGCTGGGTCAAAAAAATGAAGTATTTAAATTT
O_latialis	ATAGGATCTCCTCCTCCCTGCGGGGTCAAAAAAATGAAGTATTTAGATTT
O_orichora1	ATAGGATCTCCTCCTCCCTGCTGGATCAAAAAAATGAAGTATTTAAATTT
O_orichora2	ATAGGATCTCCTCCTCCCTGCTGGATCAAAAAAATGAAGTATTTAAATTT
O_ptunarraBPJ	ATAGGATCTCCTCCTCCCTGCGGGGTCAAAAAAATGAAGTATTTAGATTT
O_ptunarraBPJ1	ATAGGATCTCCTCCTCCCTGCGGGGTCAAAAAAATGAAGTATTTAGATTT
O_ptunarraNW	ATAGGATCTCCTCCTCCCTGCGGGGTCAAAAAAATGAAGTATTTAGATTT
V_kershawi	ATAGGATCTCCTCCTCCTTGCAGGATCGAAAAAATGAAGTATTAATATTT

A_hobartia	CGATCGTAAAAAGTATAGTAATAGCCCCTGCTAAAACAGGTAGAGAAAGT
A_hobartia2	CGATCGTAAAAAGTATAGTAATAGCCCCTGCTAAAACAGGTAGAGAAAGT
G_klugii	CGATCGTTAAAAGTATAGTAATAGCTCCAGCTAAATACAGGTAAAGAAAGT
H_cordace_1	CGGTCGTAAAAAGTATAGTAATAGCTCCAGCTAATACAGGTAAAGAAAGT
H_cordace_k	CGGTCGTAAAAAGTATAGTAATAGCTCCAGCTAATACAGGTAAAGAAAGT
H_cordace_c	CGGTCGTAAAAAGTATAGTAATAGCTCCAGCTAATACAGGTAAAGAAAGT
H_meropeWAY	CGATCGTTAAAAGTATAGTGATAGCTCCTGCTAAAACAGGTAAAGAAAGT
H_meropeWW	CGATCGTAAAAAGTATAGTGATAGCTCCTGCTAAAACAGGTAAAGAAAGT
H_penelope	CGATCGTAAAAAGTATAGTAATAGCTCCAGCTAGTACTGGTAAAGAAAGT
J_villida	CGATCGTTAAAAGTATAGTAATAGCTCCAGCTAATACTGGTAAAGAAAGA
J_villida2	CGATCGTTAAAAGTATAGTAATAGCTCCAGCTAATACTGGTAAAGAAAGA
N_leprea_e	CGATCGTAAAAAGTATGGTAATAGCTCCAGCTAATACAGGTAAAGAGAGA
N_leprea_l	CGATCGTTAAAAGTATGGTAATAGCTCCAGCTAATACAGGTAAAGAGAGA
O_correae	CGATCGTTAAAAGTATAGTAATAGCTCCTGCTAAAACAGGTAAAGAAAGT
O_kershawi	CGATCGTTAAAAGTATAGTAATAGCTCCTGCTAAAACGGGTAAAGAAAGT
O_lathoniella1	CGGTCGTTAAAAGTATAGTGATAGCTCCTGCTAGAACAGGTAAAGAAAGT
O_lathoniella2	CGGTCGTTAAAAGTATAGTGATAGCTCCTGCTAGAACAGGTAAAGAAAGT
O_latialis	CGGTCGTTAAAAGTATAGTAATAGCCCCTGCTAAAACAGGTAAAGAAAGT
O_orichora1	CGGTCGTTAAAAGTATAGTAATAGCTCCTGCTAAAACAGGTAAAGAAAGT
O_orichora2	CGGTCGTTAAAAGTATAGTAATAGCTCCTGCTAAAACAGGTAAAGAAAGT
O_ptunarraBPJ	CGGTCGTTAAAAGTATAGTAATAGCTCCTGCTAAAACAGGTAAAGAAAGT
O_ptunarraBPJ1	CGGTCGTTAAAAGTATAGTAATAGCTCCTGCTAAAACAGGTAAAGAAAGT
O_ptunarraNW	CGGTCGTTAAAAGTATAGTAATAGCTCCTGCTAAAACAGGTAAAGAAAGT
V_kershawi	CGATCGTGAAAAGTATAGTAATAGCCCCTGCTAAAACAGGTAAAGAAAGT

A_hobartia	AATAATAATAAAGCTGTAATACCAACAGCTCAAACAAATAAGGGTATTTG
A_hobartia2	AATAATAATAAAGCTGTAATACCAACAGCTCAAACAAATAAGGGTATTTG
G_klugii	AATAAAAGTAATGCTGTAATACCTACAGCTCAAACAAATAAAGGTATTTG
H_cordace_1	AATAATAATAATGCTGTAATTCCAACGGCTCATACGAATAAGGGTATTTG
H_cordace_k	AATAATAATAATGCTGTAATTCCAACGGCTCATACGAATAAGGGTATTTG
H_cordace_c	AATAATAATAATGCTGTAATTCCAACGGCTCATACGAATAAGGGTATTTG
H_meropeWAY	AGTAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAGGGGTATTTG
H_meropeWW	AGTAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAAAGGTATTTG
H_penelope	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAGGGGTATTTG
J_villida	ACTAATAATAATGCTGTAATTCCTACAGCTCAAACAAATAAAGGTATTTG
J_villida2	ACTAATAATAATGCTGTAATTCCTACAGCTCAAACAAATAAAGGTATTTG
N_leprea_e	AGTAATAATAATGCTGTAATTCCAACAGCTCAGACAAATAAAGGTATTTG
N_leprea_l	AGTAATAATAATGCTGTAATTCCAACAGCTCAGACAAATAAAGGTATTTG
O_correae	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAAAGGTATTTG
O_kershawi	AATAATAATAGTGCTGTAATTCCAACAGCTCAAACAAATAAAGGTATTTG
O_lathoniella1	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAATGGTATTTG
O_lathoniella2	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAATGGTATTTG
O_latialis	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAGGGGTATTTG
O_orichora1	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAAAGGTATTTG
O_orichora2	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAAAGGTATTTG
O_ptunarraBPJ	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAGGGGTATTTG
O_ptunarraBPJ1	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAGGGGTATTTG
O_ptunarraNW	AATAATAATAATGCTGTAATTCCAACAGCTCAAACAAATAGGGGTATTTG
V_kershawi	AATAATAATAATGCTGTAATACCTACTGCTCAAACAAATAACGGTATTTG

A_hobartia	ATCGTAAGATATACTATTAACTCGTATATTAATAATTGTTGTAATAAAAT
A_hobartia2	ATCGTAAGATATACTATTAACTCGTATATTAATAATTGTTGTAATAAAAT
G_klugii	GTCAAAGGATATACTATTAACTCGTATGTTAATAATAGTTGTAATAAAAT
H_cordace_1	ATCATAGCTTATATTATTGACACGTATATTAATAATTGTTGTAATAAAAT
H_cordace_k	ATCATAGCTTATATTATTGACACGTATATTAATAATTGTTGTAATAAAAT
H_cordace_c	ATCATAGCTTATATTATTGACACGTATATTAATAATTGTTGTAATAAAAT
H_meropeWAY	ATCATAACTTATATTATTAACTCGTATGTTAATAATAGTTGTAATAAAAT
H_meropeWW	ATCATAACTTATATTATTAACACGTATGTTAATAATTGTTGTAATAAAAT
H_penelope	ATCATAATTTATATTATTAACACGTATATTAATAATTGTTGTAATAAAAT
J_villida	ATCAAAAGATATACCATGTACTCGTATATTAATAATTGTTGTAATAAAAT
J_villida2	ATCAAAAGATATACCATGTACTCGTATATTAATAATTGTTGTAATAAAAT
N_leprea_e	ATCATAAGATATATTGTTAACTCGTATATTAATAATTGTTGTAATAAAAT
N_leprea_l	ATCATAAGATATATTGTTAACTCGTATATTAATAATTGTTGTAATAAAAT
O_correae	ATCATAAGCTATATTATTAACTCGTATATTAATAATTGTTGTAATAAAAT
O_kershawi	ATCATAAGCTATACTATTAATTCGTATATTAATAATTGTGGTAATAAAAT
O_lathoniella1	GTCGTAAGCTATATTATTAACTCGTATATTAATAATTGTTGTAATAAAAT
O_lathoniella2	GTCGTAAGCTATATTATTAACTCGTATATTAATAATTGTTGTAATAAAAT
O_latialis	ATCATAATTTATATTATTAACTCGTATATTAATAATAGTTGTAATAAAAT
O_orichora1	ATCATAAGCTATATTATTAATTCGTATATTAATAATTGTTGTAATAAAAT
O_orichora2	ATCATAAGCTATATTATTAATTCGTATATTAATAATTGTTGTAATAAAAT
O_ptunarraBPJ	ATCATAATTTATATTATTAACTCGTATATTAATAATAGTTGTAATAAAAT
O_ptunarraBPJ1	ATCATAATTTATATTATTAACTCGTATATTAATAATAGTTGTAATAAAAT
O_ptunarraNW	ATCATAATTTATATTATTAACTCGTATATTAATAATAGTTGTAATAAAAT
V_kershawi	ATCATARGATATACTATTAACTCGTATATTAATAATAGTAGTAATAAAAT

CO1

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A_hobartia      TAATAGCTCCTAAAATAGATGAGATTCCAGCTAGGTGAAGGGAAAAAATT
A_hobartia2     TAATAGCTCCTAAAATAGATGAGATTCCAGCTAGGTGAAGGGAAAAAATT
G_klugii        TAATTGCTCCTAAAATTGATGAAATACCAGCTAAATGAAGAGAAAAAATT
H_cordace_l     TAATAGCTCCTAAAATTGAAGAAATTCCAGCTAGATGAAGGGAGAAAATT
H_cordace_k     TAATAGCTCCTAAAATTGAAGAAATTCCTGCTAGATGAAGGGAGAAAATT
H_cordace_c     TAATAGCTCCTAAAATTGAAGAAATTCCTGCTAGATGAAGGGAGAAAATT
H_meropeWAY     TAATAGCTCCTAAAATAGAAGAGATTCCTGCTAAATGTAAGGAAAAAATT
H_meropeWW      TAATAGCTCCTAAAATTGAAGAGATTCCTGCTAAATGTAAAGAAAAAATT
H_penelope      TAATAGCTCCTAAAATTGAGGAAATTCCAGCTAAATGGAGGGAAAAAATT
J_villida       TAATAGCTCCTAAAATAGAAGAAATTCCTGCTAAATGAAGAGAGAAAATT
J_villida2      TAATAGCTCCTAAAATAGAAGAAATTCCTGCTAAATGAAGAGAGAAAATT
N_leprea_e      TAATTGCTCCTAAAATTGATGAAATTCCAGCTAAATGAAGGGAAAAAATT
N_leprea_l      TAATAGCTCCTAAAATTGATGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_correae       TAATGGCTCCTAAAATTGATGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_kershawi      TAATAGCTCCTAAAATAGAAGAAATTCCAGCTAAATGAAGAGAAAAAATT
O_lathoniella1  TAATAGCTCCTAAAATAGAAGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_lathoniella2  TAATRGCTCCTAAAATAGAAGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_latialis      TAATAGCTCCTAAAATAGAAGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_orichora1     TAATAGCTCCTAAGATTGAGGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_orichora2     TAATAGCTCCTAAGATTGAGGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_ptunarraBPJ   TAATAGCTCCTAAAATAGAAGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_ptunarraBPJ1  TAATAGCTCCTAAAATAGAAGAAATTCCAGCTAAATGAAGGGAAAAAATT
O_ptunarraNW    TAATAGCTCCTAAAATAGAAGAAATTCCAGCTAAATGAAGGGAAAAAATT
V_kershawi      TAATGGCTCCCAGGATTGATGAAATACCAGCTAAATGAAAAGAAAAAATT

A_hobartia      GCTAAATCAACTGATGTTCCTCTATGAGCGATATTTGATGAAAGTGGTGG
A_hobartia2     GCTAAATCAACTGATGTTCCTCTATGAGCGATATTTGATGAAAGTGGTGG
G_klugii        GCTAAATCTACAGATGATCCTCTATGTGCAATATTAGATGAAAGTGGGGG
H_cordace_l     GCTAAATCAACTGAAGAGCCTCCGTGAGCGATATTTGATGAAAGTGGGGG
H_cordace_k     GCTAAATCAACTGAAGAGCCTCCGTGAGCGATATTTGATGAAAGTGGGGG
H_cordace_c     GCTAAATCAACTGAAGAGCCTCCGTGAGCGATATTTGATGAAAGTGGGGG
H_meropeWAY     GCTAAATCTACAGATGATCCTCCATGAGCAATATTAGATGAAAGTGGGGG
H_meropeWW      GCTAAATCAACGGAAGAGCCTCCATGAGCAATATTAGATGAAAGTGGGGG
H_penelope      GTTAAGTCTACAGAAGAGCCTCCATGGGCAATATTGGATGAAAGTGGGGG
J_villida       GCTAAATCAACTGAAGATCCTCCGTGAGCAATATTAGATGAAAGTGGGGG
J_villida2      GCTAAATCAACTGAAGATCCTCCGTGAGCAATATTAGATGAAAGTGGGGG
N_leprea_e      GCTATATCAACTGAAGAACCTCTATGAGCAATATTAGATGAAAGTGGTGG
N_leprea_l      GCTATATCAACTGAAGAACCTCTATGAGCAATATTAGATGAAAGTGGTGG
O_correae       GCTAAATCTACAGAAGATCCACCATGAGCAATATTAGAAGAAAGGGGGGG
O_kershawi      GCTAAATCTACAGATGAACCACCATGGGCAATATTAGAAGAGAGGGGGGG
O_lathoniella1  GCTAAATCTACAGATGAACCACCATGAGCAATATTAGATGAAAGAGGAGG
O_lathoniella2  GCTAAATCTACAGATGAACCACCATGAGCAATATTAGATGAAAGAGGAGG
O_latialis      GCTAAATCTACAGATGAGCCACCATGAGCAATATTAGAAGAAAGAGGGGG
O_orichora1     GCTAAATCTACGGAAGATCCACCATGGGCAATATTAGAGGAAAGGGGGGG
O_orichora2     GCTAAATCTACGGAAGATCCACCATGGGCAATATTAGAGGAAAGGGGGGG
O_ptunarraBPJ   GCTAAATCTACAGATGATCCACCATGAGCAATATTAGAAGAAAGGGGGGG
O_ptunarraBPJ1  GCTAAATCTACAGATGATCCACCATGAGCAATATTAGAAGAAAGGGGGGG
O_ptunarraNW    GCTAAATCTACAGATGATCCACCATGAGCAATATTAGAAGAAAGGGGGGG
V_kershawi      GCTAAATCTACTGAGGAGCCTCCATGAGCAATATTAGATGAAAGTGGGGG

A_hobartia      GTAAACTGTTCATCCTGTTCCGGCTCCATTTTCAACAAGACTTCTAGAAA
A_hobartia2     GTAAACTGTTCATCCTGTTCCGGCTCCATTTTCAACAAGACTTCTAGAAA
G_klugii        GTAAACTGTTCATCCTGTTCCTGCTCCGTTTTCGACAATTCTACTAGAAA
H_cordace_l     ATAAACTGTTCATCCTGTTCCGGCTCCATTTTCAACAATACTTCTTGAAA
H_cordace_k     ATAAACTGTTCATCCTGTTCCGGCTCCATTTTCAACAATACTTCTTGAAA
H_cordace_c     ATAAACTGTTCATCCTGTTCCGGCTCCATTTTCAACAATACTTCTTGAAA
H_meropeWAY     GTAAACTGTTCATCCTGTACCAGCTCCGTTTTCAACAATACTACTTGAAA
H_meropeWW      GTAAACTGTTCATCCTGTACCAGCTCCGTTTTCAACAATACTACTTGAAA
H_penelope      ATAAACTGTTCATCCTGTTCCAGCTCCATTTTCGACAACACTACTTGAAA
J_villida       GTACACTGTTCATCCTGTTCCTGCTCCATTTTCTACAATTCTACTAGAAA
J_villida2      GTACACTGTTCATCCTGTTCCTGCTCCATTTTCTACAATTCTACTAGAAA
N_leprea_e      GTAAACTGTTCATCCTGTTCCAGCTCCATTTTCTACGATACTACTTGAAA
N_leprea_l      GTAAACTGTTCATCCTGTTCCAGCTCCATTTTCTACGATACTACTTGAAA
O_correae       ATATACTGTTCATCCTGTTCCAGCTCCATTTTCAACAATACTTCTTCTAA
O_kershawi      ATAAACTGTTCATCCTGTTCCAGCTCCATTTTCAACAATACTTCTTCTAA
O_lathoniella1  GTAAACTGTTCATCCTGTTCCAGCTCCATTTTCAACGATACTTCTTGAGA
O_lathoniella2  GTAAACTGTTCATCCTGTTCCAGCTCCATTTTCAACGATACTTCTTGAGA
O_latialis      ATAAACTGTTCATCCTGTTCCAGCTCCATTTTCAACAATGCTTCTTGAAA
O_orichora1     GTAAACTGTTCATCCTGTTCCAGCTCCGTTTTCAACAATACTTCTTCTAA
O_orichora2     GTAAACTGTTCATCCTGTTCCAGCTCCGTTTTCAACAATACTTCTTCTAA
O_ptunarraBPJ   ATAAACTGTTCATCCTGTTCCAGCTCCATTTTCAACAATGCTTCTTGAAA
O_ptunarraBPJ1  ATAAACTGTTCATCCTGTTCCAGCTCCATTTTCAACAATGCTTCTTGAAA
O_ptunarraNW    ATAAACTGTTCATCCTGTTCCAGCTCCATTTTCAACAATGCTTCTTGAAA
V_kershawi      ATAAACTGTTCATCCAGTTCCAGCTCCGTTTTCTACAATTCTACTAGAAA

A_hobartia      TTAATAATAYTAAAGAAGGGGGAAGAAGTCAAAATCTTATATTATTTATT
A_hobartia2     TTAATAATAYTAAAGAAGGGGGAAGAAGTCAAAATCTTATATTATTTATT
G_klugii        TTAATAATATTAATGATGGGGGTAAAAGTCAAAATCTTATATTATTTATA
H_cordace_l     TTAATAGTATTAAAGAGGGGGGTAGAAGTCAAAAACTTATATTATTTATT
H_cordace_k     TTAAAAGTATTAAAGAAGGGGGTAGAAGTCAAAATCTTATATTATTTATT
H_cordace_c     TTAAAAGTATTAAAGAAGGGGGTAGAAGTCAAAATCTTATATTATTTATT
H_meropeWAY     TTAATAGTACTAATGAAGGAGGTAAAAGTCAAAATCTTATATTATTTATT
H_meropeWW      TTAAAAGTACTAAGGAAGGAGGTAAAAGTCAAAATCTTATATTATTTATT
H_penelope      TTAAAAGTACTAAAGATGGGGGTAAAAGTCAAAATCTTATATTATTTATT
J_villida       TTAACAATACTAATGATGGGGGTAGTAGTCAAAATCTTATATTATTTATT
J_villida2      TTAACAATACTAATGATGGGGGTAGTAGTCAAAATCTTATATTATTTATT
N_leprea_e      TTAGTAATATTAATGAGGGGGGTAGAAGTCAAAATCTTATATTATTTATT
N_leprea_l      TTAGTAATATTAAAGAGGGGGGTAGAAGTCAAAATCTTATATTATTTATT
O_correae       TTAATAAAATTAAAGAGGGGGGTAAAAGTCAAAAACTTATATTATTTATT
O_kershawi      TTAGTAAAATTAATGAGGGGGGTAAGAGTCAGAAACTTATATTATTTATT
O_lathoniella1  TTAGTAAAACTAAAGAGGGGGGTAAAAGTCAAAAACTTATATTATTTATT
O_lathoniella2  TTAGTAAAACTAAAGAGGGGGGTAAAAGTCAAAAACTTATATTATTTATT
O_latialis      TTAATAAAATTAAAGAGGGGGGTAAGAGTCAAAAACTTATATTATTTATT
O_orichora1     TTAATAAAATTAAAGAGGGGGGTAAAAGTCAAAAACTTATATTATTTATT
O_orichora2     TTAATAAAATTAAAGAGGGGGGTAAAAGTCAAAAACTTATATTATTTATT
O_ptunarraBPJ   TTAATAAAATTAAAGAGGGGGGTAAAAGTCAAAAACTTATATTATTTATT
O_ptunarraBPJ1  TTAATAAAATTAAAGAGGGGGGTAAAAGTCAAAAACTTATATTATTTATT
O_ptunarraNW    TTAATAAAATTAAAGAGGGGGGTAAAAGTCAAAAACTTATATTATTTATT
V_kershawi      TTAATARTATTAAAGATGGAGGTAAAAGTCAAAATCTTATATTATTTATA
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CO1

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A_hobartia      CGGGGGAAGGCTATATCTGGGGCTCCTAATATAAGAGGTACTAATCAATT
A_hobartia2     CGGGGGAAGGCTATATCTGGGGCTCCTAATATAAGAGGTACTAATCAATT
G_klugii        CGTGGAAAAGCTATATCAGGAGCTCCTAATATTAAAGGAACTAATCAATT
H_cordace_1     CGGGGGAAAGCTATATCAGGAGCTCCTAATATAAGAGGGATTAATCAATT
H_cordace_k     CGGGGGAAAGCTATATCTGGGGCTCCTAATATAAGAGGGATTAATCAATT
H_cordace_c     CGGGGGAAAGCTATATCTGGGGCTCCTAATATAAGAGGGATTAATCAATT
H_meropeWAY     CGTGGGAAAGCTATATCTGGAGCTCCTAGTATAAGAGGGACTAATCAATT
H_meropeWW      CGTGGGAAAGCTATATCTGGAGCTCCTAGTATAAGAGGGACTAATCAATT
H_penelope      CGGGGGAAAGCTATATCTGGGGCTCCTAGTATGAGGGGTACTAGTCAATT
J_villida       CGCGGAAAAGCTATATCTGGGGCTCCTAATATAAGAGGTACTAATCAATT
J_villida2      CGCGGAAAAGCTATATCTGGGGCTCCTAATATAAGAGGTACTAATCAATT
N_leprea_e      CGAGGGAAAGCTATATCTGGGGCTCCTAATATGAGAGGGATTAATCAATT
N_leprea_1      CGAGGGAAAGCTATATCTGGGGCTCCTAATATGAGAGGGATTAATCAATT
O_correae       CGGGGGAAAGCTATGTCAGGGGCTCCTAATATAATAGGGACTAGTCAATT
O_kershawi      CGGGGGAAAGCTATGTCAGGGGCTCCTAATATAATAGGGACTAGTCAGTT
O_lathoniella1  CGAGGGAAAGCTATATCAGGAGCTCCTAATATAATAGGAACTAGTCAATT
O_lathoniella2  CGAGGGAAAGCTATATCAGGAGCTCCTAATATAATAGGAACTAGTCAATT
O_latialis      CGAGGGAAAGCCATATCAGGAGCTCCTAATATAATAGGGACTAATCAATT
O_orichora1     CGGGGGAAAGCTATATCAGGAGCTCCTAATATAATAGGAACTAATCAATT
O_orichora2     CGGGGGAAAGCTATATCAGGAGCTCCTAATATAATAGGAACTAATCAATT
O_ptunarraBPJ   CGGGGGAAAGCCATATCAGGAGCTCCTAATATAATAGGGACCAATCAATT
O_ptunarraBPJ1  CGGGGGAAAGCCATATCAGGAGCTCCTAATATAATAGGGACCAATCAATT
O_ptunarraNW    CGGGGGAAAGCCATATCAGGAGCTCCTAATATAATAGGGACCAATCAATT
V_kershawi      CGTGGGAAAGCTATATCTGGAGCACCTAATATAAGGGGGACTAATCAATT

A_hobartia      TCCAAATCCTCCGATTATAATTGGTATTACTATAAAAAAAATTATAATAA
A_hobartia2     TCCAAATCCTCCGATTATAATTGGTATTACTATAAAAAAAATTATAATAA
G_klugii        ACCAAATCCTCCAATTATAATTGGTATAACTATAAAAAAAATTATAATAA
H_cordace_1     TCCAAATCCTCCAATTATGATGGGTATAACCATAAAAAAAATTATGATAA
H_cordace_k     TCCAAATCCTCCAATTATGATGGGTATAACTATAAAAAAAATTATGATAA
H_cordace_c     TCCAAATCCTCCAATTATGATGGGTATAACTATAAAAAAAATTATGATAA
H_meropeWAY     ACCAAATCCTCCAATTATAATAGGTATAACTATAAAAAAAATTATAATGA
H_meropeWW      ACCAAATCCTCCAATTATAATAGGTATAACTATAAAAAAAATTATAATAA
H_penelope      TCCAAATCCTCCAATTATGATTGGTATAACTATAAAAAAAATTATAATAA
J_villida       ACCAAATCCTCCTATTATAATTGGTATTACTATAAAAAAAATTATAATAA
J_villida2      ACCAAATCCTCCTATTATAATTGGTATTACTATAAAAAAAATTATAATAA
N_leprea_e      ACCGAATCCTCCAATTATAATAGGTATAACTATAAAAAAAATTATAATAA
N_leprea_1      ACCGAATCCTCCAATTATAATAGGTATAACTATAAAAAAAATTATAATAA
O_correae       TCCAAATCCTCCAATTATAATGGGCATTACTATAAAAAAAATTATAATAA
O_kershawi      TCCGAATCCTCCAATTATGATAGGTATAACTATAAAAAAAATTATAATAA
O_lathoniella1  TCCAAATCCTCCAATTATAATAGGTATTACTATAAAAAAAATTATAATAA
O_lathoniella2  TCCAAATCCTCCAATTATAATAGGTATTACTATAAAAAAAATTATAATAA
O_latialis      TCCAAATCCTCCAATTATAATAGGTATAACCATAAAAAAAATTATAATGA
O_orichora1     TCCAAATCCTCCAATTATAATGGGTATTACCATAAAAAAAATTATAATAA
O_orichora2     TCCAAATCCTCCAATTATAATGGGTATTACCATAAAAAAAATTATAATAA
O_ptunarraBPJ   TCCAAATCCTCCAATTATAATAGGTATAACCATAAAAAAAATTATAATGA
O_ptunarraBPJ1  TCCAAATCCTCCAATTATAATAGGTATAACCATAAAAAAAATTATAATGA
O_ptunarraNW    TCCAAATCCTCCAATTATAATAGGTATAACCATAAAAAAAATTATAATGA
V_kershawi      TCCAAATCCTCCGATTATAATCGGCATAACTATAAAAAAAATTATAATAA

A_hobartia      AAGCATGAGCTGTAACGATAGTATTATAGATTTGATCATCACCAATTAAA
A_hobartia2     AAGCATGAGCTGTAACGATAGTATTATAGATTTGATCATCACCAATTAAA
G_klugii        AAGCATGAGCTGTAACAATTGTATTATAAATTTGATCATCTCCAATTAAA
H_cordace_1     AAGCATGTGCTGTTACAATAGTATTATAAATTTGATCATCTCCAATTAAA
H_cordace_k     AAGCATGTGCTGTTACAATTGTATTATAAATTTGATCATCTCCAATTAAA
H_cordace_c     AAGCATGTGCTGTTACAATTGTATTATAAATTTGATCATCTCCAATTAAA
H_meropeWAY     ATGCGTGGGCTGTAACAATAGTATTATAAATTTGGTCATCTCCAATTAAA
H_meropeWW      AAGCGTGGGCTGTAACAATTGTATTATAAATTTGGTCATCTCCAATTAAA
H_penelope      AAGCATGAGCTGTTACAATTGTGTTATAAATTTGATCGTCACCAATTAAA
J_villida       AAGCATGAGCTGTAACAATAGTATTATAAATTTGATCATCTCCAATTAAT
J_villida2      AAGCATGAGCTGTAACAATAGTATTATAAATTTGATCATCTCCAATTAAT
N_leprea_e      AAGCATGAGCTGTGACAATAGTATTATAAATTTGATCATCTCCAATTAAA
N_leprea_1      AAGCATGAGCTGTGACAATAGTATTATAAATTTGATCATCTCCAATTAAC
O_correae       ATGCATGTGCTGTTACAATAGTATTATAAATTTGATCATCACCAATTAAA
O_kershawi      ATGCATGAGCTGTTACAATAGTATTATAAATTTGATCGTCACCGATTAAA
O_lathoniella1  ATGCATGGGCTGTTACAATAGTATTATAAATTTGATCATCTCCAATTAAA
O_lathoniella2  ATGCATGGGCTGTTACAATAGTATTATAAATTTGATCATCTCCAATTAAA
O_latialis      ATGCATGAGCTGTTACAATAGTATTGTAAATTTGGTCATCTCCAATTAAA
O_orichora1     ATGCATGTGCTGTTACAATAGTATTATAAATTTGATCATCTCCAATTAAA
O_orichora2     ATGCATGTGCTGTTACAATAGTATTATAAATTTGATCATCTCCAATTAAA
O_ptunarraBPJ   ATGCATGAGCTGTTACAATAGTATTGTAAATTTGGTCATCTCCAATTAAA
O_ptunarraBPJ1  ATGCATGAGCTGTTACAATAGTATTGTAAATTTGGTCATCTCCAATTAAA
O_ptunarraNW    ATGCATGAGCTGTTACAATAGTATTGTAAATTTGGTCATCTCCAATTAAA
V_kershawi      AGGCATGAGCAGTAACAATTGTATTATAAATTTGATCATCTCCAATTAAA

A_hobartia      AATCCAGGGTTACCTAATTCTGTTCGAATGATAAGACTTAGAGATGTTCC
A_hobartia2     AATCCAGGGTTACCTAATTCTGTTCGAATGATAAGACTTAGAGATGTTCC
G_klugii        GATCCTGGGTTACCTAATTCAGTTCGAATAATAAAACTAAGTGATGTTCC
H_cordace_1     AATCCAGGGTTTCCTAATTCTGTTCGAATAATTAAGCTAAGAGAAGTTCC
H_cordace_k     AATCCAGGGTTACCTAATTCTGTTCGAATAATTAAACTAAGAGATGTTCG
H_cordace_c     AATCCAGGGTTACCTAATTCTGTTCGAATAATTAAACTAAGAGATGTTCC
H_meropeWAY     AATCCAGGGTTACCTAATTCTGTTCGAATAATTAAACTAAGAGAGGTTCC
H_meropeWW      AATCCAGGGTTACCTAATTCTGTTCGAATAATTAAACTAAGAGAAGTTCC
H_penelope      AATCCAGGGTTTCCTAATTCTGTTCGAATAATTAAACTGAGAGAAGTTCC
J_villida       GATCCTGGGTTYCCTAACTCAGTTCGAATAATAAMCCTMATGGRTGTTCC
J_villida2      GATCCTGGGTTYCCTAACTCAGTTCGAATAATAAMCCTMATGGRTGTTCC
N_leprea_e      AATCCGGGGGTTCCTAATTCTGTTCGGATAATAAGACTAAGGGCTGTTCC
N_leprea_1      AATCCGGGGGCTCCTAATTCTGTTCGGATAATAAGACTAAGGGCTGTTCC
O_correae       AATCCAGGGTTTCCTAATTCTGTTCGGATAATTAGGCTAGGAGAGGTTCC
O_kershawi      AATCCGGGGTTTCCTAATTCTGTTCGAATAATTAAACTAAGAGAAGTTCC
O_lathoniella1  GATCCGGGGTTTCCTAATTCTGTTCGAATAATTAAGCTAAGAGAGGTTCC
O_lathoniella2  GATCCGGGGTTTCCTAATTCTGTTCGAATAATTAAGCTAAGAGAGGTTCC
O_latialis      AATCCTGGGTTTCCTAATTCTGTTCGAATAATTAAACTAAGGGAGGTTCC
O_orichora1     AATCCAGGGTTTCCTAATTCTGTTCGAATAATTAAGCTAAGAGAAGTTCA
O_orichora2     AATCCAGGGTTTCCTAATTCTGTTCGAATAATTAAGCTAAGAGAAGTTCA
O_ptunarraBPJ   AATCCTGGGTTTCCTAATTCTGTTCGGATAATTAAACTAAGGGAGGTTCC
O_ptunarraBPJ1  AATCCTGGGTTTCCTAATTCTGTTCGGATAATTAAACTAAGGGAGGTTCC
O_ptunarraNW    AATCCTGGGTTTCCTAATTCTGTTCGGATAATTAAACTAAGGGAGGTTCC
V_kershawi      AATCCAGGGTTACCTAATTCTATTCGAATAATAAGACTTAAAGATGTTCC
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CO1

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A_hobartia      WACTATACCTGCTCAAATT------------------------------
A_hobartia2     WACTATACCTGCTCAAATT------------------------------
G_klugii        TACTATTCCTGCTCAAATT------------------------------
H_cordace_l     TACTATTCCTGCTCAAATT------------------------------
H_cordace_k     TACTATACCTGCTCAGATT------------------------------
H_cordace_c     TACTATACCTGCTCAAATT------------------------------
H_meropeWAY     AACTATACCTGCTCAAATT------------------------------
H_meropeWW      AACTATTCCTGCTCAAATT------------------------------
H_penelope      TACTATACCTGCTCGAATT------------------------------
J_villida       TACTATACCTGCTCAMATT------------------------------
J_villida2      TACTATACCTGCTCAMATT------------------------------
N_leprea_e      TACTATACCTGCTCAGATT------------------------------
N_leprea_l      TACTATACCTGCTCAGATT------------------------------
O_correae       TACTATCCCTGCTCAAATT------------------------------
O_kershawi      TACTATTCCTGCCCAAATT------------------------------
O_lathoniella1  TACTATTCCTGCTCATATT------------------------------
O_lathoniella2  TACTATTCCTGCTCATATT------------------------------
O_latialis      TACTATGCCTGCTCAAATT------------------------------
O_orichoral     TACTATTCCTGCTCAAATT------------------------------
O_orichora2     TACTATTCCTGCTCAAATT------------------------------
O_ptunarraBPJ   TACTATGCCTGCTCAAATT------------------------------
O_ptunarraBPJ1  TACTATGCCTGCTCAAATT------------------------------
O_ptunarraNW    TACTATGCCTGCTCAAATT------------------------------
V_kershawi      TACTATTCCTGCTCAAATT------------------------------
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A_hobartia      ACGTTGAAACCCACATTGTCTCCGGGCACAGCCTCAGGGAGAGCTTCGTG
A_hobartia2     ACGTTGAAACCCACNTTGTCTCCGGGCACAGCCTCAGGGAGAGCTTCGTG
G_klugii        ACGTTGAATCCTACNTTGTCTCCGGGCACAGCCTCGGGGAGGGCTTCGTG
H_cordace_1     ACGTTGAAACCCACACTGTCTCCAGGCACTGCCTCGGGCAGAGCTTCGTG
H_cordace_k     ACGTTGAAACCCACTTTCTCTCCAGGCACTGCCTCGGGCAGAGCTTCGGG
H_cordace_c     ACGTTGAAACCCACACTGTCTCCAGGCACTGCCTCGGGCAGAGCTTCGTG
H_meropeWAY     ACGTTGAAACCCACACTGTCTCCAGGCACAGCCTCGGGAAGAGCTTCGTG
H_meropeWW      ACGTTGAAACCCACACTGTCTCCAGGCACAGCCTCGGGAAGAGCTTCGTG
H_penelope      ACGTTGAAACCCACATTGTCTCCAGGCACAGCCTCGGAAAGAGCTTCGTG
J_villida       ACGTTGAAACCTACNTTGTCTCCGGGCACAGCCTCCTGGAGAGCTTCGTG
J_villida2      ACGTTGAAACCTACGTTGTCTCCGGGCACAGCCTCCTGGAGAGCTTCGTG
N_leprea_e      ACGTTGAAACCAACATTGTCCCCAGGCATAGCCTCAGAGAGGGCTTCGTG
N_leprea_1      ACGTTGAAACCAACATTGTCCCCAGGCATAGCCTCAGAGAGGGCTTCATG
O_correae       ACGTTGAAACCCACTTTGTCACCAGGCAAAGCCTCGGGGAGAGCTTCGTG
O_kershawi      ACGTTGAAACCCACTTTGTCTCCGGGCACAGCCTCAGGGAGAGCTTCATG
O_lathoniella1  ----------------------------------------------------
O_lathoniella2  ----------------------------------------------------
O_latialis      ACGTTGAAGCCCACGTTGTCTCCAGGCATAGCCTCTGAGAGAGCTTCGTG
O_orichora1     ACGTTGAAACCCACATTGTCTCCAGGCAAAGCCTCAGGGAGAGCTTCATG
O_orichora2     ACGTTGAAAACCACATTGACTCCAGGCAAAGCCTCAGGGAGAGCTTCGTG
O_ptunarraBPJ   ACGTTGAAGCCCACGTTGTCTCCAGGCATAGCCTCTGAGAGAGCTTCGTG
O_ptunarraBPJ1  ACGTTGAAGCCCACGTTGTCTCCAGGCATAGCCTCTGAGAGAGCTTCGTG
O_ptunarraNW    ACGTTGAAGCCCACGTTGTCTCCAGGCATAGCCTCTGAGAGAGCTTCGTG
V_kershawi      ACGTTGAAACCCACATTSTCTCCGGGCACAGCCTCGTGGAGAGCTTCGTG

A_hobartia      ACGTTGAAACCCACATTGTCTCCGGGCACAGCCTCAGGGAGAGCTTCGTG
A_hobartia2     ACGTTGAAACCCACNTTGTCTCCGGGCACAGCCTCAGGGAGAGCTTCGTG
G_klugii        ACGTTGAATCCTACNTTGTCTCCGGGCACAGCCTCGGGGAGGGCTTCGTG
H_cordace_1     ACGTTGAAACCCACACTGTCTCCAGGCACTGCCTCGGGCAGAGCTTCGTG
H_cordace_k     ACGTTGAAACCCACTTTCTCTCCAGGCACTGCCTCGGGCAGAGCTTCGGG
H_cordace_c     ACGTTGAAACCCACACTGTCTCCAGGCACTGCCTCGGGCAGAGCTTCGTG
H_meropeWAY     ACGTTGAAACCCACACTGTCTCCAGGCACAGCCTCGGGAAGAGCTTCGTG
H_meropeWW      ACGTTGAAACCCACACTGTCTCCAGGCACAGCCTCGGGAAGAGCTTCGTG
H_penelope      ACGTTGAAACCCACATTGTCTCCAGGCACAGCCTCGGAAAGAGCTTCGTG
J_villida       ACGTTGAAACCTACNTTGTCTCCGGGCACAGCCTCCTGGAGAGCTTCGTG
J_villida2      ACGTTGAAACCTACGTTGTCTCCGGGCACAGCCTCCTGGAGAGCTTCGTG
N_leprea_e      ACGTTGAAACCAACATTGTCCCCAGGCATAGCCTCAGAGAGGGCTTCGTG
N_leprea_1      ACGTTGAAACCAACATTGTCCCCAGGCATAGCCTCAGAGAGGGCTTCATG
O_correae       ACGTTGAAACCCACTTTGTCACCAGGCAAAGCCTCGGGGAGAGCTTCGTG
O_kershawi      ACGTTGAAACCCACTTTGTCTCCGGGCACAGCCTCAGGGAGAGCTTCATG
O_lathoniella1  ----------------------------------------------------
O_lathoniella2  ----------------------------------------------------
O_latialis      ACGTTGAAGCCCACGTTGTCTCCAGGCATAGCCTCTGAGAGAGCTTCGTG
O_orichora1     ACGTTGAAACCCACATTGACTCCAGGCAAAGCCTCAGGGAGAGCTTCGTG
O_orichora2     ACGTTGAAACCCACATTGTCTCCAGGCAAAGCCTCAGGGAGAGCTTCATG
O_ptunarraBPJ   ACGTTGAAGCCCACGTTGTCTCCAGGCATAGCCTCTGAGAGAGCTTCGTG
O_ptunarraBPJ1  ACGTTGAAGCCCACGTTGTCTCCAGGCATAGCCTCTGAGAGAGCTTCGTG
O_ptunarraNW    ACGTTGAAGCCCACGTTGTCTCCAGGCATAGCCTCTGAGAGAGCTTCGTG
V_kershawi      ACGTTGAAACCCACATTSTCTCCGGGCACAGCCTCGTGGAGAGCTTCGTG
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A_hobartia      GTGCATCTCAACAGACTTTACTTCAGTAGTGATGTTGGCGGGAGCGAAAA
A_hobartia2     GTGCATCTCAACAGACTTTACTTCAGTAGTGATGTTGGCGGGAGCGAAAA
G_klugii        GTGCATCTCAACTGACTTAACTTCAGTGGTGATGTTGGCGGGAGCAAAAA
H_cordace_1     GTGCATCTCAACAGACTTAACTTCAGTGGTGATGTTGGCAGGAGCAAAAA
H_cordace_k     GTGCATCTCAACAGACTTAACTTCAGTGGTGATGTTGGCAGGAGCAAAAA
H_cordace_c     GTGCATCTCAACAGACTTAACTTCAGTGGTGATGTTGGCAGGAGCAAAAA
H_meropeWAY     GTGCATCTCAACAGACTTAACTTCAGTGGTGATGTTGGCAGGAGCAAAAA
H_meropeWW      GTGCATCTCAACAGACTTAACTTCAGTGGTGATGTTGGCAGGAGCAAAAA
H_penelope      GTGCATCTCAACAGACTTAACTTCAGTGGTGATGTTGGCAGGAGCAAAAA
J_villida       GTGCATCTCCACAGATTTTACTTCAGTGGTGATGTTGGCGGGGGCGAAAA
J_villida2      GTGCATCTCCACAGATTTTACTTCAGTGGTGATGTTGGCGGGGGCGAAAA
N_leprea_e      GTGCATCTCAACGGACTTAACTTCAGTGGTGATGTTGGCAGGAGCGAAAA
N_leprea_1      GTGCATCTCAACGGACTTAACTTCAGTGGTGATGTTGGCAGGAGCGAAAA
O_correae       GTGCATCTCAACAGACTTAACTTCTGTGGTGATGTTGGCAGGAGCAAAAA
O_kershawi      GTGCATCTCAACTGACTTAACTTCCGTGGTGATGTTAGCGGGAGCAAAAA
O_lathoniella1  ----------------------------------------------------
O_lathoniella2  ----------------------------------------------------
O_latialis      GTGCATCTCAACGGACTTAACTTCCGTGGTGATGTTGGCGGGAGCAAAAA
O_orichora1     GTGCATCTCAACAGACTTAACTTCCGTGGTGATGTTGGCGGGTGCAAAAA
O_orichora2     GTGCATCTCAACAGACTTAACTTCCGTGGTGATGTTGGCGGGTGCAAAAA
O_ptunarraBPJ   GTGCATCTCAACGGACTTAACTTCCGTGGTGATGTTGGCGGGAGCAAAAA
O_ptunarraBPJ1  GTGCATCTCAACGGACTTAACTTCCGTGGTGATGTTGGCGGGAGCAAAAA
O_ptunarraNW    GTGCATCTCAACGGACTTAACTTCCGTGGTGATGTTGGCGGGAGCAAAAA
V_kershawi      GTGCATCTCCACAGACTTTACTTCAGTGGTGATGTTGGCGGGAGCGAAAA

A_hobartia      CAACAATGGTACCGGGCTTAAGTACACCAGTTTCTACTCTGCCTACGGGC
A_hobartia2     CAACAATGGTACCGGGCTTAAGTACACCAGTTTCTACTCTGCCTACGGGC
G_klugii        CAACAATGGTACCGGGTTTGAGGACACCAGTTTCTACTCTGCCTACAGGC
H_cordace_1     CAACAATGGTACCAGGTTTGAGAACACCAGTTTCTACTCTGCCTACGGGC
H_cordace_k     CAACAATGGTACCAGGTTTGAGAACACCAGTTTCTACTCTGCCTACGGGC
H_cordace_c     CAACAATGGTACCAGGTTTGAGAACACCAGTTTCTACTCTGCCTACGGGC
H_meropeWAY     CAACAATGGTACCAGGTTTGAGAACACCAGTTTCTACTCTGCCTACGGGC
H_meropeWW      CAACAATGGTACCAGGTTTGAGAACACCAGTTTCTACTCTGCCTACGGGC
H_penelope      CAACAATGGTACCCGGTTTGAGAACACCAGTTTCTACTCTGCCTACGGGC
J_villida       CGACAATGGTACCGGGTTTGAGGACACCAGTTTCCACTCTGCCTACGGGC
J_villida2      CGACAATGGTACCGGGTTTGAGGACACCAGTTTCCACTCTGCCTACGGGC
N_leprea_e      CAACAATGGTACCAGGTTTAAGGATACCGGTTTCAACTCTGCCTACTGGC
N_leprea_1      CAACAATGGTACCAGGTTTAAGGATACCGGTTTCAACTCTGCCTACTGGC
O_correae       CAACAATGGTACCAGGTTTCAGAACACCTGTTTCTACTCTGCCTACTGGC
O_kershawi      CAACAATGGTACCAGGTTTCAGAACACCTGTTTCTACTCTGCCTACTGGC
O_lathoniella1  ----------CACCAGTTTCGACTCTGCCTACTGGC
O_lathoniella2  ----------CACCAGTTTCGACTCTGCCTACTGGC
O_latialis      CGACAATGGTACCAGGTTTCAGAACACCTGTTTCTACTCTGCCTACTGGC
O_orichora1     CAACAATAGTACCAGGTTTCAGAACACCTGTTTCTACTCTGCCTACTGGC
O_orichora2     CAACAATAGTACCAGGTTTCAGAACACCTGTTTCTACTCTGCCTACTGGC
O_ptunarraBPJ   CGACAATGGTACCAGGTTTCAGAACACCTGTTTCTACTCTGCCTACTGGC
O_ptunarraBPJ1  CGACAATGGTACCAGGTTTCAGAACACCTGTTTCTACTCTGCCTACTGGC
O_ptunarraNW    CGACAATGGTACCAGGTTTCAGAACACCTGTTTCTACTCTGCCTACTGGC
V_kershawi      CAACAATGGTACCGGGCTTGAGGACACCAGTTTCAACTCTGCCTACTGGC
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EF-1α

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A_hobartia      ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
A_hobartia2     ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
G_klugii        ACTGTTCCAATACCACCAATTTTGTAGACGTCCTGAAGGGGAAGCCGCAG
H_cordace_1     ACTGTACCAATTCCACCGATTTTGTAGACGTCCTGAAGGGGAAGTCGCAG
H_cordace_k     ACTGTACCAATTCCGCCGATTTTGTAGACGTCCTGAAGGGGAAGTCGCAG
H_cordace_c     ACTGTACCAATTCCACCGATTTTGTAGACGTCCTGAAGGGGAAGTCGCAG
H_meropeWAY     ACTGTACCAATTCCACCGATTTTGTAGACGTCCTGAAGGGGAAGTCGCAG
H_meropeWW      ACTGTACCAATTCCACCGATTTTGTAGACGTCCTGAAGGGGAAGTCGCAG
H_penelope      ACTGTACCAATTCCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
J_villida       ACTGTACCAATACCGCCGATTTTGTATACGTCTTGCAGGGGAAGACGCAG
J_villida2      ACTGTACCAATACCGCCGATTTTGTATACGTCCTGCAGGGGAAGACGCAG
N_leprea_e      ACTGTTCCAATACCACCGATTTTGTAGACATCCTGAAGGGGAAGTCGAAG
N_leprea_1      ACTGTTCCAATACCACCGATTTTGTAGACATCCTGAAGGGGAAGTCGAAG
O_correae       ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
O_kershawi      ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
O_lathoniella1  ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
O_lathoniella2  ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
O_latialis      ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
O_orichora1     ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
O_orichora2     ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
O_ptunarraBPJ   ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAG
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O_ptunarraNW    ACTGTACCAATACCACCAATTTTGTAGACATCCTGAAGGGGAAGTCGCAA
V_kershawi      ACTGTACCAATACCACCGATTTTGTAAACGTCCTGCAGGGGAAGACGCAG

A_hobartia      GGCCTTGTCTGTGGGACGCGCTGGGGGCAGGATGGCGTCCAAAGCNTCAA
A_hobartia2     GGCCTTGTCTGTGGGACGCGCTGGGGGCAGGATGGCATCCAAAGCTTCAA
G_klugii        GGCCTTGTCTGTGGGACGCGCAGGGGGCAGGATGGCGTCCAAGGCTTCAA
H_cordace_1     TGGCTTGTCTGTGGGACGCGCTGGGGGCAGGATAGCGTCCAAGGCTTCAA
H_cordace_k     TGGCTTGTCTGTGGGACGCGCTGGGGGCAGGATAGCGTCCAAGGCTTCAA
H_cordace_c     TGGCTTGTCTGTGGGACGCGCTGGGGGCAGGATAGCGTCCAAGGCTTCAA
H_meropeWAY     GGGCTTGTCTGTGGGACGCGCTGGGGGCAGGATAGCATCCAAGGCTTCAA
H_meropeWW      GGGCTTGTCTGTGGGACGCGCTGGGGGCAGGATAGCGTCCAAGGCTTCAA
H_penelope      GGGCTTGTCTGTGGGACGTGCAGGAGGCAGGATGGCGTCCAAGGCCTCAA
J_villida       GGCCTTGTCTGTGGGACGAGCTGGGGGAAGGATGGCGTCGAGGGCCTCAA
J_villida2      GGCCTTGTCTGTGGGACGAGCTGGGGGAAGGATGGCGTCGAGGGCCTCAA
N_leprea_e      GGCCTTGTCTGTGGGACGCGCGGGGGGCAGGATGGCGTCCAAAGCTTCGA
N_leprea_1      GGCCTTGTCTGTGGGACGCGCGGGGGGCAGGATGGCGTCCAAAGCTTCGA
O_correae       AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCAA
O_kershawi      GGCCTTGTCGGTAGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCGA
O_lathoniella1  AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCTA
O_lathoniella2  AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCTA
O_latialis      AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCTA
O_orichora1     AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCAA
O_orichora2     AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCAA
O_ptunarraBPJ   AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCTA
O_ptunarraBPJ1  AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCGTCCAGGGCTTCTA
O_ptunarraNW    AGCCTTGTCTGTGGGACGCGCCGGGGGCAGGATGGCATCCAGGGCTTCTA
V_kershawi      GGCTTTGTCTGTGGGACGCGCTGGAGGAAGGATGGCATCCAAAGCCTCAA

A_hobartia      TGAGGCACTTGCCGTCAGCCTTGCCCTCCTTGCGCTCAACTTGCCATCCC
A_hobartia2     TGAGGCACTTGCCGTCAGCCTTGCCCTCCTTGCGCTCAACTTGCCATCCC
G_klugii        TGAGGCACTTGCCTTCAGCCTTGCCCTCCTTGCGCTCAACTTGCCATCCC
H_cordace_1     TGAGGCACTTGCCTTCATTCTTACCTTCCTTGCGCTCAACTTGCCATCCC
H_cordace_k     TGAGGCACTTGCCTTCATTCTTACCTTCCTTGCGCTCAACTTGCCATCCC
H_cordace_c     TGAGGCACTTGCCTTCATTCTTACCTTCCTTGCGCTCAACTTGCCATCCC
H_meropeWAY     TGAGGCACTTGCCTTCATTCTTACCTTCCTTGCGCTCAACTTGCCATCCC
H_meropeWW      TGAGGCACTTGCCTTCATTCTTACCTTCCTTGCGCTCAACTTGCCATCCC
H_penelope      TGAGGCACTTGCCTTCATTCTTACCTTCCTTACGCTCAACTTGCCATCCC
J_villida       TGAGGCATTTACCTTCAGCCTTGCCTTCTTTGCGCTCCACTTGCCATCCC
J_villida2      TGAGGCATTTACCTTCAGCCTTGCCTTCTTTGCGCTCCACTTGCCATCCC
N_leprea_e      TGAGGCACTTGCCATCAGCCTTACCCTCCTTGCGCTCCACTGCCCATCCC
N_leprea_1      TGAGGCACTTGCCATCAGCCTTACCCTCCTTGCGCTCCACTGCCCATCCC
O_correae       TGAGGCACATGCCTTCAGCTTTGCCCTCCTTGCGCTCAACTTTCCATCCC
O_kershawi      TGAGGCACTTGCCTTCAGCTTTGCCCTCCTTGCGCTCAACTTGCCATCCC
O_lathoniella1  TGAGGCACTTGCCTTCAGCTTTGCCCTCCTTACGCTCAACTGCCCACCCT
O_lathoniella2  TGAGGCACTTGCCTTCAGCTTTGCCCTCCTTACGCTCAACTGCCCACCCT
O_latialis      TGAGGCACTTGCCTTCAGCTTTGCCCTCCTTGCGCTCAACTGCCCACCCC
O_orichora1     TGAGGCACATGCCTTCAGCTTTGCCCTCCTTGCGCTCAACTTTCCATCCC
O_orichora2     TGAGGCACATGCCTTCAGCTTTGCCCTCCTTGCGCTCAACTTTCCATCCC
O_ptunarraBPJ   TGAGGCACTTGCCTTCAGCTTTGCCCTCCTTGCGCTCAACTGCCCACCCC
O_ptunarraBPJ1  TGAGGCACTTGCCTTCAGCTTTGCCCTCCTTGCGCTCAACTGCCCACCCC
O_ptunarraNW    TGAGGCACTTGCCTTCAGCTTTGCCCTCCTTGCGCTCAACTGCCCACCCC
V_kershawi      TAAGGCATTTACCTTCAGCTTTACCTTCTTTACGCTCCACTTGCCATCCC

A_hobartia      TTGAACCAGGGCATTTTGGTGGACGGCTCCAACATGTTGTCTCCGTGCCA
A_hobartia2     TTGAACCAGGGCATTTTGGTGGACGGCTCCAACATGTTGTCTCCGTGCCA
G_klugii        TTGAACCAGGGCATTTTGGTGGATGGCTCCAACATGTTGTCTCCGTGCCA
H_cordace_1     TTGAACCAAGGCATCTTGGTGGATGGCTCCAGCATGTTGTCTCCGTGCCA
H_cordace_k     TTGAACCAAGGCATCTTGGTGGATGGCTCCAGCATGTTGTCTCCGTGCCA
H_cordace_c     TTGAACCAAGGCATCTTGGTGGATGGCTCCAGCATGTTGTCTCCGTGCCA
H_meropeWAY     TTGAACCAGGGCATCTTGGTGGATGGCTCCAGCATGTTGTCTCCGTGCCA
H_meropeWW      TTGAACCAGGGCATCTTGGTGGATGGCTCCAGCATGTTGTCTCCGTGCCA
H_penelope      TTGAACCAGGGCATCTTGGTGGATGGCTCCAGCATGTTGTCTCCGTGCCA
J_villida       TTGAACCAGGGCATTTTGGTAGATGCCTCCAGCATGTTGTCTCCGTGCCA
J_villida2      TTGAACCAGGGCATTTTGGTAGATGCCTCCAGCATGTTGTCTCCGTGCCA
N_leprea_e      TTGAACCATGGCATTTTGGTAGACGGCTCCAGCATGTTGTCTCCGTGCCA
N_leprea_1      TTGAACCATGGCATTTTGGTAGACGGCTCCAGCATGTTGTCTCCGTGCCA
O_correae       TTGAACCAGGGCATTTTGGTGGATGGCTCAAGCATGTTGTCTCCGTGCCA
O_kershawi      TTGAACCAGGGCATTTTGGTGGAAGGCTCAAGCATGTTGTCTCCGTGCCA
O_lathoniella1  TTGAACCAGGGCATTTTGGTGGAAGGCTCAAGCATGTTGTCTCCGTGCCA
O_lathoniella2  TTGAACCAGGGCATTTTGGTGGAAGGCTCAAGCATGTTGTCTCCGTGCCA
O_latialis      TTGAACCAGGGCATTTTGGTGGAAGGCTCAAGCATGTTGTCTCCGTGCCA
O_orichora1     TTGAACCAGGGCATTTTGGTGGATGGCTCAAGCATGTTGTCTCCGTGCCA
O_orichora2     TTGAACCAGGGCATTTTGGTGGATGGCTCAAGCATGTTGTCTCCGTGCCA
O_ptunarraBPJ   TTGAACCAGGGCATTTTGGTGGAAGGCTCAAGCATGTTGTCTCCGTGCCA
O_ptunarraBPJ1  TTGAACCAGGGCATTTTGGTGGAAGGCTCAAGCATGTTGTCTCCGTGCCA
O_ptunarraNW    TTGAACCAGGGCATTTTGGTGGAAGGCTCAAGCATGTTGTCTCCGTGCCA
V_kershawi      TTGAACCAGGGCATCTTGGTGGATGCCTCCAGCATGTTGTCTCCGTGCCA
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A_hobartia      GCCAGAAATGGGTACGAAAGCAACGGCCAATGGGTTATAACCAATTTTCT
A_hobartia2     GCCAGAAATGGGTACGAAAGCAACGGCCAATGGGTTATAACCAATTTTCT
G_klugii        GCCAGAAATGGGTACGAAAGCGACTGCAGCNGGGTTGTAACCGATTTTCT
H_cordace_1     ACCAGAAATGGGTACAAAGGGCACGGCGGCTGGGTTGTAACCGATTTTTT
H_cordace_k     ACCAGAAATGGGTACAAAAGGCACGGCGGCTGGGTTGTAACCGATTTTTT
H_cordace_c     ACCAGAAATGGGTACAAAAGGCACGGCGGCTGGGTTGTAACCGATTTTTT
H_meropeWAY     GCCAGAAATGGGTACGAAAGCAACGGCGGCCGGGTTGTAACCGATTTTTT
H_meropeWW      GCCAGAAATGGGAACGAAAGCAACGGCGGCCGGGTTGTAACCGATTTTTT
H_penelope      GCCAGAAATGGGTACGAAAGCGACGGCGGCTGGGTTATAACCGATCTTTT
J_villida       GCCAGAAATGGGTACGAAAGCGACGGCAGCTGGGTTGTAACCAATCTTCT
J_villida2      GCCAGAAATGGGTACGAAAGCGACGGCAGCTGGGTTGTAACCGATCTTCT
N_leprea_e      GCCAGAAATGGGTACGAAAGGGACGGCAAGTGGGTTGTAACCGATTTTCT
N_leprea_l      GCCAGAAATGGGTACGAAAGGGACGGCAAGTGGGTTGTAACCGATTTTCT
O_correae       GCCAGAAATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_kershawi      GCCAGAAATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_lathoniella1  GCCAGAGATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_lathoniella2  GCCAGAGATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_latialis      GCCAGAGATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_orichora1     GCCAGAAATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_orichora2     GCCAGAAATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_ptunarraBPJ   GCCAGAGATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_ptunarraBPJ1  GCCAGAGATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
O_ptunarraNW    GCCAGAGATGGGTACGAAAGGAACTGCAGCAGGGTTGTAACCAATTTTCT
V_kershawi      GCCAGAAATGGGTACGAAAGGCACGGCAGCTGGGTTGTAACCGATCTTTT

A_hobartia      TGATGTAGGAGGAGACTTCCTTCTTGATTTCCTCGAAACGAGGTTCGCTG
A_hobartia2     TGATGTAGGAGGAGACTTCCTTCTTGATTTCCTCGAAACGAGGTTCGCTG
G_klugii        TGATGTAGGATGAAACCTCCTTCTTGATTTCCTCGAACCGAGGTTCACTG
H_cordace_1     TGATATAGGAGGAGACTTCCTTCTTGATTTCCTCGAAACGCGGTTCACTG
H_cordace_k     TGATATAGGAGGAGACTTCCTTCTTGATTTCCTCGAAACGCGGTTCACTG
H_cordace_c     TGATATAGGAGGAGACTTCCTTCTTGATTTCCTCGAAACGCGGTTCACTG
H_meropeWAY     TGATATAGGAGGAAACTTCCTTCTTGATTTCCTCGAAACGCGGTTCACTG
H_meropeWW      TGATATAGGAGGAAACTTCCTTCTTGATTTCCTCGAAACGCGGTTCACTG
H_penelope      TGATATAGGAGGAGACTTCCTTCTTGATTTCCTCGAAACGCGGTTCACTG
J_villida       TGATGTAAGAGGACACTTCCTTCTTGATTTCCTCGAAACGGGACTCGCTG
J_villida2      TGATGTAAGAGGACACTTCCTTCTTGATTTCCTCGAAACGGGACTCGCTG
N_leprea_e      TAATGTAGGAGGATACTTCCTTCTTGATTTCCTCGAAACGAGGTTCACTG
N_leprea_l      TAATGTAGGAGGATACTTCCTTTCTTGATTTCCTCAAAACGAGGTTCGCTG
O_correae       TGATGTAGGAGGATACTTCTTTCTTGATTTCCTCAAAACGAGGTTCGCTG
O_kershawi      TAATGTAGGAGGATACTTCTTTCTTGATTTCCTCGAAACGAGGTTCACTG
O_lathoniella1  TAATGTAGGATGATACTTCTTTCTTGATTTCCTCGAAACGAGGTTCGCTG
O_lathoniella2  TAATGTAGGATGATACTTCTTTCTTGATTTCCTCGAAACGAGGTTCGCTG
O_latialis      TAATGTATGATGATACTTCTTTCTTGATTTCCTCGAAACGAGGTTCGCTG
O_orichora1     TGATGTAGGAGGATACTTCTTTCTTGATTTCCTCAAAACGAGGTTCGCTG
O_orichora2     TGATGTAGGAGGATACTTCTTTCTTGATTTCCTCAAAACGAGGTTCGCTG
O_ptunarraBPJ   TAATGTATGATGATACTTCTTTCTTGATTTCCTCGAAACGAGGTTCGCTG
O_ptunarraBPJ1  TAATGTATGATGATACTTCTTTCTTGATTTCCTCGAAACGAGGTTCGCTG
O_ptunarraNW    TAATGTATGATGATACTTCTTTCTTGATTTCCTCGAAACGAGGTTCGCTG
V_kershawi      TGATGTAAGAAGATACTTCCTTCTTGATTTCTTCGAAACGGCCTTCATTG
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A_hobartia      TATGGGGGTTCAGTGGAGTCCATCTTGTTGACTCCTACGATCAGCTGCTT
A_hobartia2     TATGGGGGTTCAGTGGAGTCCATCTTGTTGACTCCTACGATCAGCTGCTT
G_klugii        TACGGGGGCTCAGTGGAGTCCATCTTGTTGACTCCTACAATCAGCTGCTT
H_cordace_1     AAYTGGGGGTCAGTGGAGTCCATCTTATTGACTCCTACGATCAGCTGCTT
H_cordace_k     AAYTGGGGGTCAGTGGAGTCCATCTTATTGACTCATACGATCAGCTGCTT
H_cordace_c     AAYTGGGGGTCAGTGGAGTCCATCTTATTGACTCCTACGATCAGCTGCTT
H_meropeWAY     AATGGGGGTTCAGTGGAGTCCATCTTATTGACTCCTACGATCAGCTGCTT
H_meropeWW      AAYTGGGGGTCAGTGGAGTCCATCTTATTGACTCCTACGATCAGCTGCTT
H_penelope      AACGGGGGCTCAGTGGAGTCCATCTTATTGACTCCTACGATCAGCTGCTT
J_villida       TAYTGGGGGTCGGTGGAGTCCATTTTGTTGACGCCTACGATCAGCTGCTT
J_villida2      TAYTGGGGGTCGGTGGAGTCCATTTTGTTGACGCCTACGATCAGCTGCTT
N_leprea_e      AATGGAGGCTCAGTAGAGTCCATCTTGTTAACTCCTACGATCAGTTGCTT
N_leprea_l      AATGGAGGCTCAGTAGAGTCCATCTTGTTAACTCCTACGATCAGTTGCTT
O_correae       TACTGGGGTTCAGTGGAGTCCATCTTGTTTACTCCTACGATGAGCTGCTT
O_kershawi      AACTGGGGTTCAGTTGAGTCCATCTTGTTGACTCCTACGATGAGCTGCTT
O_lathoniella1  TACTGAGGTTCAGTGGAGTCCATCTTGTTGACTCCTACAATGAGCTGCTT
O_lathoniella2  TACTGAGGTTCAGTGGAGTCCATCTTGTTGACTCCTACAATGAGCTGCTT
O_latialis      TACTGAGGTTCAGTGGAGTCCATCTTGTTGACTCCTACAATGAGCTGCTT
O_orichora1     TACTGGGGTTCAGTGGAGTCCATCTTGTTTACTCCTACGATGAGCTGCTT
O_orichora2     TACTGGGGTTCAGTGGAGTCCATCTTGTTTACTCCTACGATGAGCTGCTT
O_ptunarraBPJ   TACTGAGGTTCAGTGGAGTCCATCTTGTTGACTCCTACAATGAGCTGCTT
O_ptunarraBPJ1  TACTGAGGTTCAGTGGAGTCCATCTTGTTGACTCCTACAATGAGCTGCTT
O_ptunarraNW    TACTGAGGTTCAGTGGAGTCCATCTTGTTGACTCCTACAATGAGCTGCTT
V_kershawi      TAYTGGGGGTCAGTGGAGTCCATTTTGTTAACACCCACAATCAGCTGCTT

A_hobartia      TACGCCGAGGGTGAAGGCGAGAAGGGCATGCTCACGGGTCTGGCCGTTCT
A_hobartia2     GACGCCGAGGGTGAAGGCGAGAAGGGCATGCTCACGGGTCTGGCCGTTCT
G_klugii        GACGCCGAGCGTGAAAGCGAGCAGGGCGTGCTCACGGGTCTGGCCGTTCT
H_cordace_1     GACACCGAGCGTGAAGGCGAGCAGTGCGTGCTCGCGGGTTTGACCGTTCT
H_cordace_k     GACACCGAGCGTGAAGGCGAGCAGTGCGTGCTCGCGGGTTTGACCGTTCT
H_cordace_c     GACACCGAGCGTGAAGGCGAGCAGTGCGTGCTCGCGGGTTTGACCGTTCT
H_meropeWAY     GACACCGAGCGTGAAGGCGAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
H_meropeWW      GACACCGAGCGTGAAGGCGAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
H_penelope      GACACCCAGCGTGAAGGCCAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
J_villida       GACACCGAGTGTGAAAGCGAGCAGAGCGTGCTCACGAGTCTGACCGTTCT
J_villida2      GACACCGAGTGTGAAAGCGAGCAGAGCGTGCTCACGAGTCTGACCGTTCT
N_leprea_e      GACGCCGAGAGTGAAGGCCAGCAGGGCGTGCTCGCGGGTCTGGCCGTTCT
N_leprea_l      GACGCCGAGAGTGAAGGCCAGCAGGGCGTGCTCGCGGGTCTGGCCGTTCT
O_correae       GACACCAAGCGTGAAAGCGAGCAGGGCATGCTCGCGGGTCTGGCCATTCT
O_kershawi      GACACCAAGTGTGAAAGCCAGCAGGGCGTGCTCNCGGGTCTGGCCGTTCT
O_lathoniella1  GACACCAAGTGTGAAAGCGAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
O_lathoniella2  GACACCAAGTGTGAAAGCGAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
O_latialis      GACACCAAGTGTGAAAGCGAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
O_orichora1     GACACCAAGCGTGAAAGCGAGCAGGGCGTGCTCGCGGGTCTGGCCATTCT
O_orichora2     GACACCAAGCGTGAAAGCGAGCAGGGCGTGCTCGCGGGTCTGGCCATTCT
O_ptunarraBPJ   GACACCAAGTGTGAAAGCGAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
O_ptunarraBPJ1  GACACCAAGTGTGAAAGCGAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
O_ptunarraNW    GACACCAAGTGTGAAAGCGAGCAGGGCGTGCTCGCGGGTCTGACCGTTCT
V_kershawi      GACACCAAGTGTGAAGGCGAGCAGAGCGTGCTCACGGGTTTGTCCGTTCT
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A_hobartia      TGGAAATACCGGCCTCGAACTCACCGGTACCGGCGGCCACGATGAGCACG
A_hobartia2     TGGAAATACCGGCCTCGAACTCACCGGTACCGGCGGCCACGATGAGCACG
G_klugii        TAGAGATACCAGCCTCGAACTCACCAGTACCGGCAGCGACAATGAGCACA
H_cordace_1     TGGAAATACCGGCCTCGAACTCACCGGTACCGGCAGCCACGATGAGCACG
H_cordace_k     TGGAGATACCGGCCTCGAACTCACCGGTACCGGCAGCCACGATGAGCACG
H_cordace_c     TGGAAATACCGGCCTCGAACTCACCGGTACCGGCAGCCACGATGAGCACG
H_meropeWAY     TGGAGATACCGGCCTCGAACTCACCGGTACCGGCGGCCACGATGAGCACG
H_meropeWW      TGGAGATACCGGCCTCGAACTCACCGGTACCGGCGGCCACGATGAGCACG
H_penelope      TGGAGATACCGGCCTCGAACTCACCGGTACCGGCGGCCACGATGAGCACG
J_villida       TGGAGATACCGGCTTCGAACTCACCGGTACCGGCGGCGACGATGAGCACG
J_villida2      TGGAGATACCGGCTTCGAACTCACCGGTACCGGCGGCGACGATGAGCACG
N_leprea_e      TGGAGATACCAGCTTCGAACTCACCTGTACCGGCGGCGACGATTAGCACG
N_leprea_1      TGGAGATACCAGCTTCGAACTCACCTGTACCGGCGGCGACGATTAGCACG
O_correae       TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACTATCAGCACA
O_kershawi      TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAACACG
O_lathoniella1  TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAGCACG
O_lathoniella2  TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAGCACG
O_latialis      TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAGCACG
O_orichora1     TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAGCACA
O_orichora2     TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAGCACA
O_ptunarraBPJ   TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAGCACG
O_ptunarraBPJ1  TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAGCACG
O_ptunarraNW    TGGAGATACCAGCTTCGAACTCACCAGTACCGGCGGCGACGATCAGCACG
V_kershawi      TAGAGATACCAGCTTCAAACTCACCAGTACCAGCGGCGACGATGAGCACA

A_hobartia      GCGCAGTCAGCCTGCGAAGTTCCCGTGATCATGTTCTTGATGAAATCCCT
A_hobartia2     GCGCAGTCAGCCTGCGAAGTTCCCGTGATCATGTTCTTGATGAAATCCCT
G_klugii        GCACAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTGATGAAATCCCT
H_cordace_1     GCGCAGTCGGCCTGCGAGGTTCCCGTGATCATGTTCTTGATGAAATCTCT
H_cordace_k     GCGCAGTCGGCCTGCGAGGTTCCCGTGATCATGTTCTTGATGAAATCTCT
H_cordace_c     GCGCAGTCGGCCTGCGAGGTTCCCGTGATCATGTTCTTGATGAAATCTCT
H_meropeWAY     GCGCAGTCGGCCTGCGAGGTTCCCGTGATCATGTTCTTGATGAAATCTCT
H_meropeWW      GCGCAGTCGGCCTGCGAGGTTCCCGTGATCATGTTCTTGATGAAATCTCT
H_penelope      GCGCAGTCGGCCTGAGAGGTTCCCGTGATCATGTTCTTGATGAAATCTCT
J_villida       GCGCAGTCGGCCTGTGAGGTTCCGGTAATCATGTTCTTGATGAAATCTCT
J_villida2      GCGCAGTCGGCCTGTGAGGTTCCGGTAATCATGTTCTTGATGAAATCTCT
N_leprea_e      GCGCAGTCAGCCTGCGAGGTTCCCGTGATCATGTTCTTGATGAAATCTCT
N_leprea_1      GCGCAGTCAGCCTGCGAGGTTCCCGTGATCATGTTCTTGATGAAATCTCT
O_correae       GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_kershawi      GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_lathoniella1  GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_lathoniella2  GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_latialis      GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_orichora1     GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_orichora2     GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_ptunarraBPJ   GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_ptunarraBPJ1  GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
O_ptunarraNW    GCGCAATCAGCCTGCGAGGTTCCCGTGATCATGTTCTTAATGAAATCCCT
V_kershawi      GCGCAATCGGCCTGTGAAGTTCCGGTGATCATGTTCTTGATGAAATCTCT
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A_hobartia      GTGCCCGGGAGCATCAATGATGGTGACGTAGTACCTGGCGGTCTCGAACT
A_hobartia2     GTGCCCGGGAGCATCGATGATGGTGACGTAGTACCTGGCGGTCTCGAACT
G_klugii        GTGTCCGGGAGCGTCAATGATAGTGACGTAGTACCTGGCGGTTTCAAACT
H_cordace_1     GTGTCCGGGAGCGTCGATGATGGTGACGTAGAACTTGGCAGTCTCGAACT
H_cordace_k     GTGTCCGGGAGCGTCGATGATGGTGACGTAGAACTTGGCAGTCTCGAATT
H_cordace_c     GTGTCCGGGAGCGTCGATGATGGTGACGTAGAACTTGGCAGTCTCGAACT
H_meropeWAY     GTGCCCGGGAGCGTCGATGATGGTGACGTAGAACTTGGCAGTCTCGAACT
H_meropeWW      GTGCCCGGGAGCGTCGATGATGGTGACGTAGAACTTGGCAGTCTCGAACT
H_penelope      GTGTCCGGGAGCGTCGATGATGGTGACGTAGAACTTGGCAGTCTCGAACT
J_villida       GTGGCCGGGAGCGTCGATGATGGTGACGTAGTATTTGGCGGTTTCGAACT
J_villida2      GTGGCCGGGAGCGTCGATGATGGTGACGTAGTATTTGGCGGTTTCGAACT
N_leprea_e      GTGACCGGGAGCGTCGATGATGGTGACGTAGTACCTAGCGGTCTCGAATT
N_leprea_1      GTGACCGGGAGCGTCGATGATGGTGACGTAGTACCTAGCGGTCTCGAATT
O_correae       GTGTCCGGGAGCGTCGATGATAGTGACGTAGTACCTGGCGGTCTCGAACT
O_kershawi      GTGTCCGGGAGCATCGATGATGGTGACGTAGTACTTGGCGGTCTCGAACT
O_lathoniella1  GTGTCCGGGAGCATCGATGATGGTGACGTAGTACCTGGCGGTCTCGAACT
O_lathoniella2  GTGTCCGGGAGCATCGATGATGGTGACGTAGTACCTGGCGGTCTCGAACT
O_latialis      GTGTCCGGGAGCATCGATGATGGTGACGTAGTACCTGGCGGTCTCGAACT
O_orichora1     GTGTCCGGGAGCGTCGATGATAGTGACGTAGTACCTGGCGGTCTCGAACT
O_orichora2     GTGTCCGGGAGCGTCGATGATAGTTACGTAGTACCTGGCGGTCTCGAACT
O_ptunarraBPJ   GTGTCCGGGAGCATCGATGATGGTGACGTAGTACCTGGCGGTCTCGAACT
O_ptunarraBPJ1  GTGTCCGGGAGCATCGATGATGGTGACGTAGTACCTGGCGGTCTCGAACT
O_ptunarraNW    GTGTCCGGGAGCATCGATGATGGTGACGTAGTACCTGGCGGTCTCGAACT
V_kershawi      GTGACCGGGAGCGTCGATGATGGTGACGTAGTATTTGGCGGTCTCGAACT

A_hobartia      TCCACAGAGCGATGTCGATGGTGATACCGCGCTCACGCTCAGCCTTCAGT
A_hobartia2     TCCACAGAGCGATGTCGATGGTGATACCGCGCTCACGCTCATCCTTCAGT
G_klugii        TCCACAGCGCGATGTCGATGGTGATACCGCGCTCGCGCTCAGCCTTTAGT
H_cordace_1     TCCACAGAGCGATATCGATGGTGATACCGCGCTCACGMTCAKCCTTAAGT
H_cordace_k     TGCACAGAGCGATATCGATGGTGATACCGCGCTCNCGGTCATACTTNCAC
H_cordace_c     TCCACAGAGCGATATCGATGGTGATACCGCGCTCACGCTCAGCCTTCAGT
H_meropeWAY     TCCACAGAGCGATGTCGATGGTGATACCACGTTCACGCTCAGCATTCAGC
H_meropeWW      TCCACAGAGCGATGTCGATGGTGATACCACGTTCACGCTCAGCCTTCAGN
H_penelope      TCCACAGAGCGATGTCGATGGTGATACCGCGCTCACGCTCAGCCTTCAGT
J_villida       TCCATAGGGCGATATCGATGGTGATACCACGTTCACGCTCGGCCTTAAGT
J_villida2      TCCATAGGGCGATATCGATGGTGATACCACGTTCACGTTCACACTTAAGT
N_leprea_e      TCCATAGGGCGATATCGATGGTGATACCGCGCTCGCGCTCAGCTTTCAGT
N_leprea_1      TCCATAGGGCGATATCGATGGTGATACCGCGCTCGCGCTCAGCTTTCAGT
O_correae       TCCACAGAGCAATGTCGATGGTGATACCGCGCTCGCGGTCAGCCTTCAGT
O_kershawi      TCCACAGAGCAATGTCGATGGTG----------------------------
O_lathoniella1  TCCACAGAGCAATGTCGATGGTGATACCACGCTCGCGCTCAGCCTTCAGT
O_lathoniella2  TCCACAGAGCAATGTCGATGGTGATACCACGCTCGCGCTCAGCCTTCAGT
O_latialis      TCCACAGAGCAATGTCGATGGTGATACCACGCTCGCGCTCAGCCTTCAGT
O_orichora1     TCCACAGAGCAATGTCGATGGTGATACCGCGCTCGCGCTCAGCCTTCAGT
O_orichora2     TCCACAGAGCAATGTCGATGGTGATACCGCGCTCGCGCTCAGCCTTCAGT
O_ptunarraBPJ   TCCACAGAGCAATGTCGATGGTGATACCACGCTCGCGCTCAGCCTTCAGT
O_ptunarraBPJ1  TCCACAGAGCAATGTCGATGGTGATACCACGCTCGCGCTCAGCCTTCAGT
O_ptunarraNW    TCCACAGAGCAATGTCGATGGTGATACCACGCTCGCGCTCAGCCTTCAGT
V_kershawi      TCCACAGAGCAATGTCGATGGTGATACCACGTTCACGCTCAGCCTTCAGT
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A_hobartia      TTGTCCA----------------------------------------
A_hobartia2     TTGTCCA----------------------------------------
G_klugii        TTGTCCA----------------------------------------
H_cordace_l     TTGTCCA----------------------------------------
H_cordace_k     TGATGCA----------------------------------------
H_cordace_c     TTGTCCA----------------------------------------
H_meropeWAY     TTGTCCA----------------------------------------
H_meropeWW      TTGTCCA----------------------------------------
H_penelope      TTGTCCA----------------------------------------
J_villida       TTGTCCA----------------------------------------
J_villida2      TTGTCCA----------------------------------------
N_leprea_e      TTGTCCA----------------------------------------
N_leprea_l      TTGTCCA----------------------------------------
O_correae       TTGTCCA----------------------------------------
O_kershawi      ----------------------------------------
O_lathoniella1  TTGTCCA----------------------------------------
O_lathoniella2  TTGTCCA----------------------------------------
O_latialis      TTGTCCA----------------------------------------
O_orichora1     TTGTCCA----------------------------------------
O_orichora2     TTGTCCA----------------------------------------
O_ptunarraBPJ   TTGTCCA----------------------------------------
O_ptunarraBPJ1  TTGTCCA----------------------------------------
O_ptunarraNW    TTGTCCA----------------------------------------
V_kershawi      TTGTCCA----------------------------------------
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Wingless

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A_hobartia      TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACGGTKAAGACGTGC
A_hobartia2     TGAATGTAAANTGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
G_klugii        ----------------------------------TGCRGGGAAGACGTGT
H_cordace_l     TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
H_cordace_k     TGAATGTAAANTGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
H_cordace_c     TGAATGTAAANTGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
H_meropeWAY     TGAATGTAAANTGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
H_meropeWW      TGAATGTAAANTGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
H_penelope      --------------------------------------------------
J_villida       TGAATGTAAAGTGTCATGGCATGTCTGGGTCCTGCACGGTTAAGACTTGC
J_villida2      TGAATGTAAAGTGTCATGGCATGTCTGGGTCCTGCACGGTTAAGACTTGC
N_leprea_e      TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACGGTCAAGACGTGC
N_leprea_l      TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACGGTCAAGACGTGC
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  TGAATGTAAANTGTCATGGCATGTCTGGGTCCTGCACGGTTAAGACGTGC
O_lathoniella2  TGAATGTAAANTGTCATGGCATGTCTGGGTCCTGCACGGTTAAGACGTGC
O_latialis      --------------------------------------------------
O_orichora1     TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACAGTAAAGACGTGC
O_orichora2     TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACAGTAAAGACGTGC
O_ptunarraBPJ   TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
O_ptunarraBPJ1  TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
O_ptunarraNW    TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACGGTGAAGACGTGC
V_kershawi      TGAATGTAAAATGTCATGGCATGTCTGGGTCCTGCACTGTCAAGACTTGT

A_hobartia      TGGATGAGGCTTCCGAGTTTTCGCTCAGTGGGCGATGCGTTAAAGGATGG
A_hobartia2     TGGATGAGGCTTCCGAGTTTTCGCTCAGTGGGCGATGCGTTAAAGGATGG
G_klugii        TGGATGAGGCTGCCGAGTTTTCGCTCAGTAGGCGATACCTTAAAGGACGG
H_cordace_l     TGGATGAGGCTGCCGAGTTTCCGGTCTGTAGGCGATGCTTTAAAGGACGG
H_cordace_k     TGGATGAGGCTGCCGAGTTTCCGGTCTGTAGGCGATGCTTTAAAGGACGG
H_cordace_c     TGGATGAGGCTGCCGAGTTTCCGGTCTGTAGGCGATGCTTTAAAGGACGG
H_meropeWAY     TGGATGAGGCTGCCGAGTTTCCGGTCCGTAGGCGACGCCTTAAAAGACGG
H_meropeWW      TGGATGAGGCTGCCGAGTTTCCGGTCCGTAGGCGACGCCTTAAAAGACGG
H_penelope      --------------------------------------------------
J_villida       TGGATGAGGCTGCCCAGTTTTCGCTCTGTGGGCGATGCATTGAAAGATCG
J_villida2      TGGATGAGGCTGCCCAGTTTTCGCTCTGTGGGCGATGCATTGAAAGATCG
N_leprea_e      TGGATGAGGCTGCCAAGTTTTCGTTCAGTAGGCGATGCCTTAAAAGATGG
N_leprea_l      TGGATGAGGCTGCCAAGTTTTCGTTCAGTAGGCGATGCCTTAAAAGATGG
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  TGGATGAGGCTGCCGAGCTTCCGATCTGTAGGCGATGCCTTAAAAGATAG
O_lathoniella2  TGGATGAGGCTGCCGAGCTTCCGATCTGTAGGCGATGCCTTAAAAGATAG
O_latialis      --------------------------------------------------
O_orichora1     TGGATGAGGCTGCCGAGCTTCCGATCTGTAGGCGATTCCTTAAAAGATGG
O_orichora2     TGGATGAGGCTGCCGAGCTTCCGATCTGTAGGCGATTCCTTAAAAGATGG
O_ptunarraBPJ   TGGATGAGGCTGCCGAGCTTCCGATCTGTAGGCGATGCCTTAAAAGATGG
O_ptunarraBPJ1  TGGATGAGGCTGCCGAGCTTCCGATCTGTAGGCGATGCCTTAAAAGATGG
O_ptunarraNW    TGGATGAGGCTGCCGAGCTTCCGATCTGTAGGCGATGCCTTAAAAGATGG
V_kershawi      TGGATGAGGCTGCCCAGTTTTCGCTCCGTGGGTGACGCGTTAAAAGATCG
```

```
A_hobartia      CTTCGACGGGGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAGGCAC
A_hobartia2     CTTCGACGGGGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAGGCAC
G_klugii        CTTCGACGGAGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAAGCGC
H_cordace_l     CTTCGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAAGCAC
H_cordace_k     CTTCGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAAGCAC
H_cordace_c     CTTCGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAAGCAC
H_meropeWAY     CTTCGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAAGCAC
H_meropeWW      CTTCGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAAGCAC
H_penelope      --------------------------------------------------
J_villida       CTTCGATGGTGCGTCACGTGTCATGATGCCCAATACAGAAATCGAAGCGC
J_villida2      CTTCGATGGTGCGTCACGTGTCATGATGCCCAATACAGAAATCGAAGCGC
N_leprea_e      CTTCGATGGGGCGTCGCGGGTCATGATGCCTAACACGGAGGTGGAAGCAC
N_leprea_l      CTTCGATGGGGCGTCGCGGGTCATGATGCCTAACACGGAGGTGGAAGCAC
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  CTTTGATGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAATTGC
O_lathoniella2  CTTTGATGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAATTGC
O_latialis      --------------------------------------------------
O_orichora1     CTTTGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAATTGC
O_orichora2     CTTTGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAATTGC
O_ptunarraBPJ   CTTCGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAATTGC
O_ptunarraBPJ1  CTTCGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAATTGC
O_ptunarraNW    CTTCGACGGTGCGTCGCGGGTCATGATGCCCAACACGGAGGTGGAATTGC
V_kershawi      TTTCGATGGAGCGTCGCGGGTCATGATGCCTAACACAGAAATCGAAGCGC

A_hobartia      CTCTCCAGCGGAACGACGCCGTGCCGCACAGGGTCCCGCGACGAGACCGA
A_hobartia2     CTCTCCAGCGGAACGACGCCGTGCCGCACAGGGTCCCGCGACGAGACCGA
G_klugii        CACTCCAGCGGAACGACGCCGCTCCGCACAGAGTCCCGCGACGGGATCGA
H_cordace_l     CTCTCCAGCGGAACGACGCCGCCCCGCACAGGGTGCCGCGACGAGACCGA
H_cordace_k     CTCTCCAGCGGAACGACGCCGCCCCGCACAGGGTGCCGCGACGAGACCGA
H_cordace_c     CTCTCCAGCGGAACGACGCCGCCCCGCACAGGGTGCCGCGACGAGACCGA
H_meropeWAY     CCCTCCAGCGGAACGACGCCGCTCCGCACAGGGTGCCGCGCCGGGACCGA
H_meropeWW      CCCTCCAGCGGAACGACGCCGCTCCGCACAGGGTGCCGCGCCGGGACCGA
H_penelope      --------------------------------------------------
J_villida       CCGTACAGCGAAACGACGTAGCGCCTCACAGAGTTCCACGAAGAGATCGG
J_villida2      CCGTACAGCGAAACGACGTAGCGCCTCACAGAGTTCCACGAAGAGATCGG
N_leprea_e      CACTTCAGCGAAACGACGCCGCCCCGCACAGAGTACCGCGACGAGATCGA
N_leprea_l      CACTTCAGCGAAACGACGCCGCCCCGCACAGAGTACCGCGACGAGATCGA
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  CTCTGCAGCGGAATGACGCCGCTCCGCACAGAGTCCCGCGGCGAGACCGC
O_lathoniella2  CTCTGCAGCGGAATGACGCCGCTCCGCACAGAGTCCCGCGGCGAGACCGC
O_latialis      --------------------------------------------------
O_orichora1     CTCTGCAGCGGAACGACGCCGCTCCGCACAGAGTCCCGCGGCGAGACCGC
O_orichora2     CTCTGCAGCGGAACGACGCCGCTCCGCACAGAGTCCCGCGGCGAGACCGC
O_ptunarraBPJ   CTCTGCAGCGGAACGACGCCGCTCCGCACAGAGTCCCGCGGCGAGACCGC
O_ptunarraBPJ1  CTCTGCAGCGGAACGACGCCGCTCCGCACAGAGTCCCGCGGCGAGACCGC
O_ptunarraNW    CTCTGCAGCGGAACGACGCCGCTCCGCACAGAGTCCCGCGGCGAGACCGC
V_kershawi      CCGTACAGCGAAATGACGCAGCGCCTCACAGAGTTCCAAGAAGAGATCGG
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Wingless

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A_hobartia      TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACGCCCGGGGT
A_hobartia2     TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACGCCCGGGGT
G_klugii        TACAGGTTTCAACTCCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
H_cordace_l     TACAGGTTTCAGCTCCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
H_cordace_k     TACAGGTTTCAGCTCCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
H_cordace_c     TACAGGTTTCAGCTCCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
H_meropeWAY     TACAGGTTTCAGCTCCGGCCGCACAATCCTGACCACAAAACACCGGGGGT
H_meropeWW      TACAGGTTTCAGCTCCGGCCGCACAATCCTGACCACAAAACACCGGGGGT
H_penelope      --------------------------------------------------
J_villida       TACAGGTTCCAACTCAGGCCGCACAATCCCGATCATAAGACACCGGGATC
J_villida2      TACAGGTTCCAACTCAGGCCGCACAATCCCGATCATAAGACACCGGGATC
N_leprea_e      TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
N_leprea_l      TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  TACAGGTTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGT
O_lathoniella2  TACAGGTTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGT
O_latialis      --------------------------------------------------
O_orichora1     TACAGGTTTCAACTTCGGCCGCACAACCCTGACCATAAAACACCCGGAGT
O_orichora2     TACAGGTTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGAGT
O_ptunarraBPJ   TACAGGTTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGT
O_ptunarraBPJ1  TACAGGTTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGT
O_ptunarraNW    TACAGGTTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGT
V_kershawi      TACAGATTCCAGCTTCGGCCGCACAATCCCGATCATAAAACACCGGGGGC

A_hobartia      CAAGGACCTAGTATACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
A_hobartia2     CAAGGACCTAGTATACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
G_klugii        CAAGGACCTAGTGTACCTGGAATCGTCGCCGGGTTTCTGCGAAAAGAACC
H_cordace_l     CAAGGACTTAGTGTACCTGGAATCTTCGCCGGGTTTCTGCGAAAAGAACC
H_cordace_k     CAAGGACTTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
H_cordace_c     CAAGGACTTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
H_meropeWAY     CAAGGACCTAGTGTACCTGGAATCGTCGCCGGGTTTCTGCGAAAAGAACC
H_meropeWW      CAAGGACCTAGTGTACCTGGAATCGTCGCCGGGTTTCTGCGAAAAGAACC
H_penelope      --------------------------------------------------
J_villida       CAAAGACCTAGTGTACCTCGAATCATCGCCGGGTTTCTGTGAAAAGAACC
J_villida2      CAAAGACCTAGTGTACCTCGAATCATCGCCGGGTTTCTGTGAAAAGAACC
N_leprea_e      CAAGGACCTAGTATACCTGGAATCGTCGCCGGGTTTCTGCGAAAAGAACC
N_leprea_l      CAAGGACCTAGTATACCTGGAATCGTCGCCGGGTTTCTGCGAAAAGAACC
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  CAAGGACCTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
O_lathoniella2  CAAGGACCTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
O_latialis      --------------------------------------------------
O_orichora1     CAAGGACCTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
O_orichora2     CAAGGACCTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
O_ptunarraBPJ   CAAGGACCTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
O_ptunarraBPJ1  CAAGGACCTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
O_ptunarraNW    CAAGGACCTAGTGTACCTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
V_kershawi      AAAAGACCTAGTCTACCTTGAATCATCACCGGGTTTTTGTGAAAAGAACC
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A_hobartia      CGCGGCTGGGCATTCCCGGTACGCACGGGCGTGCCTGCAACGATACGAGC
A_hobartia2     CGCGGCTGGGCATTCCCGGTACGCACGGGCGTGCCTGCAACGATACGAGC
G_klugii        CGCGGCTGGGCATTCCCGGTACGCACGGGCGCGCCTGCAACGACACGAGC
H_cordace_l     CGCGGCTGGGCATCCCCGGCACGCACGGGCGAGCCTGCAACGACACGAGT
H_cordace_k     CGCGGCTGGGCATCCCCGGCACGCACGGGCGAGCCTGCAACGACACGAGT
H_cordace_c     CGCGGCTGGGCATCCCCGGCACGCACGGGCGAGCCTGCAACGACACGAGT
H_meropeWAY     CGCGGCTCGGCATCCCCGGCACGCACGGGCGAGCCTGCAACGACACGAGC
H_meropeWW      CGCGGCTCGGCATCCCCGGCACGCACGGGCGAGCCTGCAACGACACGAGC
H_penelope      --------------------------------------------------
J_villida       CGAGGCTGGGCATTCCCGGCACGCACGGGCGTGCCTGCAACGATACGAGC
J_villida2      CGAGGCTGGGCATTCCCGGCACGCACGGGCGTGCCTGCAACGATACGAGC
N_leprea_e      CACGGCTGGGCATTCCCGGTACGCACGGGCGTGCCTGCAACGATACGAGT
N_leprea_l      CACGGCTGGGCATTCCCGGTACGCACGGGCGTGCCTGCAACGATACGAGT
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  CGCGGCTGGGCATCCCCGGTACGCACGGGCGTGCCTGCAACGATACGAGT
O_lathoniella2  CGCGGCTGGGCATCCCCGGTACGCACGGGCGTGCCTGCAACGATACGAGT
O_latialis      --------------------------------------------------
O_orichora1     CGCGACTGGGCATCCCCGGTACGCACGGGCGTGCCTGCAACGATACGAGT
O_orichora2     CGCGACTGGGCATCCCCGGTACGCACGGGCGTGCCTGCAACGATACGAGT
O_ptunarraBPJ   CGCGGCTGGGCATCCCCGGTACGCACGGGCGTACCTGCAACGATACGAGT
O_ptunarraBPJ1  CGCGGCTGGGCATCCCCGGTACGCACGGGCGTACCTGCAACGATACGAGT
O_ptunarraNW    CGCGGCTGGGCATCCCCGGTACGCACGGGCGTACCTGCAACGATACGAGT
V_kershawi      CGAGGCTGGGCATTCCCGGCACGCACGGGCGTGCCTGCAACGATACCAGC

A_hobartia      ATCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
A_hobartia2     ATCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
G_klugii        ATCGGCGTGGACGGCTGCGACCTGATGTGCTGCGGCCGCGGTTACCGGAC
H_cordace_l     ATCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGCTACCGCAC
H_cordace_k     ATCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGCTACCGCAC
H_cordace_c     ATCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGCTACCGCAC
H_meropeWAY     ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGCTACCGCAC
H_meropeWW      ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGCTACCGCAC
H_penelope      --------------------------------------------------
J_villida       ATCGGCGTCGACGGCTGCGATCTCATGTGTTGCGGCCGTGGCTACCGGAC
J_villida2      ATCGGCGTCGACGGCTGCGATCTCATGTGTTGCGGCCGTGGCTACCGGAC
N_leprea_e      ATCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
N_leprea_l      ATCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  ATCGGCGTCGACGGCTGCGACCTCATGTGCTGTGGCCGCGGGTACCGGAC
O_lathoniella2  ATCGGCGTCGACGGCTGCGACCTCATGTGCTGTGGCCGCGGGTACCGGAC
O_latialis      --------------------------------------------------
O_orichora1     ATCGGCGTTGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
O_orichora2     ATCGGCGTTGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
O_ptunarraBPJ   ATCGGCGTCGACGGCTGCGACCTCATGTGCTGTGGCCGCGGGTACCGGAC
O_ptunarraBPJ1  ATCGGCGTCGACGGCTGCGACCTCATGTGCTGTGGCCGCGGGTACCGGAC
O_ptunarraNW    ATCGGCGTCGACGGCTGCGACCTCATGTGCTGTGGCCGCGGGTACCGGAC
V_kershawi      ATCGGCGTCGACGGCTGCGACCTCATGTGTTGCGGTCGTGGTTACCGGAC
```

Wingless

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A_hobartia      CGAGACGATGGTCGTCGTGGAGCGATGCAACTGTACATTCCATTGGTGCG
A_hobartia2     CGAGACGATGGTCGTCGTTGAGCGATGCAACTGTACATTCCATTGGTGCG
G_klugii        CGACACGATGTTCGTCGTGGAGCGATGCAACTGTACATTCCATTGGTGCG
H_cordace_l     CGAGACGATGATCTTCGACGAGCGATGCAACTGTACATTCCATTGGTGCN
H_cordace_k     CGAGACGATGATCGTCGACGAGCGATGCAACTGTACATTCCATTGGTGCG
H_cordace_c     CGAGACGATGATCGTCGACGAGCGATGCAACTGTACATTCCATTGGTGCG
H_meropeWAY     CGAGACGATGATCGTCACAGCGCGGTGCAACTGCACATTCCAC-------
H_meropeWW      CGAGACGATGATCGTCACAGCGCGGTGCAACTGCACATTCCAC-------
H_penelope      --------------------------------------------------
J_villida       CGAAACAATGTTTGTTGTGGAACGATGCAATTGNACATTCCANTGGTGCG
J_villida2      CGAAACAATGTTTGTTGTGGAACGATGCAATTGNACATTCCANTGGTGCG
N_leprea_e      CGAGACGATGTTTGTCGTGGAGCGATGCAACTGTACATTCCATTGGTGCC
N_leprea_l      CGAGACGATGTTTGTCGTGGAGCGATGCAACTGTACATTCCATTGGTGCC
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  TGAAACAATGTTTGTCGTGGAGCGATGCAACTGTACATTCCANTGGTGCC
O_lathoniella2  TGAAACAATGTTTGTCGTGGAGCGATGCAACTGTACATTCCANTGGTGCC
O_latialis      --------------------------------------------------
O_orichora1     CGAGACAATGTTTGTCGTGGAGCGATGCAACTGTACATTCCATTGGTGCG
O_orichora2     CGAGACAATGTTTGTCGTGGAGCGATGCAACTGTACATTCCATTGGTGCG
O_ptunarraBPJ   CGAGACTATGTTTGTCGTGGAACGATGCAACTGNACATTCCATTGGTGCG
O_ptunarraBPJ1  CGAGACTATGTTTGTCGTGGAACGATGCAACTGNACATTCCATTGGTGCG
O_ptunarraNW    CGAGACTATGTTTGTCGTGGAACGATGCAACTGTACATTCCATTGGTGCG
V_kershawi      CGAAACAATGCTTGTTGTGGAACGATGCAATTGTACATTCCANTGGTGCN

A_hobartia      GCGCAGTAA----------------------------------------
A_hobartia2     GCGCAGTAA----------------------------------------
G_klugii        GCGCAGTAA----------------------------------------
H_cordace_l     GCGCAGTAA----------------------------------------
H_cordace_k     GCGCAGTAA----------------------------------------
H_cordace_c     GCGCAGTAA----------------------------------------
H_meropeWAY     --------------------------------------------------
H_meropeWW      --------------------------------------------------
H_penelope      --------------------------------------------------
J_villida       GCGCAGTAA----------------------------------------
J_villida2      GCGCAGTAA----------------------------------------
N_leprea_e      GCGCAGTAA----------------------------------------
N_leprea_l      GCGCAGTAA----------------------------------------
O_correae       --------------------------------------------------
O_kershawi      --------------------------------------------------
O_lathoniella1  GCGCAGTAA----------------------------------------
O_lathoniella2  GCGCAGTAA----------------------------------------
O_latialis      --------------------------------------------------
O_orichora1     GCGCAGTAA----------------------------------------
O_orichora2     GCGCAGTAA----------------------------------------
O_ptunarraBPJ   GCGCAGTAA----------------------------------------
O_ptunarraBPJ1  GCGCAGTAA----------------------------------------
O_ptunarraNW    GCGCAGTAA----------------------------------------
V_kershawi      GCGCAGTAA----------------------------------------
```

Appendix 7 - Log/Det sequence divergence values

CO1

	A hobartia1	*A hobartia2*	*G klugii*	*H cordace l*	*H cordace k*	*H cordace c*	*H merope* WAY	*H merope* WW	*H penelope*	*J villida1*	*J villida2*	*N leprea e*	*N leprea l*	*O correae*	*O kershawi*	*O lathoniella1*	*O lathoniella2*	*O latialis*	*O orichora1*	*O orichora2*	*O ptunarra* BPJ	*O ptunarra* BPJ1	*O ptunarra* NW	*V kershawi*
A hobartia1	-																							
A hobartia2	0.00																							
G klugii	0.11	0.11																						
H cordace l	0.10	0.10	0.12																					
H cordace k	0.10	0.10	0.13	0.02																				
H cordace c	0.09	0.09	0.13	0.02	0.00																			
H merope WAY	0.11	0.11	0.11	0.11	0.10	0.10																		
H merope WW	0.11	0.11	0.11	0.09	0.09	0.08	0.03																	
H penelope	0.12	0.12	0.12	0.09	0.09	0.08	0.10	0.09																
J villida1	0.11	0.11	0.09	0.12	0.11	0.11	0.12	0.12	0.13															
J villida2	0.11	0.11	0.09	0.12	0.11	0.11	0.12	0.12	0.13	0.00														
N leprea e	0.10	0.10	0.11	0.10	0.10	0.10	0.11	0.11	0.11	0.11	0.11													
N leprea l	0.10	0.10	0.12	0.10	0.10	0.10	0.11	0.11	0.11	0.11	0.11	0.01												
O correae	0.10	0.10	0.12	0.09	0.10	0.10	0.10	0.11	0.10	0.12	0.12	0.10	0.10											
O kershawi	0.12	0.12	0.12	0.11	0.12	0.12	0.12	0.12	0.11	0.13	0.13	0.11	0.11	0.06										
O lathoniella1	0.11	0.11	0.11	0.10	0.11	0.11	0.09	0.10	0.11	0.13	0.13	0.11	0.11	0.06	0.08									
O lathoniella2	0.11	0.11	0.11	0.10	0.11	0.11	0.09	0.10	0.11	0.13	0.13	0.11	0.11	0.06	0.08	0.00								
O latialis	0.12	0.12	0.11	0.09	0.11	0.10	0.08	0.10	0.10	0.13	0.13	0.11	0.11	0.07	0.08	0.06	0.06							
O orichora1	0.11	0.11	0.10	0.07	0.10	0.10	0.10	0.09	0.10	0.12	0.12	0.11	0.11	0.05	0.06	0.06	0.06	0.06						
O orichora2	0.11	0.11	0.10	0.07	0.10	0.10	0.10	0.09	0.10	0.12	0.12	0.11	0.11	0.05	0.06	0.06	0.06	0.06	0.00					
O ptunarra BPJ	0.12	0.12	0.11	0.09	0.11	0.10	0.08	0.10	0.10	0.13	0.13	0.11	0.11	0.06	0.08	0.07	0.07	0.01	0.06	0.06				
O ptunarra BPJ1	0.12	0.12	0.11	0.09	0.11	0.10	0.08	0.10	0.10	0.13	0.13	0.11	0.11	0.06	0.08	0.07	0.07	0.01	0.06	0.06	0.00			
O ptunarra NW	0.12	0.12	0.11	0.09	0.11	0.10	0.08	0.10	0.10	0.13	0.13	0.11	0.11	0.06	0.08	0.07	0.07	0.01	0.06	0.06	0.00	0.00		
V kershawi	**0.11**	**0.11**	**0.08**	**0.12**	**0.12**	**0.12**	**0.11**	**0.11**	**0.12**	**0.12**	**0.12**	**0.12**	**0.12**	**0.11**	**0.13**	**0.13**	**0.13**	**0.11**	**0.11**	**0.11**	**0.12**	**0.12**	**0.12**	
Age (mya)																								
*38	33.98	33.98	34.84	33.42	33.47	33.59	33.77	33.97	33.30	33.42	33.42	33.38	33.30	33.79	33.14	33.05	33.11	33.74	33.75	33.75	33.55	33.55	33.49	38.00
***35**	**31.30**	**31.30**	**32.09**	**30.78**	**30.83**	**30.94**	**31.10**	**31.29**	**30.67**	**30.78**	**30.78**	**30.74**	**30.67**	**31.12**	**30.52**	**30.44**	**30.50**	**31.07**	**31.08**	**31.08**	**30.90**	**30.90**	**30.85**	**35.00**

EF-1α

	A hobartia1	*A hobartia2*	*G klugii*	*H cordace l*	*H cordace k*	*H cordace c*	*H merope* WAY	*H merope* WW	*H penelope*	*J villida1*	*J villida2*	*N leprea e*	*N leprea l*	*O correae*	*O kershawi*	*O lathoniella1*	*O lathoniella2*	*O latialis*	*O orichora1*	*O orichora2*	*O ptunarra* BPJ	*O ptunarra* BPJ1	*O ptunarra* NW	*V kershawi*
A hobartia1	-																							
A hobartia2	0.00																							
G klugii	0.08	0.08																						
H cordace l	0.09	0.09	0.10																					
H cordace k	0.11	0.11	0.11	0.03																				
H cordace c	0.09	0.09	0.10	0.00	0.03																			
H merope WAY	0.08	0.08	0.09	0.03	0.05	0.03																		
H merope WW	0.08	0.08	0.09	0.03	0.05	0.03	0.01																	
H penelope	0.08	0.08	0.09	0.05	0.06	0.04	0.04	0.03																
J villida1	0.10	0.11	0.11	0.12	0.13	0.12	0.11	0.10	0.11															
J villida2	0.11	0.11	0.11	0.12	0.13	0.12	0.11	0.11	0.11	0.01														
N leprea e	0.09	0.09	0.10	0.11	0.13	0.11	0.11	0.11	0.10	0.13	0.13													
N leprea l	0.10	0.10	0.10	0.12	0.13	0.11	0.11	0.11	0.11	0.13	0.14	0.00												
O correae	0.09	0.09	0.08	0.10	0.11	0.10	0.10	0.09	0.10	0.13	0.13	0.10	0.11											
O kershawi	0.08	0.08	0.08	0.11	0.11	0.11	0.10	0.09	0.10	0.12	0.12	0.10	0.10	0.05										
O lathoniella1	0.09	0.09	0.09	0.12	0.13	0.11	0.11	0.10	0.11	0.13	0.13	0.10	0.10	0.04	0.04									
O lathoniella2	0.09	0.09	0.09	0.12	0.13	0.11	0.11	0.10	0.11	0.13	0.13	0.10	0.10	0.04	0.04	0.00								
O latialis	0.10	0.09	0.09	0.12	0.13	0.11	0.11	0.10	0.11	0.13	0.13	0.10	0.10	0.05	0.05	0.01	0.01							
O orichora1	0.09	0.09	0.08	0.10	0.12	0.10	0.10	0.09	0.10	0.13	0.13	0.10	0.10	0.02	0.04	0.04	0.04	0.05						
O orichora2	0.09	0.09	0.08	0.11	0.12	0.10	0.10	0.10	0.10	0.13	0.13	0.10	0.10	0.02	0.04	0.04	0.04	0.05	0.01					
O ptunarra BPJ	0.10	0.09	0.09	0.12	0.13	0.11	0.11	0.10	0.11	0.13	0.13	0.10	0.10	0.05	0.05	0.01	0.01	0.00	0.05	0.05				
O ptunarra BPJ1	0.10	0.09	0.09	0.12	0.13	0.11	0.11	0.10	0.11	0.13	0.13	0.10	0.10	0.05	0.05	0.01	0.01	0.00	0.05	0.05	0.00			
O ptunarra NW	0.10	0.09	0.09	0.12	0.13	0.12	0.11	0.11	0.11	0.13	0.13	0.10	0.10	0.05	0.05	0.01	0.01	0.00	0.05	0.05	0.00	0.00		
V kershawi	**0.11**	**0.11**	**0.11**	**0.11**	**0.13**	**0.11**	**0.11**	**0.10**	**0.11**	**0.08**	**0.08**	**0.13**	**0.14**	**0.12**	**0.12**	**0.12**	**0.12**	**0.13**	**0.12**	**0.12**	**0.13**	**0.13**	**0.13**	
Age (mya)																								
*38	33.80	33.84	33.69	33.66	33.08	33.76	33.95	34.03	33.90	34.92	34.84	32.96	32.86	33.38	33.47	33.38	33.38	33.19	33.43	33.38	33.19	33.19	33.19	38.00
***35**	**31.14**	**31.17**	**31.03**	**31.00**	**30.47**	**31.09**	**31.27**	**31.35**	**31.22**	**32.16**	**32.09**	**30.35**	**30.27**	**30.74**	**30.83**	**30.75**	**30.75**	**30.57**	**30.79**	**30.74**	**30.57**	**30.57**	**30.57**	**35.00**

Wingless

	A hobartia1	*A hobartia2*	*G klugii*	*H cordace l*	*H cordace k*	*H cordace c*	*H merope* WAY	*H merope* WW	*J villida1*	*J villida2*	*N leprea e*	*N leprea l*	*O lathoniella1*	*O lathoniella2*	*O orichora1*	*O orichora2*	*O ptunarra* BPJ	*O ptunarra* BPJ1	*O ptunarra* LMLE1	*O ptunarra* LMLE2	*O ptunarra* NW	*V kershawi*
A hobartia1	-																					
A hobartia2	0.00																					
G klugii	0.07	0.07																				
H cordace l	0.06	0.06	0.08																			
H cordace k	0.06	0.06	0.08	0.00																		
H cordace c	0.06	0.06	0.08	0.00	0.00																	
H merope WAY	0.09	0.09	0.08	0.05	0.05	0.05																
H merope WW	0.09	0.09	0.08	0.05	0.05	0.05	0.00															
J villida1	0.14	0.14	0.16	0.15	0.15	0.15	0.16	0.16														
J villida2	0.14	0.14	0.16	0.15	0.15	0.15	0.16	0.16	0.00													
N leprea e	0.05	0.06	0.07	0.07	0.07	0.07	0.09	0.09	0.13	0.13												
N leprea l	0.05	0.06	0.07	0.07	0.07	0.07	0.09	0.09	0.13	0.13	0.00											
O lathoniella1	0.08	0.08	0.10	0.08	0.08	0.08	0.10	0.10	0.14	0.14	0.07	0.07										
O lathoniella2	0.08	0.08	0.10	0.08	0.08	0.08	0.10	0.10	0.14	0.14	0.07	0.07	0.00									
O orichora1	0.08	0.08	0.09	0.08	0.08	0.08	0.10	0.10	0.14	0.14	0.07	0.07	0.03	0.03								
O orichora2	0.07	0.08	0.09	0.08	0.08	0.08	0.10	0.10	0.14	0.14	0.07	0.07	0.03	0.03	0.00							
O ptunarra BPJ	0.07	0.07	0.09	0.07	0.07	0.07	0.09	0.09	0.14	0.14	0.07	0.07	0.02	0.02	0.03	0.02						
O ptunarra BPJ1	0.07	0.07	0.09	0.07	0.07	0.07	0.09	0.09	0.14	0.14	0.07	0.07	0.02	0.02	0.03	0.02	0.00					
O ptunarra LMLE1	0.07	0.07	0.09	0.07	0.07	0.07	0.09	0.09	0.14	0.14	0.07	0.07	0.02	0.02	0.03	0.02	0.00	0.00				
O ptunarra LMLE2	0.07	0.07	0.09	0.07	0.07	0.07	0.09	0.09	0.14	0.14	0.07	0.07	0.02	0.02	0.03	0.02	0.00	0.00	0.00			
O ptunarra NW	0.07	0.07	0.09	0.07	0.07	0.07	0.09	0.09	0.14	0.14	0.07	0.07	0.02	0.02	0.03	0.02	0.00	0.00	0.00	0.00		
V kershawi	**0.14**	**0.15**	**0.17**	**0.17**	**0.16**	**0.16**	**0.17**	**0.17**	**0.08**	**0.08**	**0.13**	**0.13**	**0.15**	**0.15**	**0.16**	**0.16**	**0.16**	**0.16**	**0.16**	**0.16**	**0.16**	
Age (mya)																						
*38	32.51	32.41	31.59	31.60	31.75	31.75	31.37	31.37	35.08	35.08	32.93	32.93	32.24	32.24	31.93	31.85	32.07	32.07	32.10	32.10	32.10	38.00
***35**	**29.95**	**29.85**	**29.10**	**29.10**	**29.24**	**29.24**	**28.89**	**28.89**	**32.31**	**32.31**	**30.33**	**30.33**	**29.70**	**29.70**	**29.41**	**29.33**	**29.54**	**29.54**	**29.56**	**29.56**	**29.56**	**35.00**

Combined

	A hobartia1	*A hobartia2*	*G klugii*	*H cordace l*	*H cordace k*	*H cordace c*	*H merope* WAY	*H merope* WW	*H penelope*	*J villida1*	*J villida2*	*N leprea e*	*N leprea l*	*O correae*	*O kershawi*	*O lathoniella1*	*O lathoniella2*	*O latialis*	*O orichora1*	*O orichora2*	*O ptunarra* BPJ	*O ptunarra* BPJ1	*O ptunarra* NW	*V kershawi*
A hobartia1	-																							
A hobartia2	0.00																							
G klugii	0.09	0.09																						
H cordace l	0.09	0.09	0.10																					
H cordace k	0.09	0.09	0.11	0.02																				
H cordace c	0.08	0.08	0.10	0.01	0.01																			
H merope WAY	0.09	0.09	0.10	0.06	0.07	0.06																		
H merope WW	0.09	0.09	0.09	0.05	0.06	0.05	0.01																	
H penelope	0.10	0.10	0.10	0.07	0.07	0.06	0.06	0.06																
J villida1	0.12	0.12	0.12	0.13	0.13	0.12	0.13	0.12	0.12															
J villida2	0.12	0.12	0.12	0.13	0.13	0.12	0.13	0.12	0.12	0.00														
N leprea e	0.09	0.09	0.10	0.10	0.10	0.10	0.11	0.10	0.11	0.12	0.12													
N leprea l	0.09	0.09	0.10	0.10	0.11	0.10	0.11	0.11	0.11	0.12	0.13	0.01												
O correae	0.10	0.10	0.09	0.10	0.11	0.10	0.10	0.10	0.10	0.13	0.13	0.10	0.10											
O kershawi	0.10	0.10	0.10	0.11	0.11	0.11	0.10	0.11	0.10	0.13	0.13	0.11	0.10	0.05										
O lathoniella1	0.09	0.09	0.10	0.10	0.11	0.10	0.10	0.10	0.11	0.13	0.13	0.09	0.09	0.05	0.06									
O lathoniella2	0.09	0.09	0.10	0.10	0.11	0.10	0.10	0.10	0.11	0.13	0.13	0.09	0.09	0.05	0.06	0.00								
O latialis	0.11	0.10	0.10	0.10	0.12	0.11	0.10	0.10	0.10	0.13	0.13	0.10	0.10	0.06	0.06	0.04	0.04							
O orichora1	0.09	0.09	0.09	0.09	0.10	0.09	0.10	0.10	0.10	0.13	0.13	0.10	0.10	0.03	0.05	0.04	0.04	0.05						
O orichora2	0.09	0.09	0.09	0.09	0.10	0.09	0.10	0.10	0.10	0.13	0.13	0.10	0.10	0.03	0.05	0.04	0.04	0.05	0.00					
O ptunarra BPJ	0.10	0.09	0.10	0.10	0.11	0.10	0.09	0.10	0.10	0.13	0.13	0.09	0.09	0.06	0.06	0.03	0.03	0.01	0.05	0.05				
O ptunarra BPJ1	0.10	0.09	0.10	0.10	0.11	0.10	0.09	0.10	0.10	0.13	0.13	0.09	0.09	0.06	0.06	0.03	0.03	0.01	0.05	0.05	0.00			
O ptunarra NW	0.10	0.09	0.10	0.10	0.11	0.10	0.09	0.10	0.10	0.13	0.13	0.10	0.10	0.06	0.06	0.04	0.04	0.01	0.05	0.05	0.00	0.00		
V kershawi	**0.12**	**0.12**	**0.12**	**0.13**	**0.13**	**0.13**	**0.12**	**0.12**	**0.11**	**0.09**	**0.09**	**0.13**	**0.13**	**0.12**	**0.12**	**0.13**	**0.13**	**0.12**	**0.13**	**0.13**	**0.13**	**0.13**	**0.13**	
Age (mya)																								
*38	33.55	33.54	33.60	33.08	32.89	33.22	33.28	33.38	33.68	34.47	34.43	33.08	33.02	33.58	33.35	32.98	33.00	33.45	33.17	33.13	33.04	33.04	33.02	38.00
***35**	**30.90**	**30.89**	**30.95**	**30.47**	**30.29**	**30.60**	**30.65**	**30.74**	**31.02**	**31.75**	**31.72**	**30.47**	**30.41**	**30.93**	**30.72**	**30.37**	**30.39**	**30.81**	**30.55**	**30.51**	**30.43**	**30.43**	**30.41**	**35.00**

Appendix 8 - Phylogenetic Trees

CO1

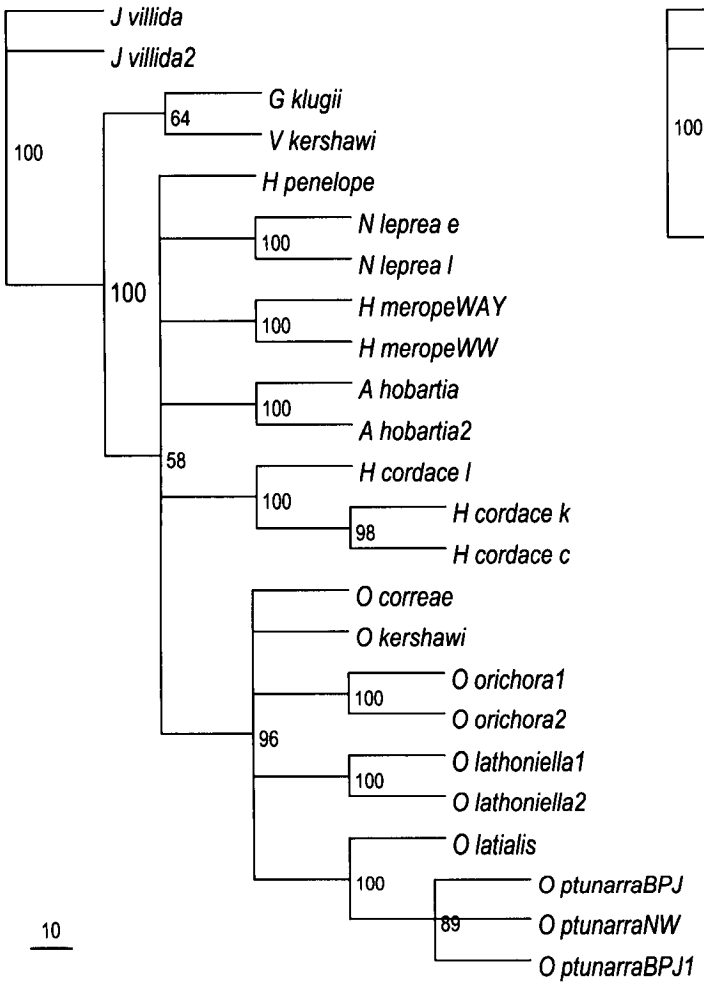

Figure A8.1 Bootstrap consensus of the most parsimonious tree (MP analysis) retrieved from CO1 sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 455, CI = 0.545, RI = 0.715).

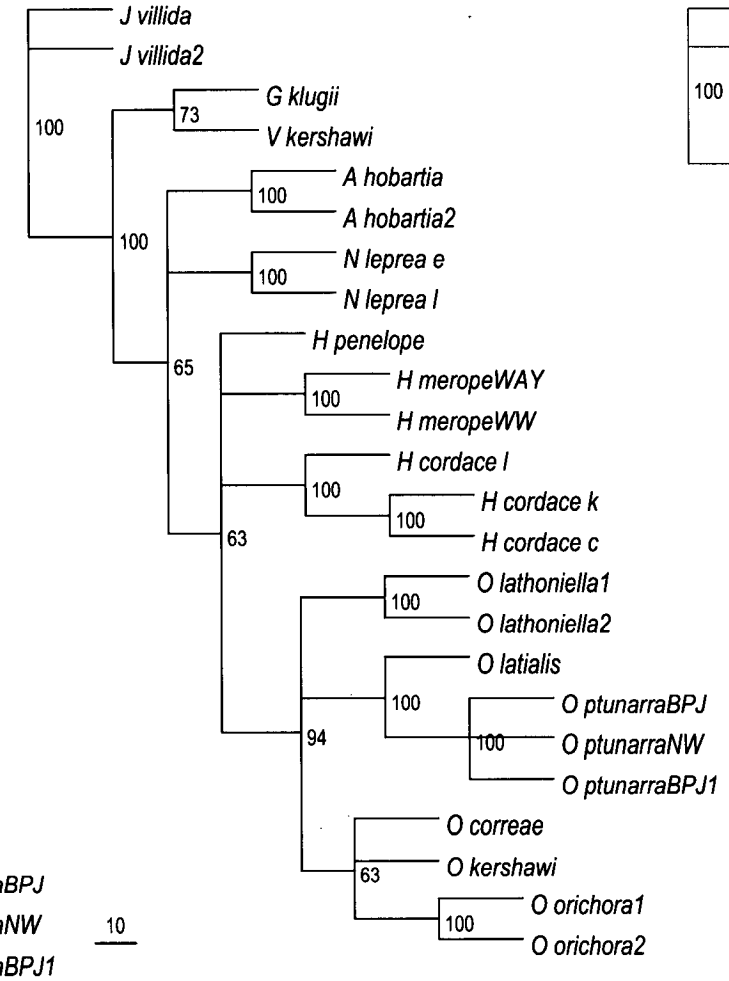

Figure A8.2 Bootstrap consensus of the minimum evolution tree (ME analysis) retrieved from CO1 sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 458, CI = 0.541, RI = 0.711).

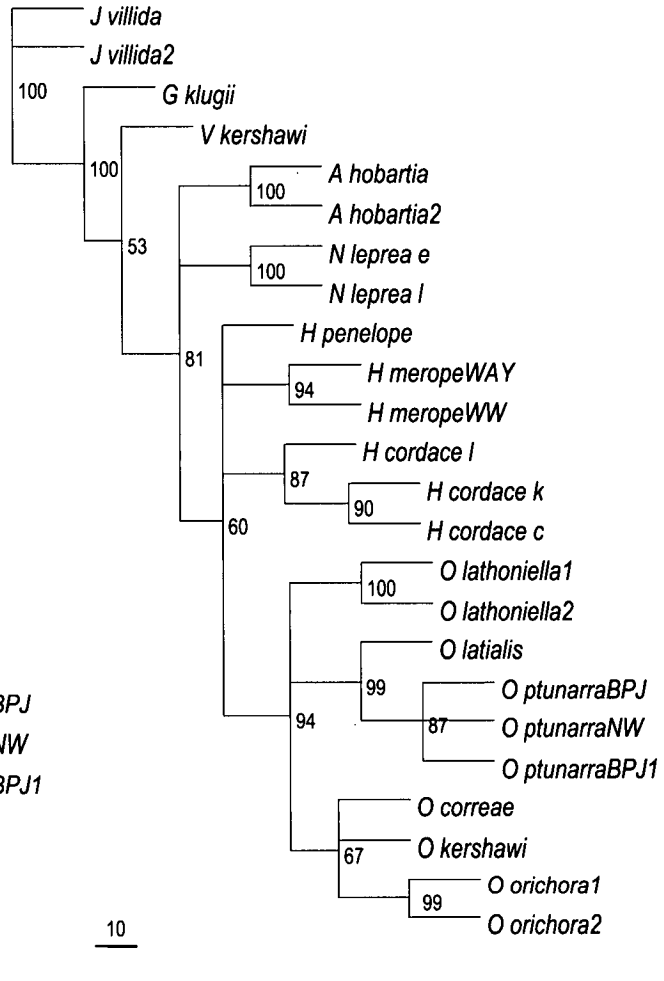

Figure A8.3 Maximum likelihood tree (ML analysis) retrieved from CO1 sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 458, CI = 0.541, RI = 0.711).

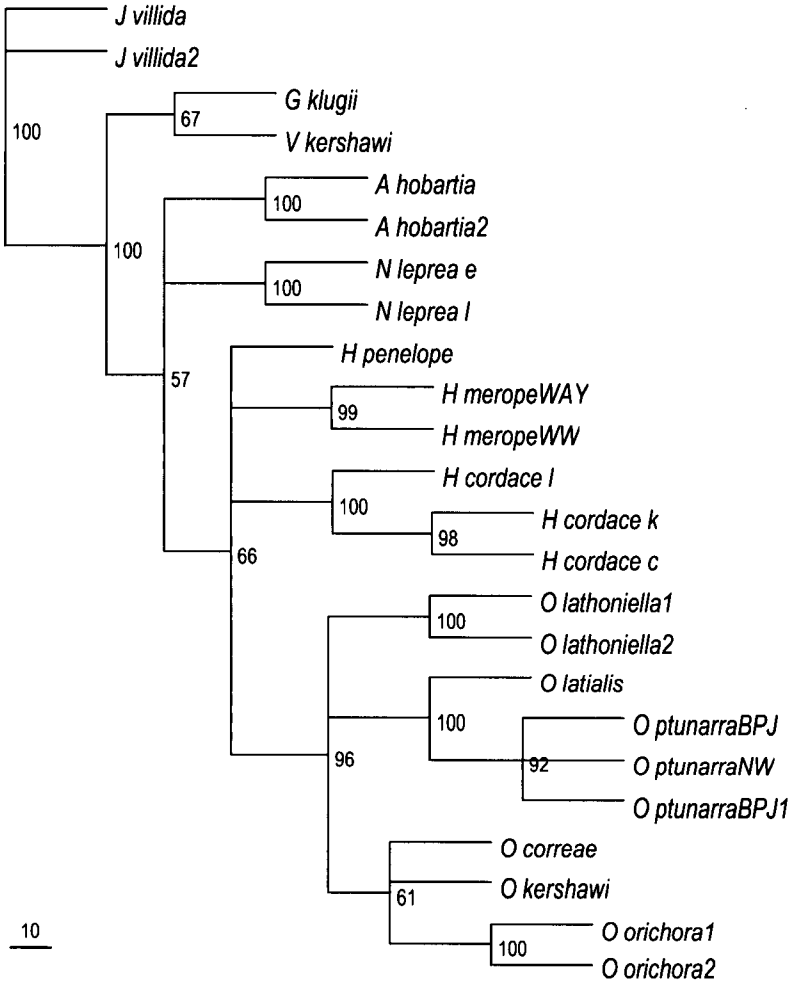

Figure A8.4 Bootstrap consensus tree resulting from the down weighting of third position nucleotide retrieved from CO1 sequence, unweighted analysis. Values above branches are bootstrap vales >50% (length 523, CI = 0.581, RI = 0.746).

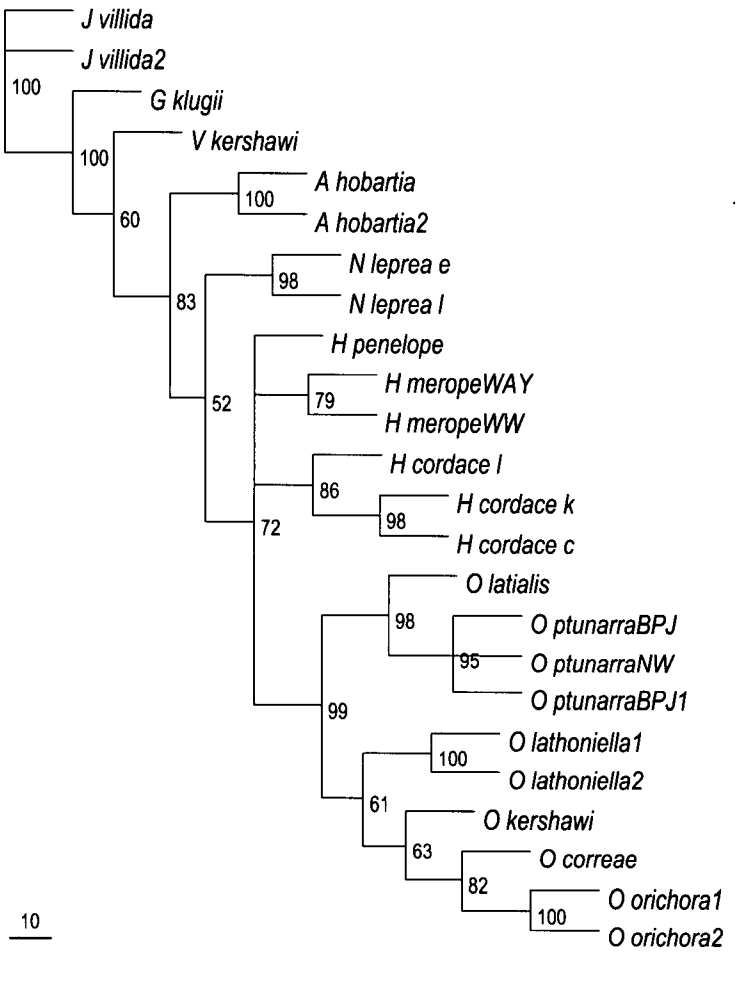

Figure A8.5 Bootstrap consensus tree resulting from analysis of the transition/transversion *ratio* retrieved from CO1 sequence, unweighted analysis. Values above branches are bootstrap vales >50% (length 2310, CI = 0.501, RI = 0.738).

EF-1α

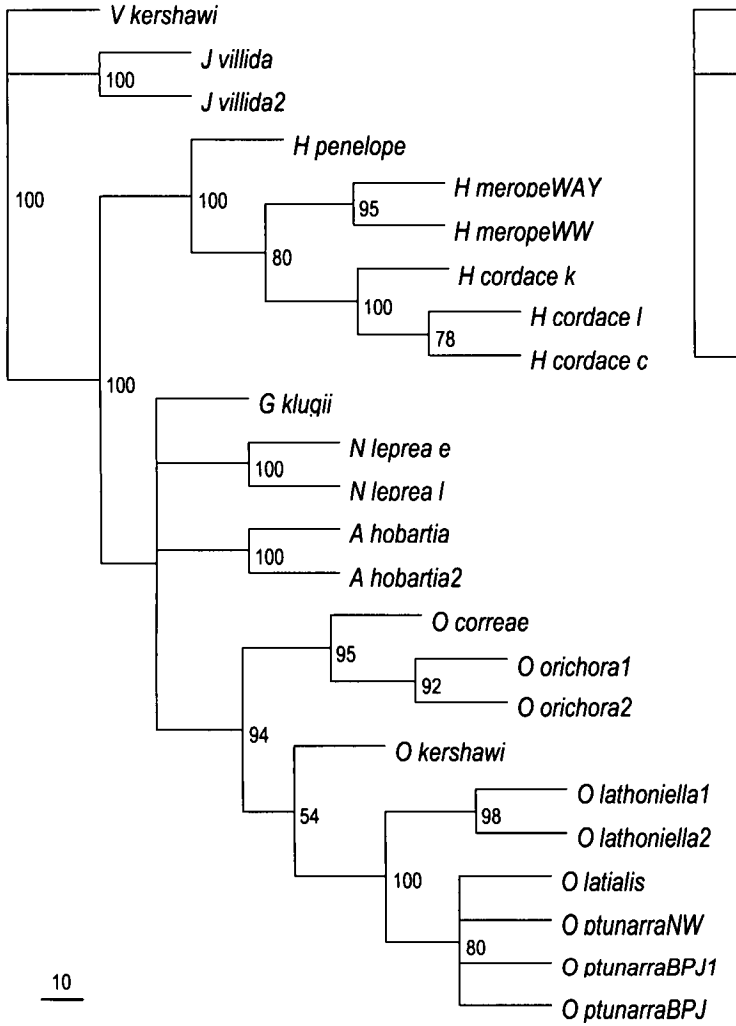

Figure A8.6 Bootstrap consensus of the most parsimonious tree (MP analysis) retrieved from EF-1α sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 442, CI = 0.658, RI = 0.826)

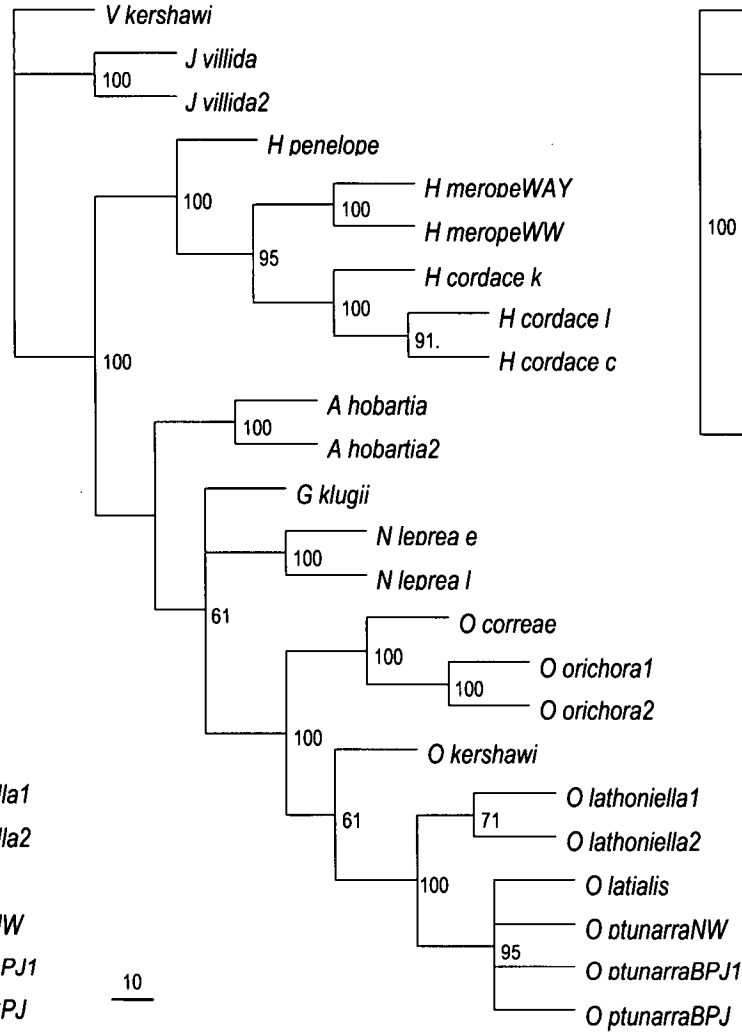

Figure A8.7 Bootstrap consensus of the minimum evolution tree (ME analysis) retrieved from EF-1α sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 443, CI = 0.657, RI = 0.825).

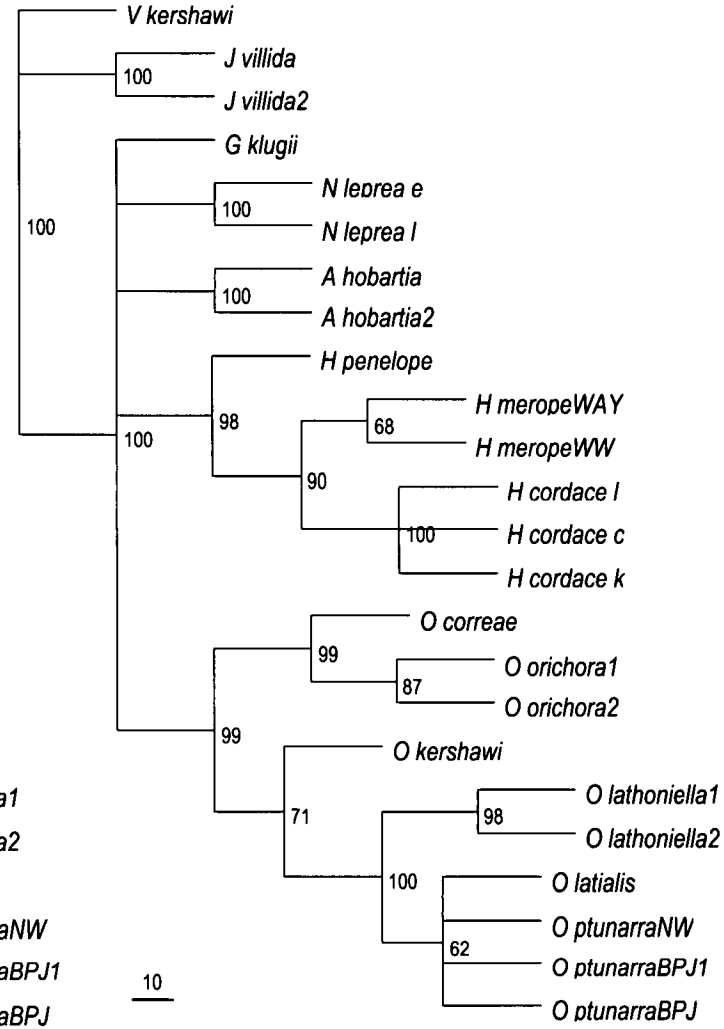

Figure A8.8 Maximum likelihood tree (ML analysis) retrieved from EF-1α sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 458, CI = 0.541, RI = 0.711).

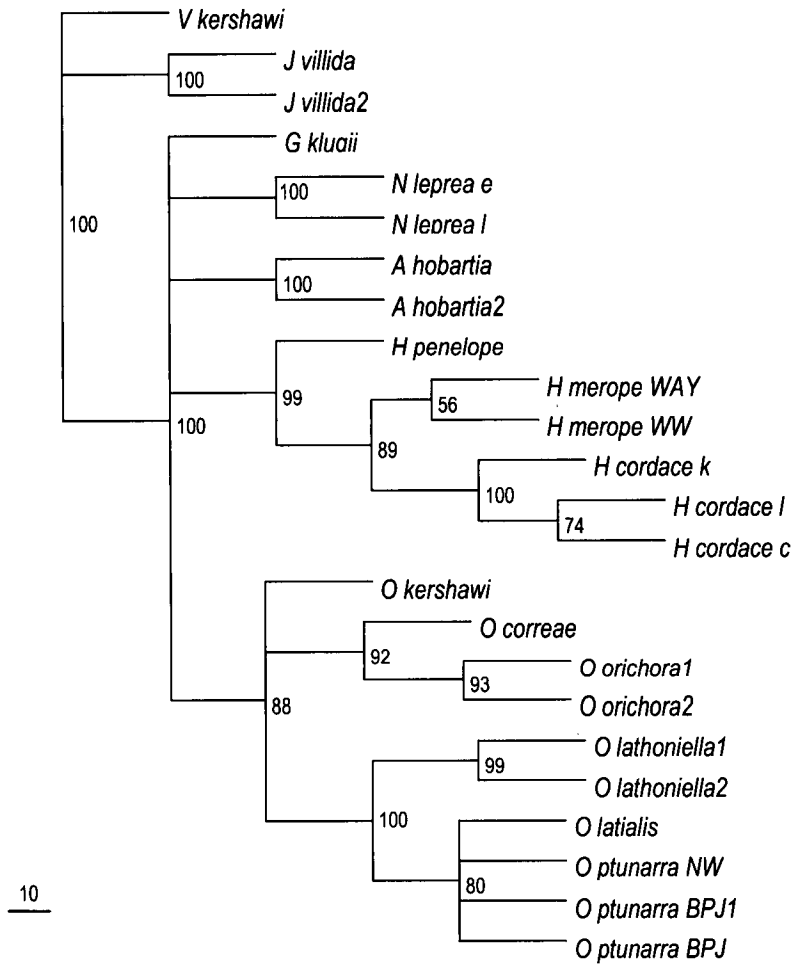

Figure A8.9 Bootstrap consensus tree resulting from the down weighting off third position nucleotide retrieved from EF-1α sequence, unweighted analysis. Values above branches are bootstrap vales >50% (length 594, CI = 0.631, RI = 0.794).

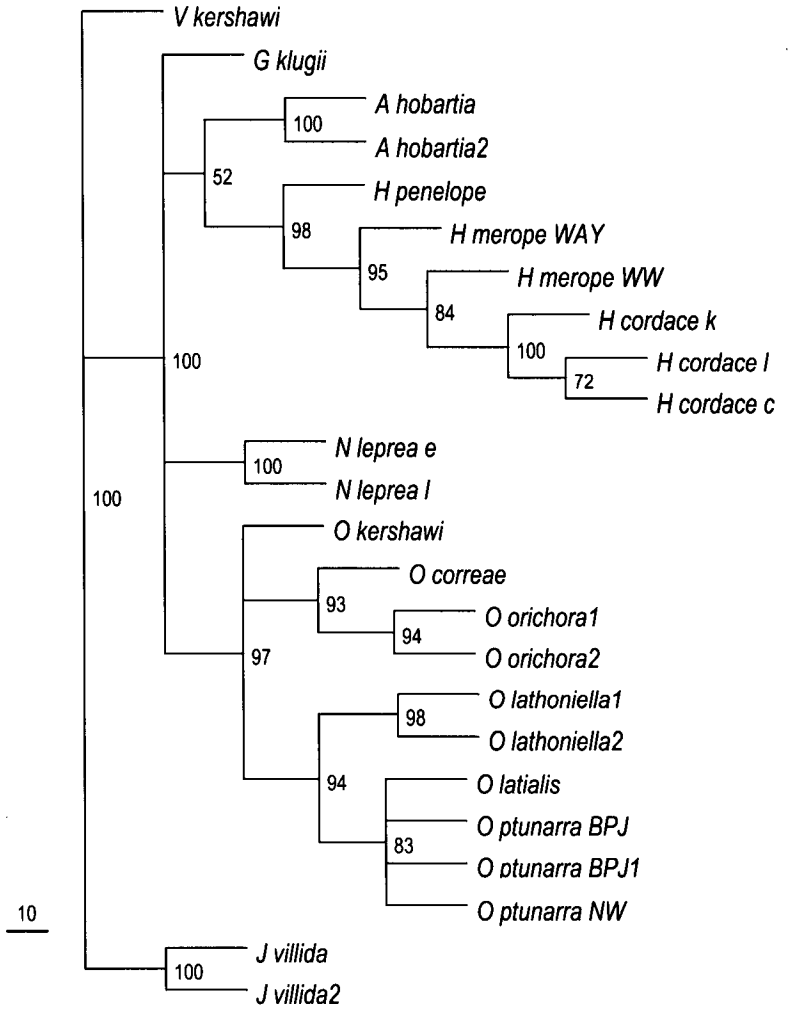

Figure A8.10 Bootstrap consensus tree resulting from analysis of the transition/transversion *ratio* retrieved from EF-1α sequence, unweighted analysis. Values above branches are bootstrap vales >50% (length 1849, CI = 0.688, RI = 0.834).

Wingless

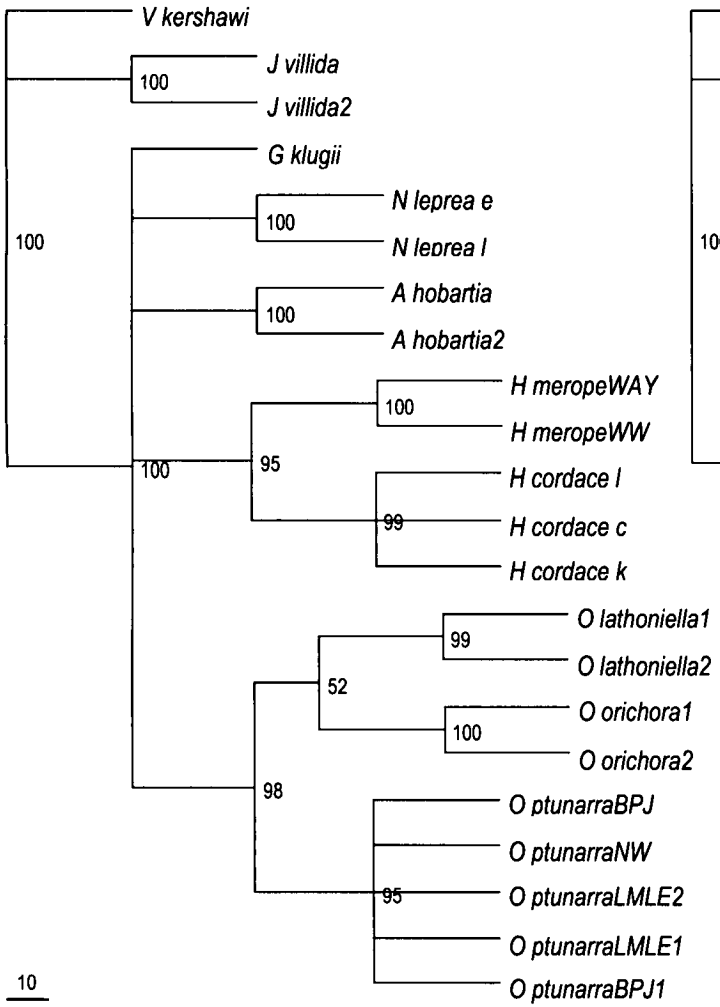

Figure A8.11 Bootstrap consensus of the most parsimonious tree (MP analysis) retrieved from wingless sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 196, CI = 0.766, RI = 0.883)

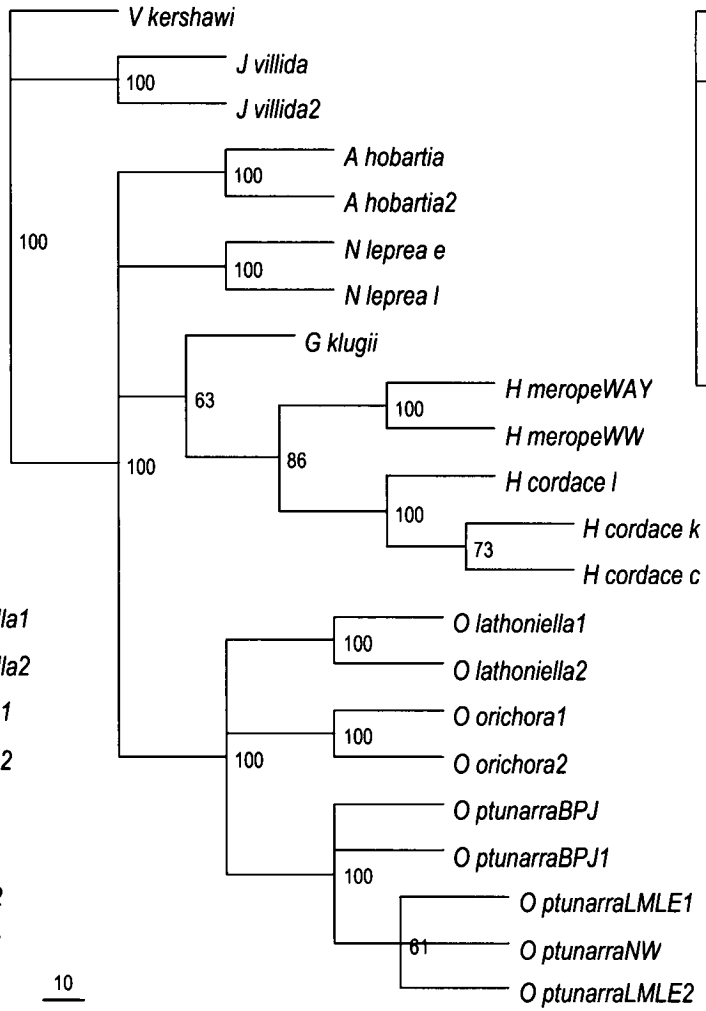

Figure A8.12 Bootstrap consensus of the minimum evolution tree (ME analysis) retrieved from wingless sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 196, CI = 0.766, RI = 0.883)

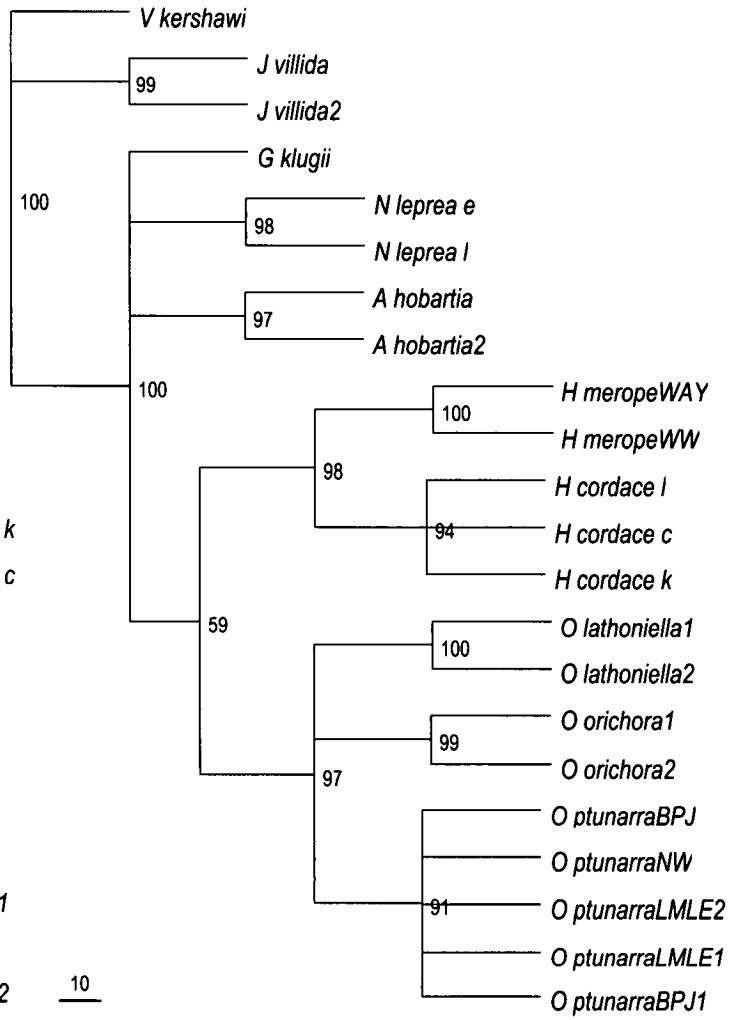

Figure A8.13 Maximum likelihood tree (ML analysis) retrieved from wingless sequence, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 196, CI = 0.766, RI = 0.883)

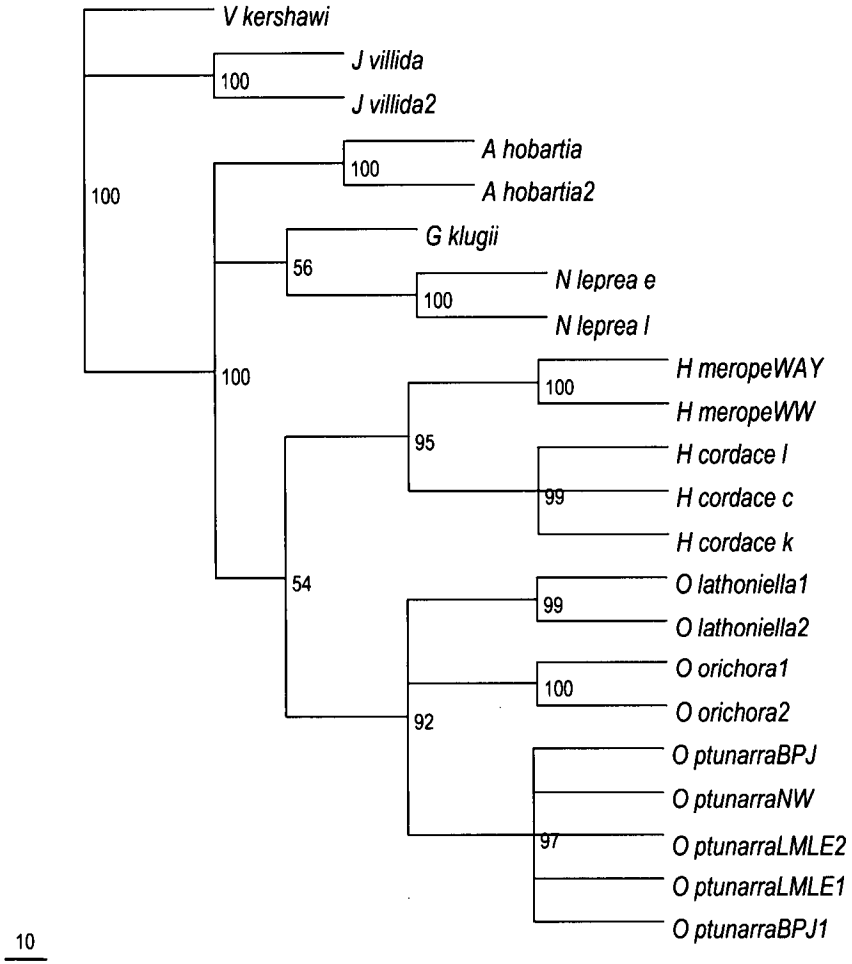

Figure A8.14 Bootstrap consensus tree resulting from the down weighting off third position nucleotide retrieved from wingless sequence, unweighted analysis. Values above branches are bootstrap vales >50% (length 389, CI = 0.740, RI = 0.870).

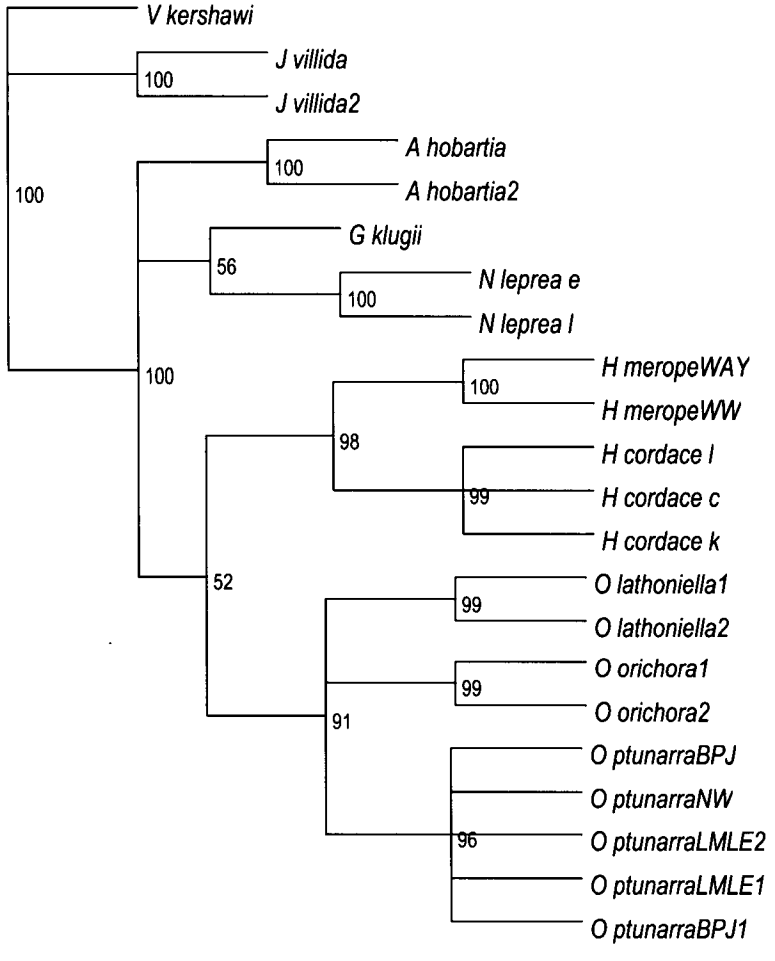

Figure A8.15 Bootstrap consensus tree resulting from analysis of the transition/transversion *ratio* retrieved from wingless sequence, unweighted analysis. Values above branches are bootstrap vales >50% (length 777, CI = 0.763, RI = 0.882).

Combined

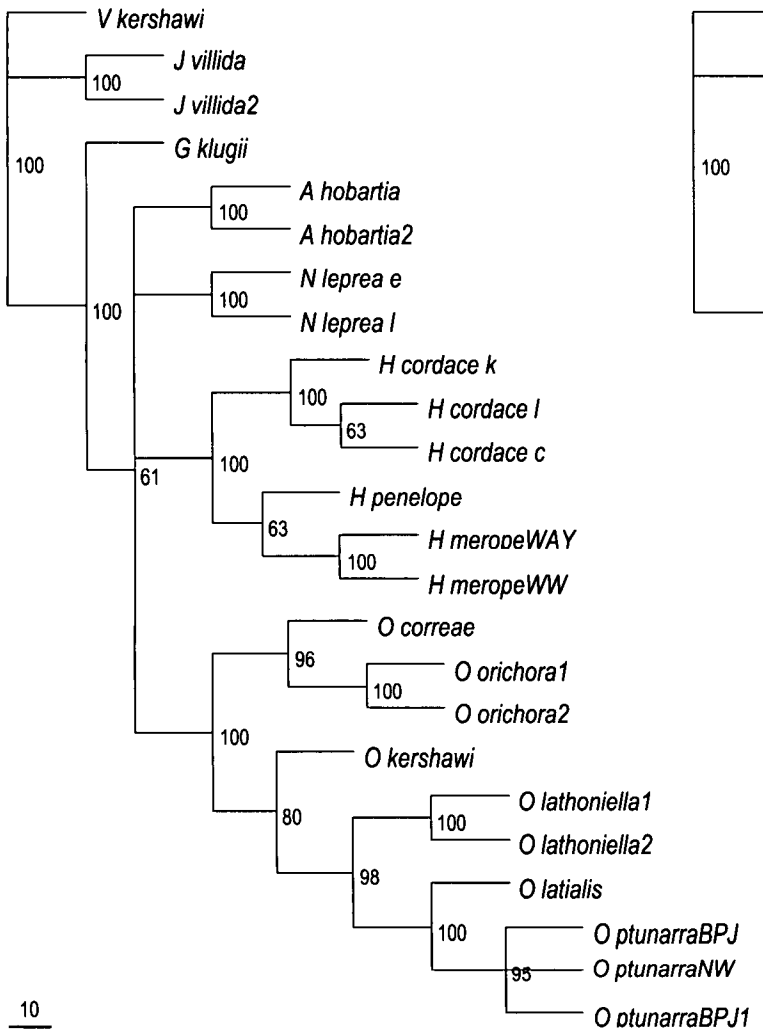

Figure A8.16 Bootstrap consensus of the most parsimonious tree (MP analysis) retrieved from combined sequences, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 1113, CI = 0.621, RI = 0.782)

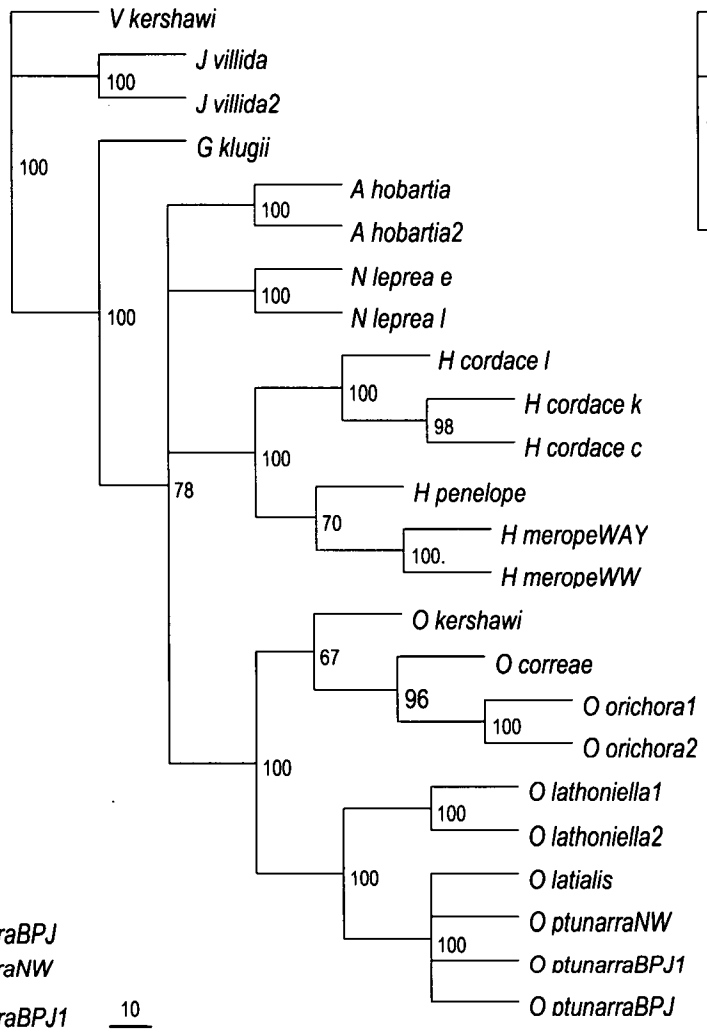

Figure A8.17 Bootstrap consensus of the minimum evolution tree (ME analysis) retrieved from combined sequences, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 1122, CI = 0.616, RI = 0.778)

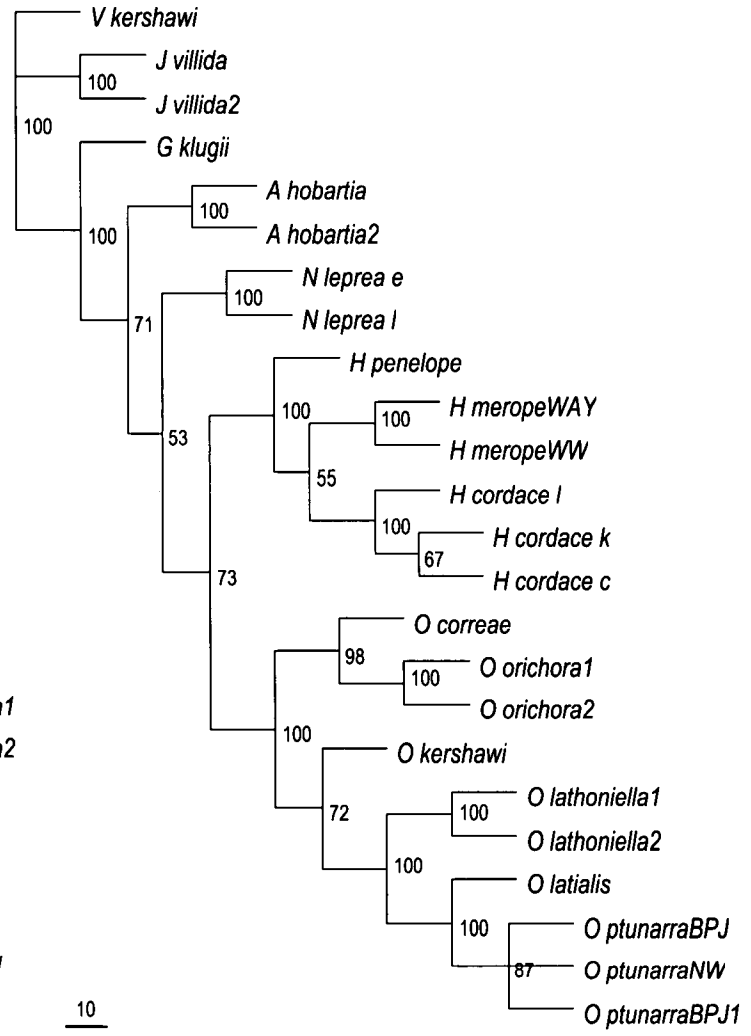

Figure A8.18 Maximum likelihood tree (ML analysis) retrieved from combined sequences, unweighted analysis.
Values above branches are bootstrap vales >50%
(Length 1113, CI = 0.621, RI = 0.782)

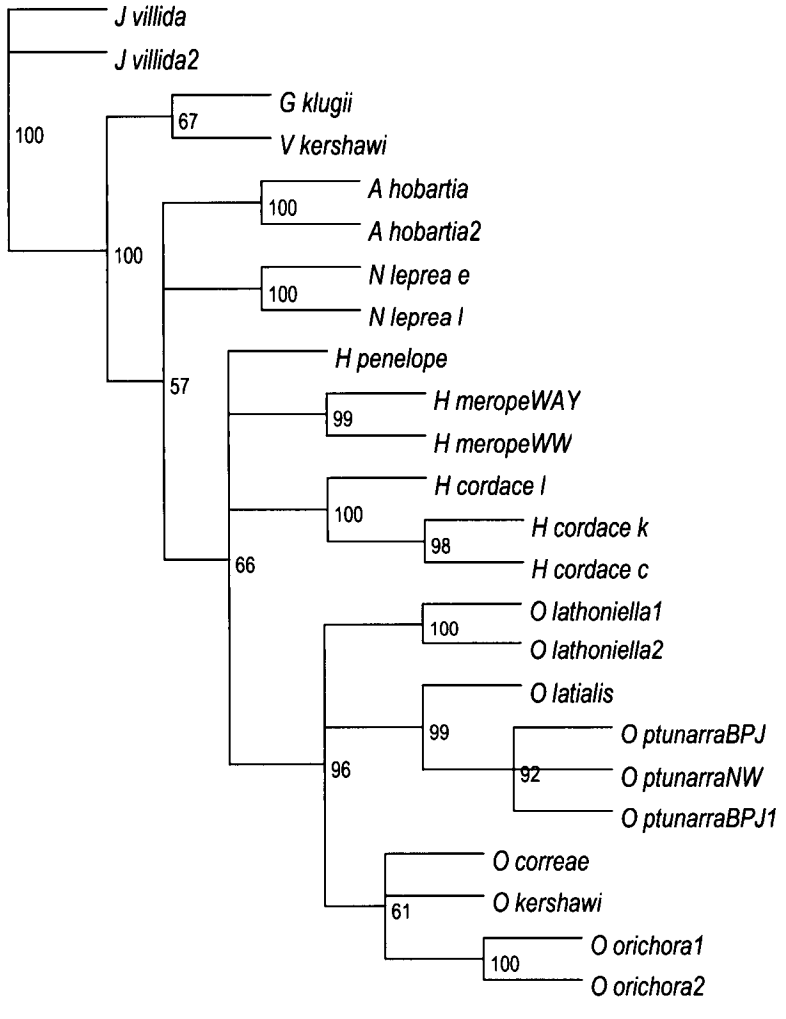

Figure A8.19 Bootstrap consensus tree resulting from the down weighting off third position nucleotide retrieved from combined sequences, unweighted analysis. Values above branches are bootstrap vales >50% (length 1521, CI = 0.620, RI = 0.779).

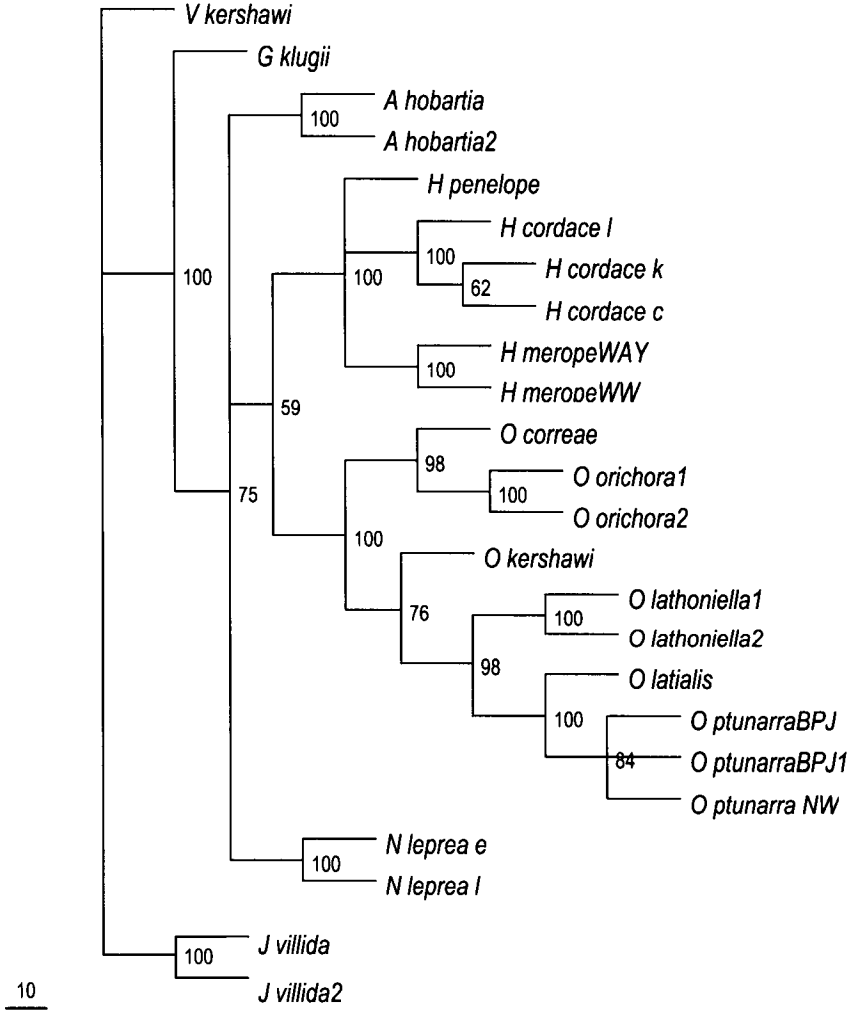

Figure A8.20 Bootstrap consensus tree resulting from analysis of the transition/transversion *ratio* retrieved from combined sequences, unweighted analysis. Values above branches are bootstrap vales >50% (length 5061, CI = 0.597, RI = 0.780).

Appendix 9 – O. ptunarra *population sequences*

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Bel2	TTAAATTTTAATTAAAATTAAAATTTCACCTAATAATTT-AATATTTA-T	Long6	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	ShR2	TTTAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T
Bel3	TTAAATTTTAATTAAAATTAAAATTTCACCTAATAATTT-AATATTTA-T	Long7	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	ShR3	TTTAATTTTAATTAAAT-TAAAATTTCACCTAATAATTG-AATATTTA-T
BPJ1	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	Long8	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	StPat1	TTTAATTTTAATTAAAT-TAAAATTTCACCTAATAATTG-AATATTTA-T
BPJ2	TTAGATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	LPLB1	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	StPat2	TTTAATTTTAATTAAAT-TAAAATTTCACCTAATAGTAG-AATATTTA-T
BPJ3	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	LPLB2	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	StPat3	TTTAATTTTAATTAAAT-TAAAATTTCACCTAATAATTG-AATATTTA-T
BPJ4	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	LPLB3	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	StPat4	TTTAATTTTAATTAAAT-TAAAATTTCACCTAATAATTG-AATATTTA-T
BTS1	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	LTC1	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	StPatME1	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTG-AATATTTA-T
BTS2	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	LTC2	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	StPatME2	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTG-AATATTTA-T
BTS3	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	LTC3	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	StPatME3	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTG-AATATTTA-T
BTS4	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	MH1	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	StPatME4	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTG-AATATTTA-T
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DM4	TTGTAATTTTATTAAGTTTAAAATTTCACCTGATAAGTT-AATATTTA-T	NB1	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	TT76_4	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T
Flag5	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	NB2	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	WSC1	TTAAAATTTTATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T
Flag6	TTAAATTTTTATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	NB3	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	WSC2	TTAAAATTTTATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T
Flag7	TTAAATTTTAATTAAATTTAAAATTTCACCTAATAATTT-AATATTTA-T	NB4	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T	Ola MtB1	TTAAATTTTAATTAAAATTAAAATTTCACCTAATAATTTTAATATTTAAT
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LC08	TGAAATTTTAATTAGAATTATAATTTCACCTAATGATTGGGATATTTA-G	PH2	TTAAATTTTAATTAAAGTTAAAATTTCACCTAATAATTT-AATATTTA-T		
LC09	TTTAATTTTAATTAGAATTAAAATTTCACCTAATGATTGTGATATTTA-G	PH3	TTAAATTTTAATTAAAGTTAAAATTTCACCTAATAATTT-AATATTTA-T		
LC10	TTTAATTTTAATTAGAATTAAAATTTCACCTAATAATTGTAATATTTA-G	PPS1 1	TTAATTTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T		
LCT1	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-GATATTTA-T	PPS1 2	TTAATTTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T		
LCT2	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-GATATTTA-T	PPS2 1	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T		
LCT3	TTAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-GATATTTA-T	PPS2 2	TAAAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T		
LCT4	TTTAATTTTAATTAAAT-TAAAATTGCACCTAATAATTG-GATATTTG-T	PPFE 1	TTTAATTTTAATTAAAT-TAAAATTTCACCTAATAATTT-AATATTTA-T		
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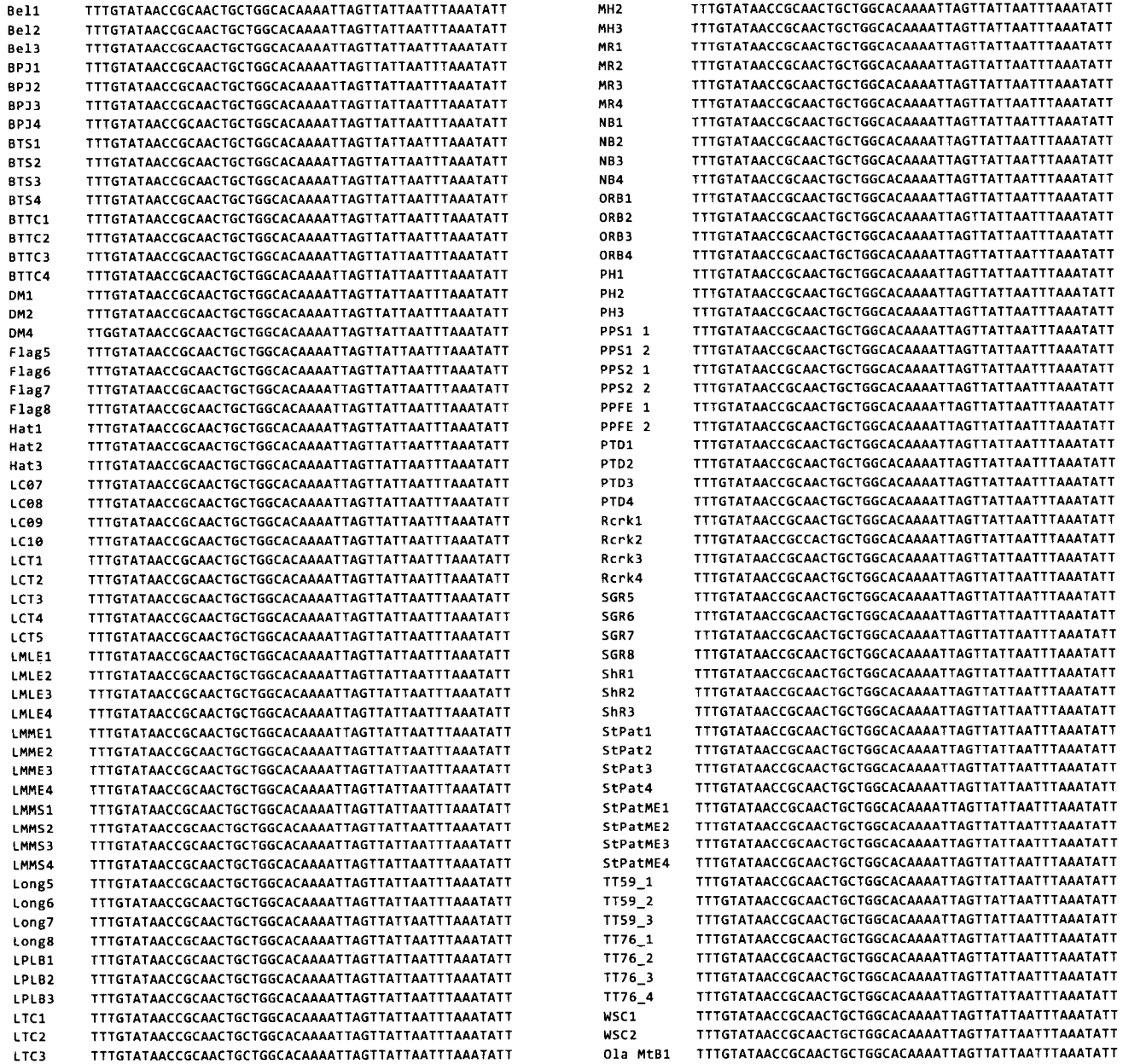
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Ola MtB1 ACTAAATCTTAATTTCTTAAATATTTAATTTTAATTACTATTAATTTTAA
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PPFE 2   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
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PTD2     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
PTD3     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
PTD4     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
Rcrk1    TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
Rcrk2    TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
Rcrk3    TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
Rcrk4    TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
SGR5     TTAATTATTATTAAAATAATTAAAATTCGATACTAAAATTT---ATATGT
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SGR7     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
SGR8     TTAATTATTATTAAAATAATTAAAATTCGATACTAAAATTT---ATATGT
ShR1     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
ShR2     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
ShR3     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
StPat1   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
StPat2   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
StPat3   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
StPat4   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
StPatME1 TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
StPatME2 TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
StPatME3 TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
StPatME4 TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
TT59_1   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
TT59_2   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
TT59_3   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
TT76_1   TTAATTTTTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
TT76_2   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
TT76_3   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
TT76_4   TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
WSC1     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
WSC2     TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTT---ATATGT
Ola MtB1 TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTTTATATATGG
Ola MtB2 TTAATTATTATTAAAATAATTAAAATTTAATACTAAAATTTTATATATGG
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Bel1     AAAATAAATTTATAATAAATTATTAAAAACACAAGTTTTTATTTATTTGC
Bel2     AAAATAAATTTATAATAAATTATTAAAAACACAAGTTTTTATTTATTTGC
Bel3     AAAATAAATTTATAATAAATTATTAAAAACACAAGTTTTTATTTATTTGC
BPJ1     AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
BPJ2     AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGC
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BTS1     AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
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Flag6    AAAATAAATTTATAATAAATTATTAAAAACACAAGTTTTTATTTATTTGC
Flag7    AAAATAAATTTATAATAAATTCATAAAAACATAAATTTTTATCTATTAGC
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LPLB2    AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
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PPFE 1   AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
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Rcrk1    AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
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SGR8     AAAATAAATTTATAATAAATTCATAAAAACATAAATTTTTATCTATTAGC
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StPatME4 AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
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TT59_2   AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
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TT76_4   AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
WSC1     AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
WSC2     AAAATAAATTTACAATAAATTATTAAAAACACAAGTTTTTATTTATTTGT
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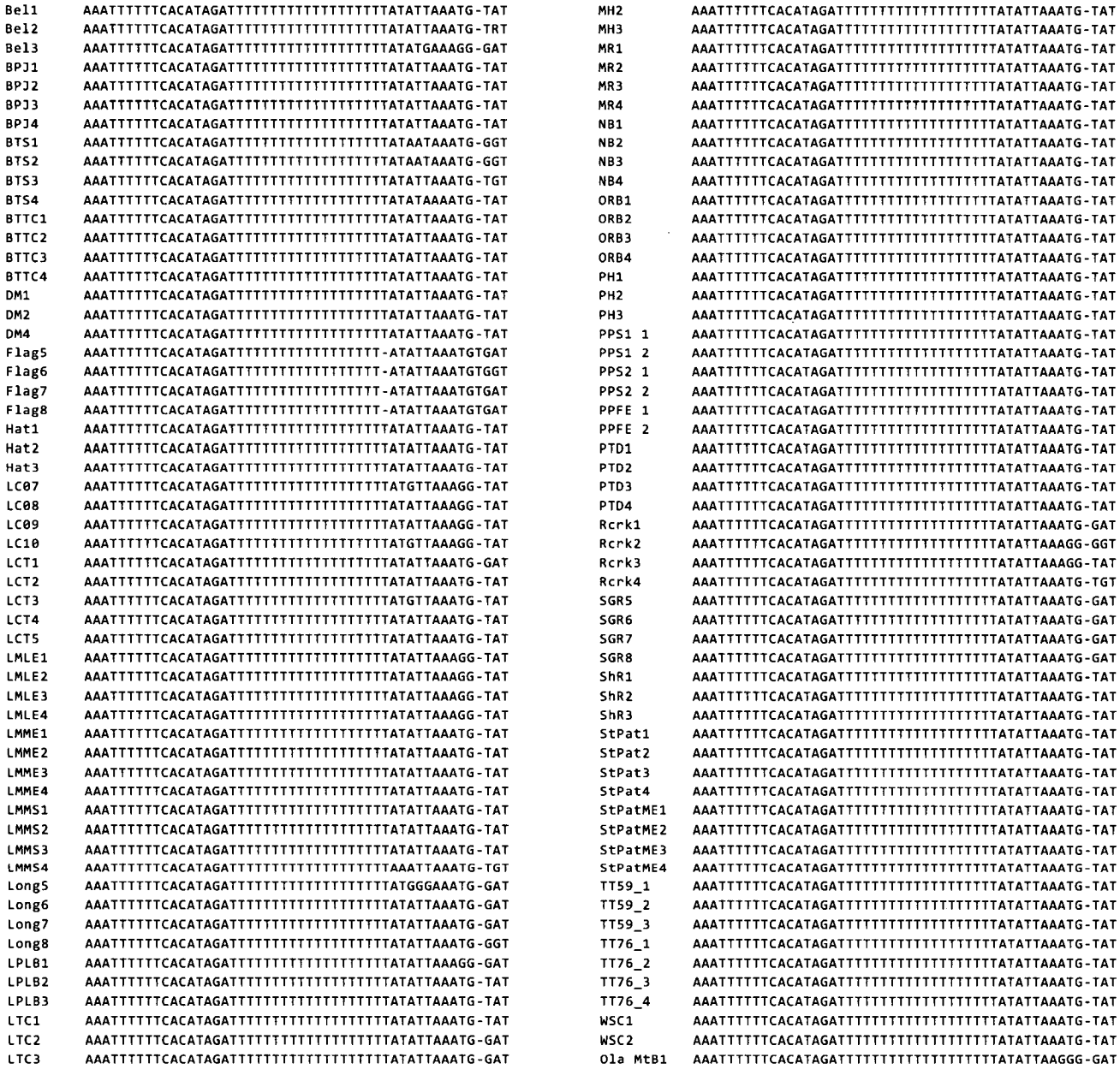
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Bel3 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATGAAAGG-GAT
BPJ1 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TAT
BPJ2 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TAT
BPJ3 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TAT
BPJ4 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TAT
BTS1 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATAATAAATG-GGT
BTS2 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATAATAAATG-GGT
BTS3 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TGT
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DM1 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TAT
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DM4 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TAT
Flag5 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTT-ATATTAAATGTGAT
Flag6 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTT-ATATTAAATGTGGT
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Flag8 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTT-ATATTAAATGTGAT
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LC07 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATGTTAAAGG-TAT
LC08 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAAGG-TAT
LC09 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAAGG-TAT
LC10 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATGTTAAAGG-TAT
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LMMS4 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTAAATTAAATG-TGT
Long5 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATGGGAAATG-GAT
Long6 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-GAT
Long7 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-GAT
Long8 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-GGT
LPLB1 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAAGG-GAT
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LTC1 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TAT
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LTC3 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-GAT
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WSC2 AAATTTTTTCACATAGATTTTTTTTTTTTTTTTTTTATATTAAATG-TAT
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BTTC2    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
BTTC3    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
BTTC4    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
DM1      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
DM2      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
DM4      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Flag5    AAAAGAAATTAATAAATTTTTATTATTTTCTCTCACTTTTTTTCAAAATA
Flag6    AATAGAAATTAATAAATTTTTATTATTTTCTCTCACTTTTTTTCAAAATA
Flag7    AATAGAAATTAATAAATTTTTATTATTTTCTCTCACTTTTTTTCAAAATA
Flag8    AATAGAAATTAATAAATTTTTATTATTTTCTCTCACTTTTTTTCAAAATA
Hat1     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Hat2     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Hat3     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LC07     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LC08     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LC09     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LC10     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LCT1     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCNAAATA
LCT2     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCAAAATA
LCT3     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LCT4     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LCT5     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCNNAATA
LMLE1    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LMLE2    AAGAGAAATTAATAAATTTTTATTATTTTCTCTCATTCTCTTTCATAATA
LMLE3    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LMLE4    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
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LMME2    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LMME3    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LMME4    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
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LMMS2    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LMMS3    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LMMS4    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Long5    AATAGAAATTAATAAATTTTTATTATTTTCTCTCCTTTTTTTTCAAAATA
Long6    AATAGAAATTAATAAATTTTTATTATTTTCTCTCCTTTTTTTTCATAATA
Long7    AATAGAAATTAATAAATTTTTATTATTTTCTCTCCTTTTTTTTCATAATA
Long8    AAAAGAAATTAATAAATTTTTATTATTTTCTCTCCTTTTTTTTCANAATA
LPLB1    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LPLB2    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LPLB3    AATAGAAATTAATAAATTTTTATTATTTTCTTTCATTTTTTTTCATAATA
LTC1     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
LTC2     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCAAAATA
LTC3     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCAAAATA
MH1      AATAGAAATTAATAAATTTTTATTACTTTCTCTCATTTTTTTTCATAATA
MH2      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
MH3      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
MR1      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
MR2      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
MR3      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
MR4      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
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NB2      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
NB3      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
NB4      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
ORB1     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
ORB2     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
ORB3     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
ORB4     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PH1      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PH2      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PH3      AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PPS1 1   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PPS1 2   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PPS2 1   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PPS2 2   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PPFE 1   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PPFE 2   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PTD1     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PTD2     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PTD3     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
PTD4     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Rcrk1    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Rcrk2    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Rcrk3    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Rcrk4    AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
SGR5     AATAGAAATTAATAAATTTTTATTATTTTCTCTCCNTTTTTTTCATAATA
SGR6     AATAGAAATTAATAAATTTTTATTATTTTCTCTCCNTTTTTTTCATAATA
SGR7     AATAGAAATTAATAAATTTTTATTATTTTCTCTCCNTTTTTTTCATAATA
SGR8     AATAGAAATTAATAAATTTTTATTATTTTCTCTCCNTTTTTTTCATAATA
ShR1     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
ShR2     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
ShR3     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
StPat1   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
StPat2   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
StPat3   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
StPat4   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
StPatME1 AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
StPatME2 AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
StPatME3 AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
StPatME4 AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
TT59_1   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
TT59_2   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
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TT76_1   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
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TT76_3   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
TT76_4   AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
WSC1     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
WSC2     AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Ola MtB1 AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
Ola MtB2 AATAGAAATTAATAAATTTTTATTATTTTCTCTCATTTTTTTTCATAATA
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Bel1     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
Bel2     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
Bel3     TCCATATTAAAAATTAATTTAATGATAATCCGAAGACAGTTCATTTTAAA
BPJ1     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
BPJ2     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
BPJ3     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCGTTTTAAA
BPJ4     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
BTS1     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
BTS2     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
BTS3     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
BTS4     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
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BTTC3    TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
BTTC4    TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
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DM2      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
DM4      TCCATATTAAAAATTAATTTAAGGATAATCCGAATACAGTTCATTTTAAA
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Flag6    TCCNNATTAAAAATTAATTTARKGANAATCCGAGTACAGTCCATTTTAAA
Flag7    TCCNNATTAAAAATTAATCTARTGANAATCCGAAAACAGTCCATTTTAAA
Flag8    TCCNNATTAAAAATTAATTTARTGANAATCCGAGTACAGTCCATTTTAAA
Hat1     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
Hat2     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
Hat3     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
LC07     TCCATATTAAAAATTAATTTAAGGATAATCCGAATACAGTTCATTTTAAA
LC08     TCCATATTAAAAATTAATTTAAGGATAATCCGAATACAGTTCATTTTAAA
LC09     TCCATATTAAAAATTAATTTAAGGATAATCCGAATACAGTTCATTTTAAA
LC10     TCCATATTAAAAATTAATTTAAGGATAATCCGAATACAGTTCATTTTAAA
LCT1     TCCNTATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
LCT2     TCCNTATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
LCT3     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
LCT4     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
LCT5     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
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LMLE2    TCCATATTAAAAATTAATTTAATGATAATCCGAATCCAGTTCATTTTAAA
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LMMS3    TCCNNATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
LMMS4    TCCATATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
Long5    TCCNNATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
Long6    TCCCTATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
Long7    TCCCNATTAAAAATTAATTTAATGATAATCCGAATACAGTCCATTTTAAA
Long8    TCCCCATTAAAAATTAATTTAATGANAATCCGAANACAGTCCATTTTAAA
LPLB1    TCCATATTAAAAGTTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
LPLB2    TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
LPLB3    TTCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
LTC1     TCCATATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
LTC2     TCCATATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
LTC3     TCCATATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
MH1      TCCATATTAAAAATTAATCTAATGATAATCCGAATACAGTTCATTTTAAA
MH2      TTTATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
MH3      TCCATATTAAAAATTAATCTAATGATAATCCGAATACAGTTCATTTTAAA
MR1      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
MR2      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
MR3      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
MR4      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
NB1      TCCATATTAAAAATTAATCTAATGATAATCCGAATACAGTTCATTTTAAA
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NB3      TCCATATTAAAAATTAATCTAATGATAATCCGAATACAGTTCATTTTAAA
NB4      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
ORB1     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
ORB2     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
ORB3     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
ORB4     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PH1      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PH2      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PH3      TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PPS1 1   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PPS1 2   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PPS2 1   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PPS2 2   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PPFE 1   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PPFE 2   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PTD1     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PTD2     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PTD3     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
PTD4     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCGTTTTAAA
Rcrk1    TCCCNATTAAAAATTAATTTAATGANAATCCGAGTACAGTCCATTTTAAA
Rcrk2    TCCCNATTAAAAATTAATTTAATGANAATCCGAGTACAGTCCATTTTAAA
Rcrk3    TCCCNATTAAAAATTAATTTAATGANAATCCGAATACAGTCCGTTTTAAA
Rcrk4    TCCCNATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
SGR5     TCCANATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
SGR6     TCCNNATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
SGR7     TCCNNATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
SGR8     TCCNNATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
ShR1     TCCNNATTAAAAATTAATTTAATGTNAATCCGAATACAGTCCATTTTAAA
ShR2     TCCATATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
ShR3     TCCANATTAAAAATTAATTTAATGANAATCCGAATACAGTCCATTTTAAA
StPat1   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
StPat2   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
StPat3   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
StPat4   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
StPatME1 TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
StPatME2 TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
StPatME3 TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
StPatME4 TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
TT59_1   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
TT59_2   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
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TT76_1   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
TT76_2   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
TT76_3   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
TT76_4   TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
WSC1     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
WSC2     TCCATATTAAAAATTAATTTAATGATAATCCGAATACAGTTCATTTTAAA
Ola MtB1 TCCATATTAAAAATTAATTTAGGGGTAATCCGAATACAGTTCATTTTAAA
Ola MtB2 TCCATATTAAAAATTAATTTAGGGGTAATCCGAATACAGTTCATTTTAAA
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Bel1     TAAGAAATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
Bel2     TAAGAGATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
Bel3     TAAGAAATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
BPJ1     TAAGAAATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
BPJ2     TAAGAAATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
BPJ3     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
BPJ4     TAAGAAATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
BTS1     TAAGAAATATTATATCCATAATATTAATTC-CCCCCAAAATTAATTAATT
BTS2     TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
BTS3     TAAGAGATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
BTS4     TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
BTTC1    TAAGAAATATTATATCTGTGATATTAATTC-CCCCAAAAATTAATTAATT
BTTC2    TAAGAAATATTATATCTATAATATTAATTC-CCCCNGAAATTTATTAATT
BTTC3    TAAGAAATATTATATCTATGATATTAATTC-CCCCAAAAATTAATTAATT
BTTC4    TAAGAAATATTATATCTATAATATTAATTC-CCCCAAAAATTAATTAATT
DM1      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
DM2      TAAGAGATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
DM4      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
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Flag6    TAAGARATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Flag7    TAAGARATATTATATCTATAATATTAATTC-CCCCCAAAATTTATTAATT
Flag8    TAAGARATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Hat1     TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
Hat2     TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
Hat3     TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
LC07     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
LC08     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
LC09     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
LC10     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
LCT1     TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
LCT2     TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
LCT3     TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
LCT4     TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
LCT5     TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
LMLE1    TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
LMLE2    TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
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LMMS1    TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTTATTAATT
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LMMS3    TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
LMMS4    TAAGARATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
Long5    TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Long6    TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Long7    TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Long8    TAAGAAATATTATATCTATAATATTAANTC-CCCCCAAAATTAATTAATT
LPLB1    TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
LPLB2    TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
LPLB3    TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTTATTAATT
LTC1     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
LTC2     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
LTC3     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
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MH2      TAAGAAATATTATATCTATAATATTAATTC-CCCCCGAAATTTATTAATT
MH3      TAAGAAATATTATATCTATAATATTAATTC-CCCCCGAAATTTATTAATT
MR1      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
MR2      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
MR3      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
MR4      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
NB1      TAAGAAATATTATATCTATAATATTAATTC-ACCCCGAAATTTATTAATT
NB2      TAAGAAATATTATATCTATAATATTAATTC-ACCCCGAAATTTATTAATT
NB3      TAAGAAATATTATATCTATAATATTAATTC-ACCCCGAAATTTATTAATT
NB4      TAAGAAATATTATATCTATAATATTAATTC-ACCCCGAAATTTATTAATT
ORB1     TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
ORB2     TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
ORB3     TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
ORB4     TAAGAGATATTATATCTATAATATTAATTC-ACCCCNAAATTAATTAATT
PH1      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
PH2      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
PH3      TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
PPS1 1   TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
PPS1 2   TAAGAAATATTATATCTATAATATTAATTC-ACCCNAAAATTAATTAATT
PPS2 1   TAAGAAATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
PPS2 2   TAAGAAATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
PPFE 1   TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
PPFE 2   TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
PTD1     TAAGAAATATTATATCTATAATATTAATTC-ACCCAAAAATTAATTAATT
PTD2     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
PTD3     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
PTD4     TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Rcrk1    TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Rcrk2    TAAGARATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Rcrk3    TAAGAGATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
Rcrk4    TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
SGR5     TAAGAAATATTATATCTATAATATTAATTC-CCCCSGAAATTTATTAATT
SGR6     TAAGAAATATTATATCTATAATATTAATTC-CCCCSGAAATTAATTAATT
SGR7     TAAGAAATATTATATCTATAATATTAATTC-CCCCSGAAATTAATTAATT
SGR8     TAAGAAATATTATATCTATAATATTAATTC-CCCCSGAAATTTATTAATT
ShR1     TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
ShR2     TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
ShR3     TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
StPat1   TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
StPat2   TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
StPat3   TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
StPat4   TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
StPatME1 TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
StPatME2 TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
StPatME3 TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
StPatME4 TAAGAAATATTATATCTATAATATTAATTC-CCCCNAAAATTAATTAATT
TT59_1   TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
TT59_2   TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
TT59_3   TAAGAAATATTATATCTATAATATTAATTC-CCCCCAAAATTAATTAATT
TT76_1   TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
TT76_2   TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
TT76_3   TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
TT76_4   TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
WSC1     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
WSC2     TAAGAAATATTATATCTATAATATTAATTC-ACCCCAAAATTAATTAATT
Ola MtB1 TAAGAAATATTATATCTATAATATTAATTCCACCCAAAAATTAATTAATT
Ola MtB2 TAAGAAATATTATATCTATAATATTAATTCCACCCAAAAATTAATTAATT
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Bel1      ATTAATATATTAATATATTAAATTATTTATATTTAAATATAATTAAATAA
Bel2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Bel3      ATTAATATATTAATATATTAAACTATTTATATATAAATATAATTAAATAA
BPJ1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BPJ2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BPJ3      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BPJ4      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BTS1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BTS2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BTS3      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BTS4      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BTTC1     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BTTC2     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
BTTC3     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
BTTC4     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
DM1       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
DM2       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
DM4       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Flag5     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Flag6     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Flag7     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
Flag8     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Hat1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Hat2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Hat3      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LC07      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LC08      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LC09      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LC10      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LCT1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LCT2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LCT3      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LCT4      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LCT5      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMLE1     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMLE2     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMLE3     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMLE4     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMME1     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMME2     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMME3     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMME4     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMMS1     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMMS2     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMMS3     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LMMS4     ATTAATATATTAATATTTTAAATTATTTATATATAAATATAATTAAATAA
Long5     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Long6     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Long7     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Long8     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LPLB1     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LPLB2     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LPLB3     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LTC1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LTC2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
LTC3      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
MH1       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
MH2       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
MH3       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
MR1       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
MR2       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
MR3       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
MR4       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
NB1       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
NB2       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
NB3       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
NB4       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
ORB1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
ORB2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
ORB3      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
ORB4      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PH1       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PH2       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PH3       ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PPS1 1    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PPS1 2    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PPS2 1    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PPS2 2    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PPFE 1    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PPFE 2    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PTD1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PTD2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PTD3      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
PTD4      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Rcrk1     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Rcrk2     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Rcrk3     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Rcrk4     ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
SGR5      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
SGR6      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
SGR7      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
SGR8      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAT
ShR1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
ShR2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
ShR3      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
StPat1    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
StPat2    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
StPat3    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
StPat4    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
StPatME1  ATTAATATATTAATACATTAAATTATTTATATATAAATATAATTAAATAA
StPatME2  ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
StPatME3  ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
StPatME4  ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
TT59_1    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
TT59_2    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
TT59_3    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
TT76_1    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
TT76_2    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
TT76_3    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
TT76_4    ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
WSC1      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
WSC2      ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Ola MtB1  ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
Ola MtB2  ATTAATATATTAATATATTAAATTATTTATATATAAATATAATTAAATAA
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Bel1     TAAATTAAATATTTAATATATAATGTNTAA-AATAATAATAAATTAAA--
Bel2     TAAATTAAATATTTAATATATAATGTGTAA-AATAATAATAAATTAAA--
Bel3     TAAATTAAATATTTAATATATAATGTGTAA-AATAATAATAAATTACA--
BPJ1     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BPJ2     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BPJ3     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BPJ4     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BTS1     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BTS2     TAAATTAAATATTTAATATACAATGTGTAA-AATAATAATAAATTAAA--
BTS3     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BTS4     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BTTC1    TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BTTC2    TATATTAAATATTTAATATTTAATGTTTAA-ATTAATAATAAATTAAA--
BTTC3    TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
BTTC4    TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
DM1      TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
DM2      TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
DM4      TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
Flag5    TAAATTAAATATTTAATATATAATGTNTAA-AATAATAATAAATTAAA--
Flag6    TAAATTAAATATTTAATATATAATGTGTAA-AATAATAATAAATTAAA--
Flag7    TATATTAAATATTTAATATTTAATGTKTAA-ATTAATAATAAATTAAA--
Flag8    TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
Hat1     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
Hat2     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
Hat3     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
LC07     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LC08     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
LC09     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
LC10     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LCT1     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LCT2     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LCT3     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LCT4     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LCT5     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LMLE1    TAAATTAAATATTTAATATACAATGTTTAA-AGTAATAATAAATTAAA--
LMLE2    TAAATTAAATATTTAATATACAAGGTTTAA-AATAATAATAAATTAAA--
LMLE3    TAAATTAAATATTTAATATACAAKGTTTAA-AATAATAATAAATTAAA--
LMLE4    TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LMME1    TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
LMME2    TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
LMME3    TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
LMME4    TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
LMMS1    TATATTAAATATTTAATATTTAATGTTTAA-AATAATAATAAATTAAA--
LMMS2    TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
LMMS3    TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LMMS4    TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
Long5    TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
Long6    TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
Long7    TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
Long8    TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAATTTAAA--
LPLB1    TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
LPLB2    TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
LPLB3    TATATTAAATATTTAATATTTAATGTTTAA-AATAATAATAAATTAAA--
LTC1     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LTC2     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
LTC3     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
MH1      TATATTAAATATTTAATATTTAATGTNTAATATTAATAATAAATTAAA--
MH2      TATATTAAATATTTAATATTTAATGTNTAATATTAATAATAAATTAAA--
MH3      TATATTAAATATTTAATATTTAATGTNTAATATTAATAATAAATTAAA--
MR1      TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
MR2      TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
MR3      TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
MR4      TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
NB1      TATATTAAATATTTAATATTTAATGTTTAATATTAATAATAAATTAAA--
NB2      TATATTAAATATTTAATATTTAATATTTAATATTAATAATAAATTAAA--
NB3      TATATTAAATATTTAATATTTAATGTTTAATATTAATAATAAATTAAA--
NB4      TATATTAAATATTTAATATTTAATGTTTAATATTAATAATAAATTAAA--
ORB1     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
ORB2     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
ORB3     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
ORB4     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
PH1      TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
PH2      TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
PH3      TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
PPS1 1   TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
PPS1 2   TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
PPS2 1   TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
PPS2 2   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
PPFE 1   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
PPFE 2   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
PTD1     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
PTD2     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
PTD3     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
PTD4     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
Rcrk1    TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
Rcrk2    TAAATTAAATATTTAATATACACGGTTTAA-AATAATAATAAATTAAA--
Rcrk3    TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
Rcrk4    TAAATTAAATATTTAATATACAGGGTTTAA-AATAATAATAAATTAAA--
SGR5     TATATTAAATATTTAATATTTAATGTTTAA-ATTAATAATAAATTAAA--
SGR6     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
SGR7     TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
SGR8     TATATTAAATATTTAATATTTAATGTTTAA-ATTAATAATAAATTAAA--
ShR1     TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
ShR2     TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
ShR3     TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
StPat1   TAAATTAAATATTTAATATATAATGTNTAA-AATAATAATAAATTAAA--
StPat2   TAAATTAAATATTTAATATACAGTGTTTAA-AATAATAATAAATTAAA--
StPat3   TAAATTAAATATTTAATATACANTGTNTAA-AATAATAATAAATTAAA--
StPat4   TAAATTAAATATTTAATATACAATGTGTAA-AATAATAATAAATTAAA--
StPatME1 TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
StPatME2 TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
StPatME3 TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
StPatME4 TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
TT59_1   TAAATTAAATATTTAATATATAATGTTTAA-AATAATAATAAATTAAA--
TT59_2   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
TT59_3   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
TT76_1   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
TT76_2   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
TT76_3   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
TT76_4   TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
WSC1     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
WSC2     TAAATTAAATATTTAATATACAATGTTTAA-AATAATAATAAATTAAA--
Ola MtB1 TAAATTAAATATTTAATATATAATGTTTAATAATAATAATAAATTAAATT
Ola MtB2 TAAATTAAATATTTAATATATAATGTTTAATAATAATAATAAATTAAATT
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Bel1      TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
Bel2      TATTTAA-TATAATATTTATACATA-TA-TGTGTA-TATATAT-ATATAT
Bel3      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
BPJ1      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
BPJ2      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
BPJ3      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
BPJ4      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
BTS1      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
BTS2      TATTTAA-TATAATATTTATACATA-TA-TGTGTA-TATATAT-ATATAT
BTS3      TATTTAA-TATAATATTTATACATA-TA-TGTGTA-TATATAT-ATATAT
BTS4      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
BTTC1     TATTTAA-TATAATATTTATACACA-TA-TGTATA-TATATAT-ATATAT
BTTC2     TATTTAA-TATAGTATT--TATATA-TA-TATATA-TATGTAT-ATTTAT
BTTC3     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
BTTC4     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
DM1       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
DM2       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
DM4       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
Flag5     TATTTAA-TATAATATTTATACACA-TA-TGTGTA-TATATAT-ATATAT
Flag6     TATTTAA-TATAATATTTATACACA-TA-TGTGTA-TATATAT-ATATAT
Flag7     TATTTAA-TATAGTATTTATATATA-TA-TATATA-TATGTAT-ATTTAT
Flag8     TATTTAA-TATAATATTTATACANA-TA-TGTRTA-TATATAT-ATATAT
Hat1      TATTTAA-TATAATATTTATACATA-TA-TGTRTA-TATATAT-ATATAT
Hat2      TATTTAA-TATAATATTTATACATA-TA-TGTRTA-TATATAT-ATATAT
Hat3      TATTTAA-TATAATATTTATACATA-TA-TGTRTA-TATATAT-ATATAT
LC07      TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
LC08      TATTTAT-TATAATATTTATACACA-TA-TGTATA-TATATAT-ATATAT
LC09      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LC10      TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
LCT1      TATTTAA-TATAATATTTATACACA-TA-GGTATA-TATATAT-ATATAT
LCT2      TATTTAA-TATAATATTTATACAGA-TA-GGTATA-TATATAT-ATATAT
LCT3      TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
LCT4      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LCT5      TATTTAA-TATAACATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LMLE1     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LMLE2     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LMLE3     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LMLE4     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LMME1     TATTTAA-TATAATATTTATACANA-TA-TGTGTA-TATATAT-ATATAT
LMME2     TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
LMME3     TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
LMME4     TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
LMMS1     TATTTAA-TATAATATTTATATATT-TA-TGTATA-TATGTAT-ATGTAT
LMMS2     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LMMS3     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LMMS4     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
Long5     TATTTAA-TATAATATTTATACACA-TA-TGTGTA-TATATAT-ATATAT
Long6     TATTTAA-TATAATATTTATACATA-TA-TGTATG-TATATAT-ATATAT
Long7     TATTTAA-TATAATATTTATACACA-TA-TGTGTA-TATATAT-ATATAT
Long8     TATTTAA-TATAATATTTATACANA-TA-TGTNTA-TATATAT-ATATAT
LPLB1     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LPLB2     TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
LPLB3     TATTTAA-TATAATATTTATATATT-TA-TATATA-TATGTAT-ATGTAT
LTC1      TATTTAA-TATAATATTTATACANA-TA-TGTGTA-TATATAT-ATATAT
LTC2      TATTTAA-TATAATATTTATACACA-TA-TGTGTA-TATATAT-ATATAT
LTC3      TATTTAA-TATAATATTTATACACA-TA-TGTGTA-TATATAT-ATATAT
MH1       TATTTAA-TATAGTATTTATATATA-TA-TATATA-TATGTAT-ATTTAT
MH2       TATTTAA-TATAGTATTTATATATA-TA-TATATA-TATGTAT-ATTTAT
MH3       TATTTAA-TATAGTATTTATATATA-TA-TATATA-TATGTAT-ATTTAT
MR1       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
MR2       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
MR3       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
MR4       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
NB1       TATTTAA-TATAGTATT--TATATA-TA-TATATA-TATGTAT-ATTTAT
NB2       TATTTAA-TATAGTATT--TATATA-TA-TATATA-TATGTAT-ATTTAT
NB3       TATTTAA-TATAGTATT--TATATA-TA-TATATA-TATGTAT-ATTTAT
NB4       TATTTAA-TATAATATT--TATATA-TA-TATATA-TATGTAT-ATTTAT
ORB1      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
ORB2      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
ORB3      TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
ORB4      TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
PH1       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PH2       TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PH3       TATTTAA-TATAATATTTATACACA-TA-TGTATA-TATATAT-ATATAT
PPS1 1    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PPS1 2    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PPS2 1    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PPS2 2    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PPFE 1    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PPFE 2    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PTD1      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PTD2      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
PTD3      TATTTAA-TATAATATTTATACATA-TA-TGTNTA-TATATAT-ATATAT
PTD4      TATTTAA-TATAATATTTATACATA-TA-TGTNTA-TATATAW-ATATAT
Rcrk1     TATTTAA-TATAATATTTATACACA-TA-TGTGTA-TATATAT-ATATAT
Rcrk2     TATTTAA-TATAATATTTATACACA-TA-TGTGTA-TATATAT-ATATAT
Rcrk3     TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
Rcrk4     TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
SGR5      TATTTAA-TATAGTATTTATATATA-TA-TATATA-TATGTAT-ATTTAT
SGR6      TATTTAA-TATAATATTTATATATA-TA-TATATA-TATATAT-ATATAT
SGR7      TATTTAA-TATAATATTTATATATA-TA-TATATA-TATATAT-ATATAT
SGR8      TATTTAA-TATAGTATTTATATATA-TA-TATATA-TATATAT-ATTTAT
ShR1      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
ShR2      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
ShR3      TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
StPat1    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
StPat2    TATTTAA-TATAATATTTATACANA-TA-TGTATA-TATATAT-ATATAT
StPat3    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
StPat4    TATTTAA-TATAATATTTATACACA-TA-TGTATA-TATATAT-ATATAT
StPatME1  TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
StPatME2  TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
StPatME3  TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
StPatME4  TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
TT59_1    TATTTAA-TATAATATTTATACAYA-TA-TGTRTA-TATATAT-ATATAT
TT59_2    TATTTAA-TATAATATTTATACAYA-TA-TGTRTA-TATATAT-ATATAT
TT59_3    TATTTAA-TATAATATTTATACAYA-TA-TGTRTA-TATATAT-ATATAT
TT76_1    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
TT76_2    TATTTAA-TATAATATTTATACATA-TA-TGTRTA-TATATAT-ATATAT
TT76_3    TATTTAA-TATAATATTTATACATA-TA-TGTGTA-TATATAT-ATATAT
TT76_4    TATTTAA-TATAATATTTATACATA-TA-TGTATA-TATATAT-ATATAT
WSC1      TATTTAA-TATAATATTTATACATA-TA-TGTATR-TATATAT-ATATAT
WSC2      TATTTAA-TATAATATTTATACATA-TA-TGTATR-TATATAT-ATATAT
Ola MtB1  TATTTAA-TATAATATTTATACATAGTACTGTATAGTGTATATCATATAT
Ola MtB2  TATTTAA-TATAATATTTATACATAGTACTGTATAGTGTATATCATATAT
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Bel1     TTA--CACGGGCGTAAATAATTTTTAATAAAGGT--AAATAATTATTATT
Bel2     TTA--CACGCGCATAAATAATTTTTAATAAAGGT--AAATAATTATTATT
Bel3     TTA--CCCGCGCCTAAATAATCTTTAATAAAGGT--AAATAATTATTATT
BPJ1     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
BPJ2     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
BPJ3     TTA--CACGTGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
BPJ4     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
BTS1     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
BTS2     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
BTS3     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
BTS4     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
BTTC1    TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAAGAATTCTTATT
BTTC2    TTA--CACGTAGATACAAATGAATTTCAAAATCT--AAATAATTTTTATT
BTTC3    TTA--CACGGGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
BTTC4    TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
DM1      TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
DM2      TTA--CACGTGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
DM4      TTA--CACGGGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
Flag5    TTA--CACGGGCATAAATAATTTTTAATAAATGT--AAATAATTATTATT
Flag6    TTA--CACGGGCATAAATAATTTTTAATAAATGT--AAATAAATCTTATT
Flag7    TTA--CACGGGCATAAATAATTTTTAATAAATGT--AAATAAATCTTATT
Flag8    TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAATTATTATT
Hat1     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
Hat2     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
Hat3     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LC07     TTA--CACGTGCATAAATAATTTTTAATAAAGGT--AAATAATTATTATT
LC08     TTA--CACGTGCATAAATAACTTTTAATAAACGT--AAATAATTCTTATT
LC09     TTA--CACGTGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
LC10     TTA--CACGTGCATAAATAATTTTTAATAAAGGT--AAATAATTATTATT
LCT1     TTA--CACGGGCATAAATAATTTTTAATAAAGGT--AAATAATTATTATT
LCT2     TTA--CACGGGCATAAATAATTTTTAATAAAGGT--AAATAATTATTATT
LCT3     TTA--CACGTGCATAAATAATTTTTAATAAAGGT--AAATAATTATTATT
LCT4     TTA--CACGTGCATAAATAATTTTTAATAAGGGT--AAATAATTATTATT
LCT5     TTA--CACGTGCATAAATAATTTTTAATAAAGGG--AAATAATTATTATT
LMLE1    TTA--CACGTACATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LMLE2    TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LMLE3    TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LMLE4    TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LMME1    TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
LMME2    TTA--CACGGGCATAAATAACTTTTAACAAATGT--AAATAATTCTTATT
LMME3    TTA--CACGTACATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
LMME4    TTA--CACGGGCATAAATAACTTTTAATAAAGGG--AAATAATTCTTATT
LMMS1    TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LMMS2    TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LMMS3    TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LMMS4    TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
Long5    TTA--CACGGGCATAAATAATTTTTAATAAAGGT--AAATAAATCTTATT
Long6    TTA--CACGGGCATAAATAATTTTTAATAAATGT--AAATAAATCTTATT
Long7    TTA--CACGGGCATAAATAATTTTTAATAAAGGT--AAATAAATCTTATT
Long8    TTA--CACGGGCATAAATAATTTTTAATAAATGT--AAATAAATCTTATT
LPLB1    TTAG-CACGTGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
LPLB2    TTAG-CACGTACATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
LPLB3    TTAG-CACGTGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
LTC1     TTA--CACGGGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LTC2     TTA--CACGGGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
LTC3     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
MH1      --------AGATACAAAT-AATTTCA--AAATCT--AAATAATTTTTATT
MH2      --------AGATACAAAT-AATTTCA--AAATCT--AAATAATTTTTATT
MH3      --------AAATACAAAT-AATTTCA--AAATCT--AAATAATTTTTATT
MR1      TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
MR2      TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
MR3      TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
MR4      TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
NB1      --------AAATACAAAT-AATTTCA--AAATCT--AAATAATTTTTATT
NB2      --------AAATACAAAT-AATTTCA--AAATCT--AAATAATTTTTATT
NB3      --------AAATACAAAT-AATTTCA--AAATCT--AAATAATTTTTATT
NB4      --------AGATACAAAT-AATTTCA--AAATCT--AAATAATTTTTATT
ORB1     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
ORB2     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
ORB3     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
ORB4     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PH1      TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAATTATTATT
PH2      TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAATTATTATT
PH3      TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAATTATTATT
PPS1 1   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PPS1 2   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PPS2 1   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PPS2 2   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PPFE 1   TTA--CACGGGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PPFE 2   TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
PTD1     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PTD2     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PTD3     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
PTD4     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
Rcrk1    TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
Rcrk2    TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
Rcrk3    TTA--CACGTGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
Rcrk4    TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
SGR5     TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAATCTTTATT
SGR6     TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAAATCTTATT
SGR7     TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAAATCTTATT
SGR8     TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAATCTTTATT
ShR1     TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
ShR2     TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
ShR3     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
StPat1   TCA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
StPat2   TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
StPat3   TTA--CACGTGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
StPat4   TTA--CACGGGCATAAATAACTTTTAATAAAGGT--AAATAATTCTTATT
StPatME1 TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
StPatME2 TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
StPatME3 TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
StPatME4 TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
TT59_1   TTA--CACGTGCATAAATAATTTTTAATAAATGT--AAATAATTATTATT
TT59_2   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
TT59_3   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
TT76_1   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
TT76_2   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
TT76_3   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
TT76_4   TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
WSC1     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
WSC2     TTA--CACGTGCATAAATAACTTTTAATAAATGT--AAATAATTCTTATT
Ola MtB1 TTATTCACGTACATAAATAATTTTTAATAAACGTAGATACAGTTCTCATT
Ola MtB2 TTATTCACGTACATAAATAATTTTTAATAAACGTAGATACAGTTCTCATT
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Bel1      TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTTGCGTAATAAA
Bel2      TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTTGCGTAATAAA
Bel3      TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTTGCGTAATAAA
BPJ1      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTA-CGTT-AATAA
BPJ2      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTA-CGTT-AATAA
BPJ3      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTA-CGTT-AATAA
BPJ4      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTA-CGTT-AATAA
BTS1      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
BTS2      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
BTS3      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
BTS4      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
BTTC1     TATTCTAATTTAGCT-GTACCATTATTTATATCTTTTTT-ACGTCAATTA
BTTC2     TATTCTAATTTAGCT-GTACCATTATTTATATCTTTTTT-ACATCAATAA
BTTC3     TATTCTAATTTAGCT-GTACCATTATTTATATCTTTTTT-ACGTCAATTA
BTTC4     TATTCTAATTTAGCT-GTACCATTATTTATATCTTTTTT-GCGTCAATAA
DM1       TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATTA
DM2       TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
DM4       TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AAGGA
Flag5     TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTACCGTAATAAA
Flag6     TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTACCGTAATAAA
Flag7     TATTT--ATTTAGCT-GTACC-ATTTTTA-ATCTTTTTTACCGTAATAAA
Flag8     TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTACCGTAATAAA
Hat1      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
Hat2      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
Hat3      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
LC07      TATTT--ACTTATTT-ATACC-ATTTTTA-ATCT-TTTTTACGTAATAAA
LC08      TATTT--AATTATTT-ATACC-ACTTT-A-ATCT-TTTTAACGTAATCAA
LC09      TATTT--AATTATTT-ATACC-ATTTTTA-ATCT-TTTTAACGTAATGAA
LC10      TATTT--ACTTATTT-ATACC-ATTTTTA-ATCT-TTTTTACGTAATAAA
LCT1      TATTT--ACTTATTT-ATACC-ATTTTTA-ATC-TTTTTTACGTAATAAA
LCT2      TATTT--ACTTATTT-ATACC-ATTTTTA-ATC-TTTTTTGCGTAATAAA
LCT3      TATTT--ACTTATTT-ATACC-ATTTTTA-ATC-TCTTTGACGTAATAAA
LCT4      TATTT--ACGTATTT-ATACC-ATTTTTA-ATC-TTTTTCACGTAATTAA
LCT5      TATTT--ACTTATTT-ATACC-ATTTTTA-ATC-TTTTTTACGTAATAAA
LMLE1     TATTT--AATTATTT-ATACC-GTTTTTA-ATCTTTTA--GCGT-AATAA
LMLE2     TATTT--AGTTATTT-ATGCC-ATTTTTA-ATCTTTTA--GCGT-AATAA
LMLE3     TATTT--AGTTATTT-ATGCC-ATTTTTA-ATCTTTTA--GCGT-AATAA
LMLE4     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTA--GCGT-AATAA
LMME1     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTAGCGTAATTAA
LMME2     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTAGCGTAATTAA
LMME3     TATTT--AATTATTT-ATACC-GTTTTTA-ATCTTTTTTAGCGTAATTAA
LMME4     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTACCGTAATTAA
LMMS1     TATTT--ATTTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACATAAATAT
LMMS2     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATTA
LMMS3     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATTA
LMMS4     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATTA
Long5     TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTACGTTAATTAA
Long6     TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTACGGTAATTAA
Long7     TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTACSGTAATTAA
Long8     TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTTACGGTAATTAA
LPLB1     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTAGCGTAAATAA
LPLB2     TATTT--AATTATTT-ATACC-GTTTTTA-ATCTTTTTTAGCGTAAATAA
LPLB3     TATTT-AATTTATTC-ATACC-GTTTTTA-ATCTTTTTTAACATAAATAT
LTC1      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTACCGTAATTAA
LTC2      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTASCGTAATTAA
LTC3      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTAGCGTAATTAA
MH1       TATTT--ATTTAGCT-GTACCATT-TTTA-ATCTTTTTT-ACATCAAATA
MH2       TATTT--ATTTAGCT-GTACCATT-TTTA-ATCTTTTTT-ACATCAAATA
MH3       TATTT--ATTTAGCT-GTACCATT-TTTA-ATCTTTTTT-ACATCAAATA
MR1       TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
MR2       TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
MR3       TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
MR4       TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
NB1       TATTT--ATTTAGCT-GTACCATT-TTTA-ATCTTTTTT-ACAT-AAAAA
NB2       TATTT--ATTTAGCT-GTACCATT-TTTA-ATCTTTTTT-ACAT-AAAAA
NB3       TATTT--ATTTAGCT-GTACCATT-TTTA-ATCTTTTTT-ACAT-AAAAA
NB4       TATTT--ATTTAGCT-GTACCATT-TTTA-ATCTTTTTT-ACAT-AAAAA
ORB1      TATTT--AATTATTT-ATACC-ATTTTTA-ATCT-TTTTTACGTAATAAA
ORB2      TATTT--AATTATTT-ATACC-ATTTTTA-ATCT-TTTTTACGTAATTAA
ORB3      TATTT--AATTATTT-ATACC-ATTTTTA-ATCT-TTTTTACGTAATTAA
ORB4      TATTT--AATTATTT-ATACC-ATTTTTA-ATCT-TTTTTACGTAATTAA
PH1       TATTT--ACTTATTT-ATACC-ATTTTTA-ATCT--TTTTACGCTAATTA
PH2       TATTT--ACTTATTT-ATACC-ATTTTTA-ATCT--TTTTACGGTAATTA
PH3       TATTT--ACTTATTT-ATACC-ATTTTTA-ATCT--TTTTACGTTAATTA
PPS1 1    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
PPS1 2    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
PPS2 1    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-GCGT-AATAA
PPS2 2    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-GCGT-AATAA
PPFE 1    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT--CGT-AATAA
PPFE 2    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT--CGT-AATAA
PTD1      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATAA
PTD2      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATAA
PTD3      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATAA
PTD4      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATAA
Rcrk1     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTT-A-CGT-AATAA
Rcrk2     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTT-A-CGT-AATAA
Rcrk3     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTT-A-CGT-AATGA
Rcrk4     TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTT-A-CGT-AATTA
SGR5      TATTT--ATTTAGCT-ATACCATTTTTTA-ATCTTTTTTAC-ATAAAATA
SGR6      TATTT--ACTTATTT-ATACCATTTTTTA-ATCTTTTTTAC-GTAATTAA
SGR7      TATTT--ACTTATTT-ATACCATTTTTTA-ATCTTTTTTAC-GTAATTAA
SGR8      TATTT--ATTTAGCT-ATACCATTTTTTA-ATCTTTTTTAC-ATAAAATA
ShR1      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTAGCGTTAATAA
ShR2      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTAGCGTTAATAA
ShR3      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTAGCGTTAATAA
StPat1    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTA-CGTTAATTA
StPat2    TATTT--AATTATTT-ATACC-ACTTTTA-ATCTTTTTTA-CGTTAATTA
StPat3    TATTT--AATTATTT-ACCCCCATTTTTA-ATCTCCCTTA-CGTAAATTA
StPat4    TATTT--AATTATTT-ATACCCATTTTTA-ATCTTTTTTA-CGTTAATTA
StPatME1  TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
StPatME2  TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
StPatME3  TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
StPatME4  TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
TT59_1    TATTT--ACTTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATAA
TT59_2    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATAA
TT59_3    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGTTAATAA
TT76_1    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
TT76_2    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
TT76_3    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
TT76_4    TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTT-ACGT-AATAA
WSC1      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTA-CGTTAATAA
WSC2      TATTT--AATTATTT-ATACC-ATTTTTA-ATCTTTTTTA-CGTTAATAA
Ola MtB1  TATTT--ACTTACTTTACACC-ATTCTTG-ATCTATTTTAGCGTCACTAC
Ola MtB2  TATTT--ACTTACTTTACACC-ATTCTTG-ATCTATTTTAGCGTCACTAC
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Appendix 10 – O. ptunarra *Population Log/Det sequence divergence values*

	Bel1	Bel2	Bel3	BPJ1	BPJ2	BPJ3	BPJ4	BTS1	BTS2	BTS3	BTS4	BTTC1	BTTC2
Bel1													
Bel2	0.0098												
Bel3	0.0195	0.0165											
BPJ1	0.0263	0.0248	0.0358										
BPJ2	0.0263	0.0248	0.0359	0.0028									
BPJ3	0.0277	0.0262	0.0372	0.0069	0.0069								
BPJ4	0.0263	0.0248	0.0358	0.0000	0.0028	0.0069							
BTS1	0.0332	0.0304	0.0400	0.0166	0.0193	0.0207	0.0166						
BTS2	0.0333	0.0262	0.0386	0.0180	0.0207	0.0221	0.0180	0.0041					
BTS3	0.0290	0.0207	0.0386	0.0124	0.0152	0.0166	0.0124	0.0097	0.0083				
BTS4	0.0263	0.0248	0.0345	0.0097	0.0124	0.0138	0.0097	0.0097	0.0110	0.0055			
BTTC1	0.0402	0.0399	0.0509	0.0249	0.0276	0.0318	0.0249	0.0276	0.0290	0.0235	0.0207		
BTTC2	0.0789	0.0802	0.0898	0.0750	0.0749	0.0778	0.0750	0.0778	0.0792	0.0736	0.0709	0.0661	
BTTC3	0.0345	0.0344	0.0454	0.0207	0.0235	0.0276	0.0207	0.0235	0.0248	0.0193	0.0166	0.0069	0.0633
BTTC4	0.0317	0.0316	0.0427	0.0221	0.0249	0.0263	0.0221	0.0262	0.0276	0.0221	0.0193	0.0151	0.0661
DM1	0.0263	0.0249	0.0359	0.0097	0.0124	0.0138	0.0097	0.0124	0.0138	0.0083	0.0055	0.0207	0.0737
DM2	0.0304	0.0262	0.0400	0.0166	0.0180	0.0180	0.0166	0.0193	0.0207	0.0124	0.0124	0.0304	0.0806
DM4	0.0373	0.0373	0.0483	0.0249	0.0262	0.0290	0.0249	0.0276	0.0290	0.0235	0.0207	0.0373	0.0889
Flag5	0.0292	0.0263	0.0389	0.0387	0.0387	0.0401	0.0387	0.0360	0.0332	0.0319	0.0346	0.0497	0.0889
Flag6	0.0267	0.0236	0.0373	0.0347	0.0347	0.0361	0.0347	0.0319	0.0277	0.0263	0.0305	0.0456	0.0862
Flag7	0.0611	0.0611	0.0693	0.0652	0.0652	0.0666	0.0652	0.0652	0.0652	0.0626	0.0610	0.0678	0.0404
Flag8	0.0208	0.0194	0.0304	0.0263	0.0263	0.0277	0.0263	0.0263	0.0264	0.0223	0.0222	0.0389	0.0766
Hat1	0.0221	0.0194	0.0317	0.0055	0.0083	0.0111	0.0055	0.0097	0.0098	0.0043	0.0028	0.0193	0.0708
Hat2	0.0221	0.0194	0.0317	0.0055	0.0083	0.0111	0.0055	0.0097	0.0098	0.0043	0.0028	0.0193	0.0708
Hat3	0.0221	0.0194	0.0317	0.0055	0.0083	0.0111	0.0055	0.0097	0.0098	0.0043	0.0028	0.0193	0.0708
LC07	0.0221	0.0235	0.0317	0.0359	0.0359	0.0345	0.0359	0.0387	0.0401	0.0345	0.0318	0.0484	0.0858
LC08	0.0434	0.0431	0.0513	0.0349	0.0377	0.0377	0.0349	0.0376	0.0390	0.0335	0.0307	0.0472	0.1004
LC09	0.0331	0.0317	0.0400	0.0248	0.0276	0.0262	0.0248	0.0276	0.0290	0.0235	0.0207	0.0399	0.0900
LC10	0.0193	0.0207	0.0290	0.0332	0.0332	0.0318	0.0332	0.0359	0.0373	0.0318	0.0290	0.0457	0.0831
LCT1	0.0153	0.0194	0.0276	0.0305	0.0305	0.0291	0.0305	0.0277	0.0291	0.0263	0.0236	0.0386	0.0777
LCT2	0.0112	0.0152	0.0262	0.0277	0.0277	0.0278	0.0277	0.0306	0.0320	0.0264	0.0237	0.0386	0.0776
LCT3	0.0180	0.0193	0.0303	0.0278	0.0278	0.0264	0.0278	0.0278	0.0291	0.0236	0.0209	0.0361	0.0738
LCT4	0.0222	0.0235	0.0345	0.0291	0.0291	0.0292	0.0291	0.0306	0.0320	0.0264	0.0237	0.0400	0.0776
LCT5	0.0166	0.0180	0.0290	0.0277	0.0277	0.0263	0.0277	0.0277	0.0291	0.0235	0.0208	0.0386	0.0750
LMLE1	0.0277	0.0263	0.0345	0.0111	0.0138	0.0167	0.0111	0.0181	0.0194	0.0139	0.0111	0.0263	0.0737
LMLE2	0.0319	0.0305	0.0387	0.0166	0.0194	0.0222	0.0166	0.0222	0.0236	0.0194	0.0167	0.0319	0.0834
LMLE3	0.0264	0.0249	0.0332	0.0111	0.0139	0.0167	0.0111	0.0181	0.0194	0.0139	0.0111	0.0263	0.0779
LMLE4	0.0222	0.0208	0.0290	0.0083	0.0111	0.0139	0.0083	0.0153	0.0167	0.0111	0.0084	0.0249	0.0737
LMME1	0.0222	0.0194	0.0331	0.0138	0.0166	0.0167	0.0138	0.0194	0.0180	0.0125	0.0125	0.0291	0.0818
LMME2	0.0263	0.0262	0.0361	0.0152	0.0180	0.0194	0.0152	0.0166	0.0179	0.0124	0.0097	0.0276	0.0777
LMME3	0.0277	0.0262	0.0373	0.0166	0.0193	0.0180	0.0166	0.0179	0.0193	0.0138	0.0111	0.0276	0.0764
LMME4	0.0249	0.0249	0.0359	0.0138	0.0166	0.0152	0.0138	0.0166	0.0180	0.0125	0.0097	0.0277	0.0792
LMMS1	0.0471	0.0456	0.0566	0.0387	0.0387	0.0417	0.0387	0.0445	0.0458	0.0403	0.0375	0.0523	0.0567
LMMS2	0.0264	0.0237	0.0359	0.0083	0.0111	0.0139	0.0083	0.0125	0.0139	0.0071	0.0056	0.0207	0.0749
LMMS3	0.0236	0.0249	0.0359	0.0111	0.0139	0.0167	0.0111	0.0154	0.0167	0.0111	0.0084	0.0234	0.0721
LMMS4	0.0319	0.0278	0.0414	0.0139	0.0166	0.0195	0.0139	0.0153	0.0167	0.0098	0.0111	0.0262	0.0803
Long5	0.0292	0.0304	0.0387	0.0305	0.0305	0.0291	0.0305	0.0346	0.0332	0.0319	0.0305	0.0470	0.0862
Long6	0.0235	0.0262	0.0344	0.0234	0.0235	0.0248	0.0234	0.0262	0.0276	0.0248	0.0221	0.0399	0.0776
Long7	0.0223	0.0235	0.0345	0.0276	0.0276	0.0263	0.0276	0.0290	0.0276	0.0249	0.0249	0.0400	0.0805
Long8	0.0292	0.0293	0.0390	0.0292	0.0292	0.0306	0.0292	0.0263	0.0264	0.0264	0.0278	0.0445	0.0837
LPLB1	0.0277	0.0263	0.0317	0.0141	0.0168	0.0154	0.0141	0.0126	0.0140	0.0113	0.0085	0.0277	0.0779
LPLB2	0.0263	0.0248	0.0358	0.0126	0.0154	0.0139	0.0126	0.0139	0.0153	0.0098	0.0070	0.0249	0.0723
LPLB3	0.0540	0.0525	0.0635	0.0471	0.0471	0.0457	0.0471	0.0485	0.0499	0.0444	0.0416	0.0566	0.0569

	Bel1	Bel2	Bel3	BPJ1	BPJ2	BPJ3	BPJ4	BTS1	BTS2	BTS3	BTS4	BTTC1	BTTC2
LTC1	0.0235	0.0207	0.0345	0.0124	0.0152	0.0166	0.0124	0.0179	0.0166	0.0111	0.0111	0.0291	0.0778
LTC2	0.0250	0.0235	0.0345	0.0166	0.0194	0.0207	0.0166	0.0193	0.0180	0.0152	0.0152	0.0317	0.0818
LTC3	0.0264	0.0235	0.0345	0.0166	0.0193	0.0207	0.0166	0.0180	0.0166	0.0138	0.0138	0.0303	0.0805
MH1	0.0714	0.0732	0.0833	0.0733	0.0733	0.0746	0.0733	0.0746	0.0750	0.0703	0.0676	0.0657	0.0225
MH2	0.0715	0.0733	0.0834	0.0734	0.0733	0.0747	0.0734	0.0746	0.0750	0.0704	0.0676	0.0658	0.0255
MH3	0.0714	0.0718	0.0819	0.0719	0.0719	0.0732	0.0719	0.0732	0.0736	0.0689	0.0662	0.0643	0.0211
MR1	0.0249	0.0235	0.0345	0.0083	0.0111	0.0124	0.0083	0.0110	0.0124	0.0069	0.0041	0.0221	0.0724
MR2	0.0249	0.0235	0.0345	0.0083	0.0111	0.0124	0.0083	0.0110	0.0124	0.0069	0.0041	0.0221	0.0724
MR3	0.0249	0.0235	0.0345	0.0083	0.0111	0.0124	0.0083	0.0110	0.0124	0.0069	0.0041	0.0221	0.0724
MR4	0.0249	0.0235	0.0345	0.0083	0.0111	0.0124	0.0083	0.0110	0.0124	0.0069	0.0041	0.0221	0.0724
NB1	0.0674	0.0687	0.0787	0.0689	0.0689	0.0703	0.0689	0.0732	0.0745	0.0689	0.0661	0.0675	0.0212
NB2	0.0660	0.0673	0.0773	0.0675	0.0675	0.0689	0.0675	0.0717	0.0731	0.0675	0.0647	0.0661	0.0255
NB3	0.0674	0.0687	0.0787	0.0689	0.0689	0.0703	0.0689	0.0732	0.0745	0.0689	0.0661	0.0675	0.0212
NB4	0.0632	0.0659	0.0759	0.0661	0.0661	0.0675	0.0661	0.0703	0.0717	0.0661	0.0633	0.0647	0.0241
ORB1	0.0249	0.0235	0.0345	0.0194	0.0221	0.0249	0.0194	0.0236	0.0249	0.0194	0.0166	0.0344	0.0830
ORB2	0.0263	0.0249	0.0359	0.0180	0.0207	0.0236	0.0180	0.0222	0.0236	0.0180	0.0152	0.0331	0.0816
ORB3	0.0221	0.0207	0.0317	0.0138	0.0166	0.0194	0.0138	0.0181	0.0194	0.0139	0.0111	0.0277	0.0775
ORB4	0.0249	0.0207	0.0345	0.0166	0.0194	0.0208	0.0166	0.0194	0.0208	0.0125	0.0125	0.0304	0.0780
PH1	0.0180	0.0193	0.0303	0.0207	0.0207	0.0221	0.0207	0.0235	0.0249	0.0193	0.0166	0.0317	0.0706
PH2	0.0180	0.0193	0.0303	0.0207	0.0207	0.0221	0.0207	0.0235	0.0249	0.0193	0.0166	0.0317	0.0706
PH3	0.0166	0.0193	0.0303	0.0207	0.0207	0.0221	0.0207	0.0235	0.0249	0.0193	0.0166	0.0289	0.0706
PPS1 1	0.0222	0.0207	0.0317	0.0083	0.0111	0.0139	0.0083	0.0125	0.0139	0.0083	0.0056	0.0221	0.0709
PPS1 2	0.0222	0.0207	0.0317	0.0083	0.0111	0.0139	0.0083	0.0125	0.0139	0.0083	0.0056	0.0221	0.0709
PPS2 1	0.0194	0.0180	0.0290	0.0069	0.0097	0.0138	0.0069	0.0138	0.0152	0.0097	0.0069	0.0221	0.0709
PPS2 2	0.0222	0.0207	0.0317	0.0069	0.0097	0.0138	0.0069	0.0138	0.0152	0.0097	0.0069	0.0221	0.0736
PPFE 1	0.0209	0.0209	0.0320	0.0069	0.0097	0.0139	0.0069	0.0138	0.0152	0.0097	0.0069	0.0221	0.0737
PPFE 2	0.0194	0.0195	0.0306	0.0083	0.0111	0.0097	0.0083	0.0124	0.0138	0.0083	0.0055	0.0235	0.0738
PTD1	0.0235	0.0221	0.0331	0.0055	0.0083	0.0124	0.0055	0.0111	0.0124	0.0069	0.0041	0.0206	0.0719
PTD2	0.0249	0.0235	0.0345	0.0069	0.0097	0.0111	0.0069	0.0097	0.0111	0.0055	0.0028	0.0220	0.0720
PTD3	0.0235	0.0209	0.0331	0.0083	0.0083	0.0097	0.0083	0.0111	0.0112	0.0056	0.0042	0.0234	0.0707
PTD4	0.0263	0.0237	0.0359	0.0111	0.0111	0.0097	0.0111	0.0111	0.0112	0.0056	0.0042	0.0234	0.0708
Rcrk1	0.0322	0.0306	0.0417	0.0194	0.0222	0.0208	0.0194	0.0194	0.0180	0.0153	0.0153	0.0305	0.0838
Rcrk2	0.0406	0.0362	0.0472	0.0278	0.0306	0.0292	0.0278	0.0250	0.0236	0.0195	0.0237	0.0389	0.0923
Rcrk3	0.0348	0.0306	0.0417	0.0180	0.0208	0.0167	0.0180	0.0208	0.0222	0.0139	0.0139	0.0291	0.0825
Rcrk4	0.0306	0.0293	0.0418	0.0167	0.0195	0.0181	0.0167	0.0167	0.0180	0.0125	0.0125	0.0264	0.0811
SGR5	0.0624	0.0637	0.0721	0.0596	0.0597	0.0611	0.0596	0.0625	0.0639	0.0611	0.0583	0.0623	0.0321
SGR6	0.0278	0.0291	0.0375	0.0264	0.0264	0.0279	0.0264	0.0279	0.0292	0.0265	0.0237	0.0388	0.0685
SGR7	0.0278	0.0291	0.0375	0.0264	0.0264	0.0279	0.0264	0.0279	0.0292	0.0265	0.0237	0.0388	0.0685
SGR8	0.0626	0.0639	0.0722	0.0598	0.0598	0.0613	0.0598	0.0626	0.0640	0.0612	0.0584	0.0624	0.0349
ShR1	0.0291	0.0290	0.0401	0.0166	0.0194	0.0180	0.0166	0.0180	0.0194	0.0139	0.0111	0.0304	0.0806
ShR2	0.0277	0.0276	0.0387	0.0152	0.0180	0.0180	0.0152	0.0180	0.0194	0.0138	0.0111	0.0290	0.0803
ShR3	0.0305	0.0291	0.0401	0.0125	0.0152	0.0180	0.0125	0.0153	0.0166	0.0111	0.0083	0.0262	0.0776
StPat1	0.0264	0.0251	0.0363	0.0153	0.0180	0.0181	0.0153	0.0181	0.0182	0.0139	0.0111	0.0262	0.0776
StPat2	0.0319	0.0319	0.0431	0.0180	0.0208	0.0208	0.0180	0.0208	0.0222	0.0166	0.0139	0.0277	0.0832
StPat3	0.0336	0.0308	0.0421	0.0182	0.0209	0.0210	0.0182	0.0209	0.0210	0.0167	0.0140	0.0304	0.0846
StPat4	0.0266	0.0265	0.0376	0.0153	0.0181	0.0181	0.0153	0.0180	0.0166	0.0138	0.0111	0.0248	0.0816
StPatME1	0.0263	0.0249	0.0359	0.0097	0.0125	0.0153	0.0097	0.0111	0.0125	0.0069	0.0042	0.0207	0.0722
StPatME2	0.0249	0.0235	0.0345	0.0083	0.0111	0.0139	0.0083	0.0097	0.0111	0.0055	0.0028	0.0193	0.0708
StPatME3	0.0249	0.0235	0.0345	0.0083	0.0111	0.0139	0.0083	0.0097	0.0111	0.0055	0.0028	0.0193	0.0708
StPatME4	0.0249	0.0235	0.0345	0.0083	0.0111	0.0139	0.0083	0.0097	0.0111	0.0055	0.0028	0.0193	0.0708
TT59_1	0.0180	0.0180	0.0303	0.0194	0.0193	0.0207	0.0194	0.0194	0.0194	0.0139	0.0125	0.0291	0.0665
TT59_2	0.0263	0.0236	0.0359	0.0083	0.0110	0.0124	0.0083	0.0083	0.0084	0.0029	0.0014	0.0193	0.0707
TT59_3	0.0263	0.0236	0.0359	0.0083	0.0110	0.0124	0.0083	0.0083	0.0084	0.0029	0.0014	0.0193	0.0707
TT76_1	0.0249	0.0235	0.0345	0.0083	0.0111	0.0124	0.0083	0.0110	0.0124	0.0069	0.0041	0.0221	0.0724
TT76_2	0.0235	0.0208	0.0331	0.0069	0.0097	0.0111	0.0069	0.0097	0.0097	0.0042	0.0028	0.0207	0.0710
TT76_3	0.0249	0.0207	0.0345	0.0083	0.0111	0.0124	0.0083	0.0110	0.0097	0.0041	0.0041	0.0221	0.0724
TT76_4	0.0235	0.0221	0.0331	0.0069	0.0097	0.0111	0.0069	0.0097	0.0110	0.0055	0.0028	0.0207	0.0710
WSC1	0.0278	0.0264	0.0375	0.0083	0.0111	0.0125	0.0083	0.0125	0.0138	0.0083	0.0055	0.0248	0.0749
WSC2	0.0278	0.0264	0.0375	0.0083	0.0111	0.0125	0.0083	0.0125	0.0138	0.0083	0.0055	0.0248	0.0749

	BTTC3	BTTC4	DM1	DM2	DM4	Flag5	Flag6	Flag7	Flag8	Hat1	Hat2	Hat3	LC07	LC08	LC09	LC10
BTTC4	0.0082															
DM1	0.0166	0.0194														
DM2	0.0262	0.0235	0.0097													
DM4	0.0304	0.0331	0.0180	0.0180												
Flag5	0.0456	0.0442	0.0374	0.0416	0.0484											
Flag6	0.0415	0.0429	0.0333	0.0361	0.0403	0.0112										
Flag7	0.0623	0.0637	0.0639	0.0695	0.0749	0.0475	0.0471									
Flag8	0.0359	0.0373	0.0250	0.0306	0.0388	0.0069	0.0084	0.0458								
Hat1	0.0152	0.0180	0.0028	0.0097	0.0180	0.0335	0.0294	0.0613	0.0224							
Hat2	0.0152	0.0180	0.0028	0.0097	0.0180	0.0335	0.0294	0.0613	0.0224	0.0000						
Hat3	0.0152	0.0180	0.0028	0.0097	0.0180	0.0335	0.0294	0.0613	0.0224	0.0000	0.0000					
LC07	0.0455	0.0455	0.0318	0.0359	0.0428	0.0388	0.0363	0.0707	0.0277	0.0291	0.0291	0.0291				
LC08	0.0459	0.0472	0.0308	0.0363	0.0417	0.0556	0.0503	0.0849	0.0449	0.0281	0.0281	0.0281	0.0250			
LC09	0.0358	0.0331	0.0179	0.0221	0.0290	0.0484	0.0431	0.0748	0.0360	0.0180	0.0180	0.0180	0.0193	0.0166		
LC10	0.0427	0.0400	0.0263	0.0304	0.0387	0.0361	0.0336	0.0680	0.0249	0.0264	0.0264	0.0264	0.0055	0.0306	0.0165	
LCT1	0.0345	0.0345	0.0264	0.0305	0.0374	0.0195	0.0194	0.0542	0.0125	0.0237	0.0237	0.0237	0.0235	0.0418	0.0332	0.0208
LCT2	0.0331	0.0304	0.0265	0.0306	0.0375	0.0224	0.0223	0.0558	0.0142	0.0236	0.0236	0.0236	0.0237	0.0434	0.0333	0.0209
LCT3	0.0346	0.0345	0.0237	0.0278	0.0374	0.0278	0.0264	0.0583	0.0166	0.0210	0.0210	0.0210	0.0207	0.0406	0.0304	0.0180
LCT4	0.0359	0.0331	0.0237	0.0278	0.0403	0.0347	0.0334	0.0654	0.0223	0.0236	0.0236	0.0236	0.0263	0.0433	0.0291	0.0207
LCT5	0.0345	0.0345	0.0236	0.0277	0.0374	0.0277	0.0264	0.0584	0.0153	0.0209	0.0209	0.0209	0.0194	0.0390	0.0276	0.0166
LMLE1	0.0221	0.0222	0.0111	0.0180	0.0263	0.0418	0.0377	0.0670	0.0293	0.0083	0.0083	0.0083	0.0347	0.0337	0.0235	0.0319
LMLE2	0.0277	0.0277	0.0167	0.0236	0.0318	0.0446	0.0418	0.0725	0.0335	0.0139	0.0139	0.0139	0.0389	0.0392	0.0291	0.0361
LMLE3	0.0222	0.0222	0.0111	0.0180	0.0263	0.0404	0.0363	0.0670	0.0279	0.0083	0.0083	0.0083	0.0333	0.0337	0.0235	0.0306
LMLE4	0.0208	0.0208	0.0084	0.0153	0.0235	0.0363	0.0321	0.0628	0.0238	0.0055	0.0055	0.0055	0.0292	0.0309	0.0208	0.0264
LMME1	0.0235	0.0207	0.0125	0.0139	0.0249	0.0307	0.0266	0.0613	0.0238	0.0084	0.0084	0.0084	0.0347	0.0324	0.0221	0.0319
LMME2	0.0221	0.0221	0.0125	0.0166	0.0249	0.0292	0.0279	0.0585	0.0236	0.0097	0.0097	0.0097	0.0373	0.0336	0.0248	0.0346
LMME3	0.0248	0.0221	0.0139	0.0152	0.0290	0.0347	0.0306	0.0625	0.0236	0.0111	0.0111	0.0111	0.0359	0.0336	0.0234	0.0332
LMME4	0.0221	0.0207	0.0125	0.0139	0.0249	0.0319	0.0278	0.0597	0.0236	0.0097	0.0097	0.0097	0.0346	0.0322	0.0221	0.0318
LMMS1	0.0482	0.0482	0.0375	0.0444	0.0527	0.0571	0.0558	0.0489	0.0475	0.0346	0.0346	0.0346	0.0541	0.0630	0.0527	0.0513
LMMS2	0.0165	0.0221	0.0028	0.0112	0.0194	0.0323	0.0321	0.0627	0.0238	0.0028	0.0028	0.0028	0.0334	0.0323	0.0222	0.0306
LMMS3	0.0193	0.0248	0.0056	0.0153	0.0222	0.0308	0.0293	0.0600	0.0210	0.0056	0.0056	0.0056	0.0306	0.0352	0.0250	0.0278
LMMS4	0.0221	0.0248	0.0083	0.0167	0.0249	0.0377	0.0349	0.0683	0.0293	0.0083	0.0083	0.0083	0.0389	0.0379	0.0277	0.0361
Long5	0.0428	0.0414	0.0347	0.0388	0.0471	0.0222	0.0180	0.0555	0.0181	0.0307	0.0307	0.0307	0.0361	0.0530	0.0443	0.0334
Long6	0.0330	0.0344	0.0249	0.0318	0.0373	0.0235	0.0180	0.0499	0.0153	0.0222	0.0222	0.0222	0.0331	0.0473	0.0372	0.0304
Long7	0.0359	0.0345	0.0277	0.0318	0.0401	0.0166	0.0125	0.0500	0.0126	0.0237	0.0237	0.0237	0.0319	0.0459	0.0373	0.0291
Long8	0.0388	0.0402	0.0306	0.0375	0.0430	0.0168	0.0127	0.0489	0.0154	0.0280	0.0280	0.0280	0.0388	0.0519	0.0430	0.0361
LPLB1	0.0236	0.0208	0.0113	0.0154	0.0264	0.0361	0.0320	0.0626	0.0237	0.0085	0.0085	0.0085	0.0332	0.0322	0.0208	0.0305
LPLB2	0.0208	0.0179	0.0098	0.0139	0.0250	0.0374	0.0334	0.0640	0.0251	0.0071	0.0071	0.0071	0.0346	0.0336	0.0221	0.0318
LPLB3	0.0525	0.0497	0.0444	0.0485	0.0595	0.0610	0.0598	0.0500	0.0515	0.0417	0.0417	0.0417	0.0595	0.0683	0.0567	0.0567
LTC1	0.0234	0.0248	0.0111	0.0180	0.0235	0.0250	0.0209	0.0555	0.0180	0.0070	0.0070	0.0070	0.0332	0.0323	0.0235	0.0304
LTC2	0.0276	0.0276	0.0152	0.0222	0.0277	0.0221	0.0180	0.0541	0.0153	0.0111	0.0111	0.0111	0.0360	0.0349	0.0276	0.0333
LTC3	0.0290	0.0290	0.0139	0.0208	0.0290	0.0249	0.0208	0.0568	0.0153	0.0098	0.0098	0.0098	0.0347	0.0335	0.0262	0.0319
MH1	0.0602	0.0658	0.0677	0.0774	0.0801	0.0800	0.0764	0.0310	0.0705	0.0680	0.0680	0.0680	0.0798	0.0960	0.0854	0.0770
MH2	0.0603	0.0658	0.0677	0.0774	0.0801	0.0801	0.0765	0.0339	0.0706	0.0680	0.0680	0.0680	0.0798	0.0961	0.0855	0.0771
MH3	0.0602	0.0658	0.0663	0.0760	0.0800	0.0800	0.0765	0.0310	0.0691	0.0666	0.0666	0.0666	0.0784	0.0946	0.0840	0.0756
MR1	0.0180	0.0207	0.0042	0.0083	0.0193	0.0360	0.0319	0.0625	0.0236	0.0014	0.0014	0.0014	0.0304	0.0294	0.0193	0.0277
MR2	0.0180	0.0207	0.0042	0.0083	0.0193	0.0360	0.0319	0.0625	0.0236	0.0014	0.0014	0.0014	0.0304	0.0294	0.0193	0.0277
MR3	0.0180	0.0207	0.0042	0.0083	0.0193	0.0360	0.0319	0.0625	0.0236	0.0014	0.0014	0.0014	0.0304	0.0294	0.0193	0.0277
MR4	0.0180	0.0207	0.0042	0.0083	0.0193	0.0360	0.0319	0.0625	0.0236	0.0014	0.0014	0.0014	0.0304	0.0294	0.0193	0.0277
NB1	0.0634	0.0661	0.0662	0.0731	0.0785	0.0789	0.0762	0.0297	0.0679	0.0636	0.0636	0.0636	0.0744	0.0906	0.0800	0.0716
NB2	0.0619	0.0647	0.0648	0.0716	0.0771	0.0775	0.0748	0.0339	0.0665	0.0622	0.0622	0.0622	0.0729	0.0892	0.0785	0.0701
NB3	0.0634	0.0661	0.0662	0.0731	0.0785	0.0789	0.0762	0.0297	0.0679	0.0636	0.0636	0.0636	0.0744	0.0906	0.0800	0.0716
NB4	0.0592	0.0620	0.0634	0.0703	0.0743	0.0747	0.0720	0.0311	0.0651	0.0608	0.0608	0.0608	0.0715	0.0878	0.0772	0.0688
ORB1	0.0303	0.0303	0.0139	0.0208	0.0290	0.0417	0.0376	0.0682	0.0293	0.0138	0.0138	0.0138	0.0235	0.0280	0.0207	0.0235
ORB2	0.0290	0.0289	0.0125	0.0194	0.0290	0.0431	0.0390	0.0696	0.0306	0.0124	0.0124	0.0124	0.0249	0.0280	0.0207	0.0249
ORB3	0.0248	0.0248	0.0083	0.0152	0.0249	0.0377	0.0336	0.0655	0.0265	0.0083	0.0083	0.0083	0.0291	0.0310	0.0193	0.0235
ORB4	0.0276	0.0276	0.0097	0.0139	0.0263	0.0362	0.0335	0.0655	0.0265	0.0097	0.0097	0.0097	0.0304	0.0323	0.0207	0.0249

	BTTC3	BTTC4	DM1	DM2	DM4	Flag5	Flag6	Flag7	Flag8	Hat1	Hat2	Hat3	LC07	LC08	LC09	LC10
PH1	0.0275	0.0331	0.0138	0.0235	0.0304	0.0318	0.0305	0.0625	0.0195	0.0139	0.0139	0.0139	0.0235	0.0431	0.0331	0.0207
PH2	0.0275	0.0331	0.0138	0.0235	0.0304	0.0318	0.0305	0.0625	0.0195	0.0139	0.0139	0.0139	0.0235	0.0431	0.0331	0.0207
PH3	0.0275	0.0331	0.0138	0.0235	0.0304	0.0291	0.0278	0.0625	0.0180	0.0139	0.0139	0.0139	0.0220	0.0404	0.0331	0.0193
PPS1 1	0.0180	0.0208	0.0056	0.0125	0.0208	0.0349	0.0307	0.0614	0.0224	0.0028	0.0028	0.0028	0.0292	0.0309	0.0208	0.0264
PPS1 2	0.0180	0.0208	0.0056	0.0125	0.0208	0.0349	0.0307	0.0614	0.0224	0.0028	0.0028	0.0028	0.0292	0.0309	0.0208	0.0264
PPS2 1	0.0180	0.0180	0.0069	0.0138	0.0221	0.0346	0.0305	0.0611	0.0222	0.0028	0.0028	0.0028	0.0304	0.0321	0.0221	0.0277
PPS2 2	0.0180	0.0180	0.0069	0.0138	0.0221	0.0374	0.0333	0.0639	0.0250	0.0028	0.0028	0.0028	0.0318	0.0307	0.0221	0.0304
PPFE 1	0.0152	0.0140	0.0042	0.0111	0.0180	0.0349	0.0307	0.0614	0.0252	0.0028	0.0028	0.0028	0.0332	0.0321	0.0193	0.0277
PPFE 2	0.0166	0.0153	0.0055	0.0097	0.0180	0.0334	0.0293	0.0600	0.0237	0.0028	0.0028	0.0028	0.0291	0.0294	0.0179	0.0263
PTD1	0.0165	0.0193	0.0042	0.0111	0.0193	0.0374	0.0333	0.0638	0.0250	0.0000	0.0000	0.0000	0.0318	0.0307	0.0207	0.0290
PTD2	0.0179	0.0206	0.0028	0.0097	0.0180	0.0360	0.0319	0.0624	0.0236	0.0000	0.0000	0.0000	0.0304	0.0294	0.0193	0.0277
PTD3	0.0193	0.0220	0.0042	0.0111	0.0194	0.0334	0.0294	0.0611	0.0222	0.0014	0.0014	0.0014	0.0290	0.0308	0.0207	0.0263
PTD4	0.0193	0.0221	0.0069	0.0138	0.0221	0.0334	0.0294	0.0612	0.0222	0.0042	0.0042	0.0042	0.0318	0.0335	0.0235	0.0291
Rcrk1	0.0264	0.0251	0.0181	0.0195	0.0277	0.0278	0.0238	0.0629	0.0213	0.0142	0.0142	0.0142	0.0418	0.0391	0.0305	0.0390
Rcrk2	0.0347	0.0334	0.0265	0.0278	0.0389	0.0348	0.0294	0.0713	0.0297	0.0226	0.0226	0.0226	0.0475	0.0447	0.0361	0.0447
Rcrk3	0.0264	0.0265	0.0153	0.0125	0.0263	0.0335	0.0309	0.0659	0.0268	0.0140	0.0140	0.0140	0.0388	0.0364	0.0263	0.0361
Rcrk4	0.0208	0.0223	0.0125	0.0167	0.0264	0.0321	0.0280	0.0629	0.0266	0.0126	0.0126	0.0126	0.0402	0.0379	0.0277	0.0375
SGR5	0.0595	0.0637	0.0584	0.0680	0.0735	0.0627	0.0614	0.0210	0.0516	0.0586	0.0586	0.0586	0.0694	0.0852	0.0749	0.0666
SGR6	0.0347	0.0361	0.0265	0.0334	0.0417	0.0237	0.0195	0.0461	0.0140	0.0238	0.0238	0.0238	0.0347	0.0491	0.0389	0.0319
SGR7	0.0347	0.0361	0.0265	0.0334	0.0417	0.0237	0.0195	0.0461	0.0140	0.0238	0.0238	0.0238	0.0347	0.0491	0.0389	0.0319
SGR8	0.0597	0.0638	0.0585	0.0682	0.0737	0.0586	0.0586	0.0209	0.0488	0.0588	0.0588	0.0588	0.0695	0.0854	0.0750	0.0667
ShR1	0.0235	0.0180	0.0111	0.0125	0.0249	0.0348	0.0333	0.0638	0.0278	0.0111	0.0111	0.0111	0.0402	0.0391	0.0249	0.0346
ShR2	0.0221	0.0166	0.0111	0.0124	0.0249	0.0375	0.0334	0.0640	0.0278	0.0111	0.0111	0.0111	0.0402	0.0392	0.0249	0.0346
ShR3	0.0221	0.0193	0.0083	0.0125	0.0249	0.0362	0.0334	0.0640	0.0251	0.0083	0.0083	0.0083	0.0375	0.0350	0.0221	0.0319
StPat1	0.0193	0.0180	0.0083	0.0153	0.0235	0.0377	0.0324	0.0643	0.0280	0.0111	0.0111	0.0111	0.0347	0.0364	0.0222	0.0292
StPat2	0.0221	0.0208	0.0111	0.0152	0.0263	0.0419	0.0378	0.0699	0.0335	0.0139	0.0139	0.0139	0.0402	0.0350	0.0249	0.0347
StPat3	0.0263	0.0250	0.0112	0.0168	0.0292	0.0449	0.0395	0.0715	0.0324	0.0140	0.0140	0.0140	0.0379	0.0366	0.0223	0.0324
StPat4	0.0207	0.0194	0.0083	0.0152	0.0235	0.0364	0.0308	0.0658	0.0296	0.0111	0.0111	0.0111	0.0363	0.0336	0.0221	0.0308
StPatME1	0.0166	0.0193	0.0069	0.0138	0.0221	0.0362	0.0321	0.0627	0.0237	0.0042	0.0042	0.0042	0.0305	0.0295	0.0194	0.0278
StPatME2	0.0152	0.0180	0.0055	0.0124	0.0207	0.0348	0.0307	0.0614	0.0224	0.0028	0.0028	0.0028	0.0292	0.0281	0.0180	0.0264
StPatME3	0.0152	0.0180	0.0055	0.0124	0.0207	0.0348	0.0307	0.0614	0.0224	0.0028	0.0028	0.0028	0.0292	0.0281	0.0180	0.0264
StPatME4	0.0152	0.0180	0.0055	0.0124	0.0207	0.0348	0.0307	0.0614	0.0224	0.0028	0.0028	0.0028	0.0292	0.0281	0.0180	0.0264
TT59_1	0.0262	0.0289	0.0152	0.0221	0.0304	0.0237	0.0224	0.0569	0.0139	0.0126	0.0126	0.0126	0.0207	0.0378	0.0290	0.0180
TT59_2	0.0165	0.0193	0.0042	0.0111	0.0193	0.0320	0.0279	0.0611	0.0222	0.0014	0.0014	0.0014	0.0318	0.0295	0.0207	0.0291
TT59_3	0.0165	0.0193	0.0042	0.0111	0.0193	0.0320	0.0279	0.0611	0.0222	0.0014	0.0014	0.0014	0.0318	0.0295	0.0207	0.0291
TT76_1	0.0180	0.0207	0.0042	0.0111	0.0193	0.0360	0.0319	0.0625	0.0236	0.0014	0.0014	0.0014	0.0304	0.0294	0.0193	0.0277
TT76_2	0.0166	0.0194	0.0028	0.0097	0.0180	0.0334	0.0293	0.0611	0.0222	0.0000	0.0000	0.0000	0.0290	0.0280	0.0179	0.0263
TT76_3	0.0180	0.0207	0.0042	0.0111	0.0193	0.0333	0.0291	0.0625	0.0222	0.0000	0.0000	0.0000	0.0304	0.0294	0.0193	0.0277
TT76_4	0.0166	0.0194	0.0028	0.0097	0.0180	0.0346	0.0305	0.0611	0.0222	0.0000	0.0000	0.0000	0.0290	0.0280	0.0179	0.0263
WSC1	0.0207	0.0222	0.0056	0.0069	0.0152	0.0375	0.0307	0.0641	0.0251	0.0028	0.0028	0.0028	0.0346	0.0321	0.0221	0.0318
WSC2	0.0207	0.0222	0.0056	0.0069	0.0152	0.0375	0.0307	0.0641	0.0251	0.0028	0.0028	0.0028	0.0346	0.0321	0.0221	0.0318

	LCT1	LCT2	LCT3	LCT4	LCT5	LMLE1	LMLE2	LMLE3	LMLE4	LMME1	LMME2	LMME3	LMME4	LMMS1	LMMS2	LMMS3	LMMS4
LCT2	0.0042																
LCT3	0.0110	0.0113															
LCT4	0.0180	0.0180	0.0153														
LCT5	0.0097	0.0097	0.0097	0.0125													
LMLE1	0.0320	0.0291	0.0294	0.0319	0.0292												
LMLE2	0.0362	0.0333	0.0335	0.0361	0.0334	0.0139											
LMLE3	0.0306	0.0278	0.0280	0.0306	0.0279	0.0083	0.0056										
LMLE4	0.0265	0.0236	0.0238	0.0264	0.0237	0.0055	0.0111	0.0055									
LMME1	0.0251	0.0223	0.0264	0.0291	0.0264	0.0152	0.0208	0.0153	0.0125								
LMME2	0.0250	0.0224	0.0263	0.0292	0.0263	0.0153	0.0208	0.0153	0.0125	0.0084							
LMME3	0.0263	0.0239	0.0249	0.0278	0.0249	0.0111	0.0222	0.0167	0.0139	0.0069	0.0097						
LMME4	0.0222	0.0210	0.0235	0.0264	0.0208	0.0167	0.0222	0.0167	0.0139	0.0070	0.0069	0.0083					
LMMS1	0.0487	0.0485	0.0462	0.0486	0.0460	0.0430	0.0471	0.0416	0.0374	0.0444	0.0446	0.0459	0.0446				
LMMS2	0.0279	0.0278	0.0252	0.0278	0.0251	0.0111	0.0167	0.0111	0.0083	0.0111	0.0139	0.0125	0.0139	0.0389			
LMMS3	0.0251	0.0250	0.0225	0.0250	0.0223	0.0139	0.0195	0.0139	0.0083	0.0139	0.0167	0.0153	0.0167	0.0389	0.0028		
LMMS4	0.0334	0.0333	0.0308	0.0333	0.0307	0.0167	0.0222	0.0167	0.0139	0.0166	0.0195	0.0181	0.0195	0.0416	0.0056	0.0083	
Long5	0.0208	0.0237	0.0250	0.0320	0.0277	0.0390	0.0431	0.0376	0.0335	0.0252	0.0306	0.0292	0.0264	0.0557	0.0334	0.0307	0.0390
Long6	0.0180	0.0195	0.0221	0.0250	0.0221	0.0292	0.0333	0.0278	0.0236	0.0250	0.0221	0.0263	0.0207	0.0472	0.0252	0.0224	0.0320
Long7	0.0153	0.0182	0.0208	0.0250	0.0221	0.0320	0.0362	0.0306	0.0265	0.0183	0.0236	0.0222	0.0195	0.0501	0.0252	0.0225	0.0320
Long8	0.0210	0.0227	0.0278	0.0307	0.0278	0.0350	0.0377	0.0336	0.0294	0.0267	0.0278	0.0291	0.0264	0.0532	0.0268	0.0241	0.0322
LPLB1	0.0250	0.0251	0.0250	0.0279	0.0250	0.0113	0.0167	0.0112	0.0085	0.0126	0.0126	0.0112	0.0112	0.0433	0.0127	0.0155	0.0182
LPLB2	0.0264	0.0237	0.0235	0.0264	0.0236	0.0070	0.0181	0.0126	0.0098	0.0111	0.0111	0.0041	0.0098	0.0419	0.0112	0.0141	0.0168
LPLB3	0.0513	0.0514	0.0485	0.0514	0.0486	0.0473	0.0542	0.0487	0.0446	0.0487	0.0486	0.0444	0.0458	0.0071	0.0460	0.0460	0.0487
LTC1	0.0236	0.0225	0.0249	0.0278	0.0249	0.0153	0.0208	0.0153	0.0097	0.0056	0.0111	0.0124	0.0097	0.0404	0.0097	0.0098	0.0153
LTC2	0.0208	0.0223	0.0278	0.0319	0.0277	0.0181	0.0236	0.0181	0.0125	0.0069	0.0125	0.0138	0.0125	0.0445	0.0139	0.0139	0.0194
LTC3	0.0221	0.0237	0.0264	0.0306	0.0263	0.0167	0.0222	0.0167	0.0111	0.0083	0.0138	0.0124	0.0152	0.0431	0.0125	0.0125	0.0180
MH1	0.0687	0.0689	0.0677	0.0745	0.0687	0.0708	0.0807	0.0750	0.0708	0.0762	0.0718	0.0731	0.0731	0.0536	0.0694	0.0664	0.0749
MH2	0.0688	0.0690	0.0678	0.0746	0.0688	0.0709	0.0807	0.0750	0.0708	0.0763	0.0720	0.0732	0.0732	0.0508	0.0694	0.0665	0.0749
MH3	0.0687	0.0689	0.0663	0.0731	0.0674	0.0694	0.0792	0.0736	0.0694	0.0762	0.0718	0.0717	0.0731	0.0522	0.0679	0.0650	0.0734
MR1	0.0249	0.0251	0.0223	0.0251	0.0222	0.0097	0.0152	0.0097	0.0070	0.0083	0.0083	0.0097	0.0083	0.0361	0.0042	0.0070	0.0097
MR2	0.0249	0.0251	0.0223	0.0251	0.0222	0.0097	0.0152	0.0097	0.0070	0.0083	0.0083	0.0097	0.0083	0.0361	0.0042	0.0070	0.0097
MR3	0.0249	0.0251	0.0223	0.0251	0.0222	0.0097	0.0152	0.0097	0.0070	0.0083	0.0083	0.0097	0.0083	0.0361	0.0042	0.0070	0.0097
MR4	0.0249	0.0251	0.0223	0.0251	0.0222	0.0097	0.0152	0.0097	0.0070	0.0083	0.0083	0.0097	0.0083	0.0361	0.0042	0.0070	0.0097
NB1	0.0675	0.0677	0.0651	0.0719	0.0662	0.0664	0.0763	0.0706	0.0664	0.0721	0.0706	0.0704	0.0718	0.0480	0.0667	0.0637	0.0722
NB2	0.0661	0.0662	0.0638	0.0704	0.0647	0.0650	0.0749	0.0692	0.0650	0.0706	0.0692	0.0690	0.0704	0.0466	0.0652	0.0623	0.0707
NB3	0.0675	0.0677	0.0651	0.0719	0.0662	0.0664	0.0763	0.0706	0.0664	0.0721	0.0706	0.0704	0.0718	0.0480	0.0667	0.0637	0.0722
NB4	0.0633	0.0635	0.0623	0.0691	0.0633	0.0636	0.0735	0.0678	0.0636	0.0679	0.0664	0.0676	0.0677	0.0452	0.0638	0.0609	0.0693
ORB1	0.0292	0.0291	0.0278	0.0249	0.0236	0.0222	0.0277	0.0222	0.0166	0.0222	0.0222	0.0236	0.0222	0.0456	0.0180	0.0180	0.0235
ORB2	0.0306	0.0305	0.0292	0.0235	0.0250	0.0208	0.0264	0.0208	0.0152	0.0208	0.0208	0.0222	0.0208	0.0443	0.0167	0.0166	0.0222
ORB3	0.0251	0.0252	0.0250	0.0222	0.0237	0.0166	0.0222	0.0166	0.0111	0.0166	0.0167	0.0181	0.0167	0.0402	0.0125	0.0125	0.0180
ORB4	0.0264	0.0267	0.0263	0.0236	0.0250	0.0180	0.0236	0.0180	0.0125	0.0180	0.0180	0.0194	0.0180	0.0417	0.0126	0.0139	0.0182
PH1	0.0194	0.0194	0.0167	0.0208	0.0167	0.0223	0.0265	0.0209	0.0167	0.0264	0.0263	0.0277	0.0263	0.0403	0.0140	0.0112	0.0195
PH2	0.0194	0.0194	0.0167	0.0208	0.0167	0.0222	0.0264	0.0209	0.0167	0.0264	0.0263	0.0277	0.0263	0.0403	0.0139	0.0112	0.0195
PH3	0.0166	0.0180	0.0153	0.0208	0.0167	0.0223	0.0265	0.0209	0.0167	0.0250	0.0249	0.0263	0.0250	0.0403	0.0140	0.0112	0.0195
PPS1 1	0.0237	0.0236	0.0210	0.0236	0.0209	0.0111	0.0167	0.0111	0.0056	0.0125	0.0125	0.0139	0.0125	0.0346	0.0056	0.0056	0.0111
PPS1 2	0.0237	0.0236	0.0210	0.0236	0.0209	0.0111	0.0167	0.0111	0.0056	0.0125	0.0125	0.0139	0.0125	0.0346	0.0056	0.0056	0.0111
PPS2 1	0.0249	0.0208	0.0223	0.0236	0.0222	0.0083	0.0139	0.0083	0.0028	0.0097	0.0111	0.0124	0.0124	0.0346	0.0056	0.0056	0.0111
PPS2 2	0.0277	0.0236	0.0250	0.0264	0.0249	0.0083	0.0139	0.0083	0.0055	0.0097	0.0111	0.0124	0.0124	0.0374	0.0056	0.0083	0.0111
PPFE 1	0.0250	0.0224	0.0250	0.0236	0.0250	0.0099	0.0155	0.0099	0.0070	0.0085	0.0098	0.0140	0.0097	0.0374	0.0056	0.0083	0.0111
PPFE 2	0.0208	0.0197	0.0208	0.0237	0.0208	0.0098	0.0155	0.0099	0.0070	0.0056	0.0084	0.0098	0.0056	0.0375	0.0055	0.0084	0.0111
PTD1	0.0263	0.0249	0.0236	0.0250	0.0235	0.0083	0.0139	0.0083	0.0055	0.0111	0.0124	0.0138	0.0125	0.0360	0.0028	0.0055	0.0083
PTD2	0.0249	0.0250	0.0223	0.0251	0.0222	0.0083	0.0139	0.0083	0.0056	0.0111	0.0111	0.0124	0.0111	0.0361	0.0028	0.0056	0.0083
PTD3	0.0236	0.0237	0.0209	0.0237	0.0208	0.0097	0.0153	0.0097	0.0070	0.0113	0.0124	0.0138	0.0125	0.0348	0.0042	0.0070	0.0097
PTD4	0.0236	0.0237	0.0209	0.0237	0.0208	0.0125	0.0181	0.0125	0.0098	0.0141	0.0125	0.0138	0.0125	0.0376	0.0070	0.0098	0.0125
Rcrk1	0.0252	0.0282	0.0307	0.0349	0.0320	0.0224	0.0281	0.0225	0.0196	0.0084	0.0140	0.0126	0.0111	0.0503	0.0140	0.0169	0.0210
Rcrk2	0.0336	0.0368	0.0391	0.0419	0.0403	0.0281	0.0309	0.0269	0.0252	0.0184	0.0238	0.0224	0.0210	0.0588	0.0226	0.0254	0.0266
Rcrk3	0.0308	0.0297	0.0306	0.0335	0.0306	0.0182	0.0238	0.0182	0.0154	0.0140	0.0168	0.0125	0.0139	0.0490	0.0099	0.0141	0.0169
Rcrk4	0.0266	0.0255	0.0292	0.0321	0.0292	0.0197	0.0225	0.0184	0.0168	0.0098	0.0126	0.0112	0.0097	0.0476	0.0084	0.0113	0.0126

	LCT1	LCT2	LCT3	LCT4	LCT5	LMLE1	LMLE2	LMLE3	LMLE4	LMME1	LMME2	LMME3	LMME4	LMMS1	LMMS2	LMMS3	LMMS4
SGR5	0.0584	0.0599	0.0570	0.0641	0.0584	0.0629	0.0698	0.0643	0.0601	0.0670	0.0640	0.0640	0.0626	0.0433	0.0602	0.0573	0.0657
SGR6	0.0236	0.0251	0.0237	0.0265	0.0237	0.0294	0.0350	0.0294	0.0252	0.0266	0.0265	0.0237	0.0251	0.0462	0.0253	0.0224	0.0308
SGR7	0.0236	0.0251	0.0237	0.0265	0.0237	0.0294	0.0350	0.0294	0.0252	0.0266	0.0265	0.0237	0.0251	0.0462	0.0253	0.0224	0.0308
SGR8	0.0584	0.0600	0.0571	0.0642	0.0585	0.0630	0.0700	0.0644	0.0602	0.0643	0.0641	0.0613	0.0627	0.0462	0.0574	0.0546	0.0630
ShR1	0.0291	0.0265	0.0291	0.0292	0.0291	0.0167	0.0222	0.0167	0.0140	0.0083	0.0111	0.0097	0.0097	0.0474	0.0111	0.0139	0.0167
ShR2	0.0291	0.0263	0.0291	0.0291	0.0292	0.0166	0.0222	0.0166	0.0139	0.0083	0.0111	0.0097	0.0097	0.0471	0.0111	0.0138	0.0166
ShR3	0.0320	0.0291	0.0292	0.0263	0.0264	0.0139	0.0194	0.0139	0.0111	0.0111	0.0111	0.0097	0.0125	0.0444	0.0083	0.0111	0.0139
StPat1	0.0264	0.0251	0.0264	0.0235	0.0237	0.0182	0.0238	0.0182	0.0125	0.0153	0.0154	0.0168	0.0125	0.0444	0.0111	0.0111	0.0166
StPat2	0.0306	0.0293	0.0319	0.0291	0.0292	0.0209	0.0266	0.0210	0.0181	0.0153	0.0153	0.0167	0.0124	0.0499	0.0139	0.0166	0.0194
StPat3	0.0336	0.0323	0.0280	0.0279	0.0280	0.0211	0.0253	0.0197	0.0182	0.0183	0.0183	0.0168	0.0154	0.0488	0.0154	0.0182	0.0210
StPat4	0.0265	0.0266	0.0280	0.0264	0.0265	0.0182	0.0238	0.0182	0.0153	0.0140	0.0139	0.0153	0.0110	0.0472	0.0111	0.0139	0.0167
StPatME1	0.0250	0.0250	0.0224	0.0222	0.0195	0.0125	0.0180	0.0125	0.0097	0.0138	0.0111	0.0125	0.0111	0.0388	0.0069	0.0097	0.0125
StPatME2	0.0236	0.0236	0.0210	0.0208	0.0181	0.0111	0.0166	0.0111	0.0083	0.0125	0.0097	0.0111	0.0097	0.0374	0.0056	0.0083	0.0111
StPatME3	0.0236	0.0236	0.0210	0.0208	0.0181	0.0111	0.0166	0.0111	0.0083	0.0125	0.0097	0.0111	0.0097	0.0374	0.0056	0.0083	0.0111
StPatME4	0.0236	0.0236	0.0210	0.0208	0.0181	0.0111	0.0166	0.0111	0.0083	0.0125	0.0097	0.0111	0.0097	0.0374	0.0056	0.0083	0.0111
TT59_1	0.0138	0.0152	0.0126	0.0152	0.0125	0.0209	0.0251	0.0195	0.0154	0.0224	0.0208	0.0222	0.0208	0.0389	0.0154	0.0126	0.0209
TT59_2	0.0222	0.0237	0.0209	0.0237	0.0208	0.0097	0.0153	0.0097	0.0070	0.0112	0.0097	0.0111	0.0097	0.0376	0.0042	0.0070	0.0097
TT59_3	0.0222	0.0237	0.0209	0.0237	0.0208	0.0097	0.0153	0.0097	0.0070	0.0112	0.0097	0.0111	0.0097	0.0376	0.0042	0.0070	0.0097
TT76_1	0.0249	0.0251	0.0223	0.0251	0.0222	0.0097	0.0152	0.0097	0.0070	0.0111	0.0111	0.0125	0.0111	0.0361	0.0042	0.0070	0.0097
TT76_2	0.0236	0.0237	0.0209	0.0237	0.0208	0.0083	0.0139	0.0083	0.0056	0.0084	0.0097	0.0111	0.0097	0.0348	0.0028	0.0056	0.0083
TT76_3	0.0249	0.0251	0.0223	0.0251	0.0222	0.0097	0.0152	0.0097	0.0070	0.0083	0.0111	0.0124	0.0111	0.0361	0.0042	0.0070	0.0097
TT76_4	0.0236	0.0237	0.0209	0.0237	0.0208	0.0083	0.0139	0.0083	0.0056	0.0097	0.0097	0.0111	0.0097	0.0348	0.0028	0.0056	0.0083
WSC1	0.0291	0.0280	0.0263	0.0291	0.0263	0.0099	0.0155	0.0099	0.0070	0.0127	0.0126	0.0140	0.0125	0.0389	0.0056	0.0084	0.0111
WSC2	0.0291	0.0280	0.0263	0.0291	0.0263	0.0099	0.0155	0.0099	0.0070	0.0127	0.0126	0.0140	0.0125	0.0389	0.0056	0.0084	0.0111

	LPLB3	LTC1	LTC2	LTC3	MH1	MH2	MH3	MR1	MR2	MR3	MR4	NB1	NB2	NB3	NB4
LTC1	0.0472														
LTC2	0.0513	0.0028													
LTC3	0.0499	0.0055	0.0014												
MH1	0.0535	0.0717	0.0758	0.0772											
MH2	0.0507	0.0718	0.0759	0.0773	0.0056										
MH3	0.0521	0.0717	0.0758	0.0758	0.0028	0.0056									
MR1	0.0430	0.0097	0.0138	0.0124	0.0690	0.0691	0.0676								
MR2	0.0430	0.0097	0.0138	0.0124	0.0690	0.0691	0.0676	0.0000							
MR3	0.0430	0.0097	0.0138	0.0124	0.0690	0.0691	0.0676	0.0000	0.0000						
MR4	0.0430	0.0097	0.0138	0.0124	0.0690	0.0691	0.0676	0.0000	0.0000	0.0000					
NB1	0.0508	0.0676	0.0717	0.0718	0.0056	0.0084	0.0028	0.0647	0.0647	0.0647	0.0647				
NB2	0.0494	0.0662	0.0703	0.0703	0.0099	0.0098	0.0070	0.0633	0.0633	0.0633	0.0633	0.0042			
NB3	0.0508	0.0676	0.0717	0.0718	0.0056	0.0084	0.0028	0.0647	0.0647	0.0647	0.0647	0.0000	0.0042		
NB4	0.0480	0.0635	0.0676	0.0690	0.0071	0.0070	0.0071	0.0619	0.0619	0.0619	0.0619	0.0042	0.0056	0.0042	
ORB1	0.0541	0.0180	0.0222	0.0208	0.0774	0.0775	0.0760	0.0152	0.0152	0.0152	0.0152	0.0720	0.0705	0.0720	0.0691
ORB2	0.0527	0.0166	0.0208	0.0194	0.0788	0.0789	0.0774	0.0138	0.0138	0.0138	0.0138	0.0734	0.0719	0.0734	0.0705
ORB3	0.0487	0.0125	0.0153	0.0139	0.0747	0.0748	0.0733	0.0097	0.0097	0.0097	0.0097	0.0692	0.0678	0.0692	0.0664
ORB4	0.0500	0.0139	0.0166	0.0153	0.0747	0.0748	0.0733	0.0111	0.0111	0.0111	0.0111	0.0693	0.0678	0.0693	0.0665
PH1	0.0486	0.0222	0.0263	0.0249	0.0645	0.0646	0.0631	0.0152	0.0152	0.0152	0.0152	0.0619	0.0604	0.0619	0.0591
PH2	0.0486	0.0222	0.0263	0.0249	0.0645	0.0645	0.0631	0.0152	0.0152	0.0152	0.0152	0.0618	0.0604	0.0618	0.0590
PH3	0.0486	0.0208	0.0235	0.0221	0.0645	0.0646	0.0631	0.0152	0.0152	0.0152	0.0152	0.0619	0.0604	0.0619	0.0591
PPS1 1	0.0418	0.0084	0.0125	0.0111	0.0680	0.0680	0.0665	0.0042	0.0042	0.0042	0.0042	0.0636	0.0621	0.0636	0.0608
PPS1 2	0.0418	0.0084	0.0125	0.0111	0.0680	0.0680	0.0665	0.0042	0.0042	0.0042	0.0042	0.0636	0.0621	0.0636	0.0608
PPS2 1	0.0430	0.0083	0.0111	0.0097	0.0690	0.0691	0.0676	0.0055	0.0055	0.0055	0.0055	0.0647	0.0633	0.0647	0.0619
PPS2 2	0.0458	0.0111	0.0138	0.0124	0.0719	0.0719	0.0705	0.0055	0.0055	0.0055	0.0055	0.0675	0.0661	0.0675	0.0647
PPFE 1	0.0458	0.0084	0.0125	0.0139	0.0692	0.0692	0.0691	0.0055	0.0055	0.0055	0.0055	0.0662	0.0648	0.0662	0.0620
PPFE 2	0.0416	0.0069	0.0111	0.0125	0.0677	0.0677	0.0677	0.0041	0.0041	0.0041	0.0041	0.0647	0.0633	0.0647	0.0605

	LPLB3	LTC1	LTC2	LTC3	MH1	MH2	MH3	MR1	MR2	MR3	MR4	NB1	NB2	NB3	NB4
PTD1	0.0444	0.0111	0.0152	0.0138	0.0701	0.0702	0.0688	0.0028	0.0028	0.0028	0.0028	0.0647	0.0633	0.0647	0.0619
PTD2	0.0430	0.0097	0.0138	0.0124	0.0687	0.0688	0.0673	0.0014	0.0014	0.0014	0.0014	0.0633	0.0619	0.0633	0.0605
PTD3	0.0416	0.0097	0.0139	0.0125	0.0674	0.0675	0.0660	0.0028	0.0028	0.0028	0.0028	0.0619	0.0605	0.0619	0.0591
PTD4	0.0417	0.0125	0.0167	0.0153	0.0674	0.0675	0.0660	0.0055	0.0055	0.0055	0.0055	0.0648	0.0634	0.0648	0.0620
Rcrk1	0.0515	0.0126	0.0125	0.0139	0.0777	0.0778	0.0777	0.0139	0.0139	0.0139	0.0139	0.0776	0.0762	0.0776	0.0735
Rcrk2	0.0599	0.0210	0.0208	0.0222	0.0863	0.0863	0.0863	0.0236	0.0236	0.0236	0.0236	0.0862	0.0848	0.0862	0.0820
Rcrk3	0.0502	0.0180	0.0208	0.0195	0.0778	0.0779	0.0764	0.0125	0.0125	0.0125	0.0125	0.0777	0.0763	0.0777	0.0749
Rcrk4	0.0488	0.0139	0.0167	0.0181	0.0722	0.0723	0.0722	0.0111	0.0111	0.0111	0.0111	0.0749	0.0735	0.0749	0.0707
SGR5	0.0431	0.0612	0.0625	0.0625	0.0227	0.0227	0.0212	0.0597	0.0597	0.0597	0.0597	0.0227	0.0240	0.0227	0.0226
SGR6	0.0461	0.0209	0.0223	0.0223	0.0651	0.0652	0.0637	0.0251	0.0251	0.0251	0.0251	0.0625	0.0610	0.0625	0.0596
SGR7	0.0461	0.0209	0.0223	0.0223	0.0651	0.0652	0.0637	0.0251	0.0251	0.0251	0.0251	0.0625	0.0610	0.0625	0.0596
SGR8	0.0460	0.0585	0.0598	0.0598	0.0255	0.0256	0.0241	0.0599	0.0599	0.0599	0.0599	0.0256	0.0269	0.0256	0.0255
ShR1	0.0486	0.0139	0.0166	0.0180	0.0745	0.0746	0.0745	0.0097	0.0097	0.0097	0.0097	0.0733	0.0719	0.0733	0.0691
ShR2	0.0486	0.0138	0.0166	0.0180	0.0747	0.0748	0.0747	0.0097	0.0097	0.0097	0.0097	0.0735	0.0720	0.0735	0.0693
ShR3	0.0487	0.0139	0.0166	0.0152	0.0748	0.0749	0.0734	0.0069	0.0069	0.0069	0.0069	0.0721	0.0707	0.0721	0.0693
StPat1	0.0459	0.0139	0.0181	0.0195	0.0678	0.0679	0.0678	0.0125	0.0125	0.0125	0.0125	0.0694	0.0680	0.0694	0.0652
StPat2	0.0514	0.0194	0.0222	0.0236	0.0748	0.0748	0.0747	0.0125	0.0125	0.0125	0.0125	0.0763	0.0749	0.0763	0.0721
StPat3	0.0503	0.0210	0.0252	0.0238	0.0791	0.0791	0.0777	0.0140	0.0140	0.0140	0.0140	0.0793	0.0778	0.0793	0.0765
StPat4	0.0487	0.0153	0.0181	0.0195	0.0722	0.0723	0.0722	0.0125	0.0125	0.0125	0.0125	0.0748	0.0733	0.0748	0.0706
StPatME1	0.0431	0.0125	0.0166	0.0153	0.0694	0.0694	0.0679	0.0055	0.0055	0.0055	0.0055	0.0679	0.0664	0.0679	0.0650
StPatME2	0.0417	0.0111	0.0153	0.0139	0.0679	0.0679	0.0665	0.0041	0.0041	0.0041	0.0041	0.0664	0.0650	0.0664	0.0636
StPatME3	0.0417	0.0111	0.0153	0.0139	0.0679	0.0679	0.0665	0.0041	0.0041	0.0041	0.0041	0.0664	0.0650	0.0664	0.0636
StPatME4	0.0417	0.0111	0.0153	0.0139	0.0679	0.0679	0.0665	0.0041	0.0041	0.0041	0.0041	0.0664	0.0650	0.0664	0.0636
TT59_1	0.0430	0.0180	0.0209	0.0195	0.0631	0.0632	0.0617	0.0138	0.0138	0.0138	0.0138	0.0605	0.0591	0.0605	0.0577
TT59_2	0.0417	0.0097	0.0125	0.0111	0.0674	0.0675	0.0660	0.0028	0.0028	0.0028	0.0028	0.0648	0.0634	0.0648	0.0620
TT59_3	0.0417	0.0097	0.0125	0.0111	0.0674	0.0675	0.0660	0.0028	0.0028	0.0028	0.0028	0.0648	0.0634	0.0648	0.0620
TT76_1	0.0430	0.0097	0.0138	0.0125	0.0691	0.0691	0.0677	0.0028	0.0028	0.0028	0.0028	0.0647	0.0633	0.0647	0.0619
TT76_2	0.0416	0.0069	0.0111	0.0097	0.0677	0.0677	0.0663	0.0014	0.0014	0.0014	0.0014	0.0633	0.0619	0.0633	0.0605
TT76_3	0.0430	0.0069	0.0111	0.0097	0.0690	0.0691	0.0676	0.0028	0.0028	0.0028	0.0028	0.0647	0.0633	0.0647	0.0619
TT76_4	0.0416	0.0083	0.0124	0.0111	0.0677	0.0677	0.0662	0.0014	0.0014	0.0014	0.0014	0.0633	0.0619	0.0633	0.0605
WSC1	0.0458	0.0111	0.0153	0.0139	0.0716	0.0717	0.0702	0.0042	0.0042	0.0042	0.0042	0.0662	0.0648	0.0662	0.0634
WSC2	0.0458	0.0111	0.0153	0.0139	0.0716	0.0717	0.0702	0.0042	0.0042	0.0042	0.0042	0.0662	0.0648	0.0662	0.0634

	ORB1	ORB2	ORB3	ORB4	PH1	PH2	PH3	PPS1 1	PPS1 2	PPS2 1	PPS2 2	PPFE 1	PPFE 2	PTD1	PTD2	PTD3	PTD4
ORB2	0.0014																
ORB3	0.0055	0.0041															
ORB4	0.0069	0.0055	0.0014														
PH1	0.0249	0.0236	0.0194	0.0208													
PH2	0.0249	0.0235	0.0194	0.0208	0.0014												
PH3	0.0249	0.0236	0.0181	0.0194	0.0028	0.0028											
PPS1 1	0.0138	0.0125	0.0083	0.0097	0.0139	0.0139	0.0139										
PPS1 2	0.0138	0.0125	0.0083	0.0097	0.0139	0.0139	0.0139	0.0000									
PPS2 1	0.0138	0.0125	0.0083	0.0111	0.0152	0.0152	0.0152	0.0028	0.0028								
PPS2 2	0.0152	0.0138	0.0111	0.0139	0.0180	0.0180	0.0180	0.0055	0.0055	0.0028							
PPFE 1	0.0139	0.0125	0.0083	0.0111	0.0180	0.0180	0.0180	0.0055	0.0055	0.0041	0.0041						
PPFE 2	0.0166	0.0152	0.0111	0.0125	0.0166	0.0166	0.0166	0.0056	0.0056	0.0055	0.0055	0.0042					
PTD1	0.0152	0.0138	0.0097	0.0125	0.0152	0.0152	0.0152	0.0028	0.0028	0.0028	0.0028	0.0028	0.0042				
PTD2	0.0152	0.0138	0.0097	0.0111	0.0138	0.0138	0.0138	0.0028	0.0028	0.0041	0.0041	0.0042	0.0028	0.0014			
PTD3	0.0167	0.0153	0.0111	0.0125	0.0125	0.0125	0.0125	0.0042	0.0042	0.0055	0.0055	0.0055	0.0042	0.0028	0.0014		
PTD4	0.0194	0.0181	0.0139	0.0152	0.0152	0.0152	0.0152	0.0070	0.0070	0.0083	0.0083	0.0083	0.0069	0.0055	0.0042	0.0028	
Rcrk1	0.0307	0.0293	0.0238	0.0251	0.0306	0.0306	0.0278	0.0182	0.0182	0.0180	0.0180	0.0167	0.0125	0.0167	0.0153	0.0156	0.0156
Rcrk2	0.0391	0.0377	0.0324	0.0323	0.0390	0.0390	0.0362	0.0267	0.0267	0.0264	0.0264	0.0250	0.0209	0.0250	0.0236	0.0240	0.0240
Rcrk3	0.0293	0.0279	0.0237	0.0223	0.0278	0.0278	0.0265	0.0168	0.0168	0.0166	0.0166	0.0181	0.0139	0.0153	0.0139	0.0153	0.0125
Rcrk4	0.0279	0.0265	0.0224	0.0237	0.0251	0.0251	0.0237	0.0154	0.0154	0.0153	0.0153	0.0139	0.0097	0.0139	0.0125	0.0139	0.0139
SGR5	0.0683	0.0697	0.0656	0.0656	0.0555	0.0555	0.0555	0.0572	0.0572	0.0583	0.0611	0.0614	0.0600	0.0611	0.0597	0.0583	0.0584
SGR6	0.0335	0.0322	0.0280	0.0279	0.0237	0.0236	0.0237	0.0224	0.0224	0.0237	0.0265	0.0266	0.0252	0.0265	0.0251	0.0237	0.0237
SGR7	0.0335	0.0322	0.0280	0.0279	0.0237	0.0236	0.0237	0.0224	0.0224	0.0237	0.0265	0.0266	0.0252	0.0265	0.0251	0.0237	0.0237
SGR8	0.0685	0.0699	0.0658	0.0657	0.0557	0.0557	0.0557	0.0573	0.0573	0.0584	0.0612	0.0615	0.0601	0.0612	0.0598	0.0585	0.0585
ShR1	0.0250	0.0236	0.0195	0.0208	0.0263	0.0263	0.0263	0.0139	0.0139	0.0125	0.0125	0.0084	0.0070	0.0125	0.0111	0.0125	0.0125
ShR2	0.0249	0.0235	0.0194	0.0207	0.0264	0.0263	0.0264	0.0138	0.0138	0.0111	0.0111	0.0070	0.0070	0.0111	0.0110	0.0125	0.0125
ShR3	0.0194	0.0180	0.0166	0.0180	0.0236	0.0236	0.0236	0.0111	0.0111	0.0083	0.0083	0.0070	0.0098	0.0083	0.0083	0.0097	0.0097
StPat1	0.0194	0.0180	0.0166	0.0180	0.0209	0.0208	0.0209	0.0111	0.0111	0.0097	0.0125	0.0083	0.0083	0.0111	0.0111	0.0125	0.0125
StPat2	0.0249	0.0235	0.0222	0.0235	0.0264	0.0264	0.0250	0.0166	0.0166	0.0152	0.0152	0.0111	0.0111	0.0139	0.0138	0.0153	0.0153
StPat3	0.0224	0.0211	0.0197	0.0211	0.0257	0.0256	0.0257	0.0168	0.0168	0.0154	0.0154	0.0140	0.0140	0.0154	0.0154	0.0168	0.0168
StPat4	0.0222	0.0208	0.0181	0.0194	0.0237	0.0237	0.0209	0.0139	0.0139	0.0125	0.0125	0.0083	0.0083	0.0111	0.0111	0.0125	0.0125
StPatME1	0.0152	0.0138	0.0125	0.0139	0.0181	0.0181	0.0181	0.0069	0.0069	0.0069	0.0069	0.0069	0.0069	0.0042	0.0042	0.0056	0.0056
StPatME2	0.0138	0.0125	0.0111	0.0125	0.0167	0.0167	0.0167	0.0055	0.0055	0.0055	0.0055	0.0055	0.0055	0.0028	0.0028	0.0042	0.0042
StPatME3	0.0138	0.0125	0.0111	0.0125	0.0167	0.0167	0.0167	0.0055	0.0055	0.0055	0.0055	0.0055	0.0055	0.0028	0.0028	0.0042	0.0042
StPatME4	0.0138	0.0125	0.0111	0.0125	0.0167	0.0167	0.0167	0.0055	0.0055	0.0055	0.0055	0.0055	0.0055	0.0028	0.0028	0.0042	0.0042
TT59_1	0.0250	0.0236	0.0195	0.0208	0.0069	0.0069	0.0055	0.0126	0.0126	0.0138	0.0166	0.0166	0.0152	0.0138	0.0124	0.0111	0.0111
TT59_2	0.0166	0.0153	0.0111	0.0125	0.0152	0.0152	0.0139	0.0042	0.0042	0.0055	0.0055	0.0055	0.0042	0.0028	0.0014	0.0028	0.0028
TT59_3	0.0166	0.0153	0.0111	0.0125	0.0152	0.0152	0.0139	0.0042	0.0042	0.0055	0.0055	0.0055	0.0042	0.0028	0.0014	0.0028	0.0028
TT76_1	0.0152	0.0139	0.0097	0.0111	0.0152	0.0152	0.0152	0.0042	0.0042	0.0055	0.0055	0.0055	0.0041	0.0028	0.0014	0.0028	0.0055
TT76_2	0.0139	0.0125	0.0083	0.0097	0.0139	0.0139	0.0139	0.0028	0.0028	0.0041	0.0041	0.0042	0.0028	0.0014	0.0000	0.0014	0.0042
TT76_3	0.0152	0.0138	0.0097	0.0111	0.0152	0.0152	0.0152	0.0042	0.0042	0.0055	0.0055	0.0055	0.0041	0.0028	0.0014	0.0014	0.0041
TT76_4	0.0139	0.0125	0.0083	0.0097	0.0139	0.0139	0.0139	0.0028	0.0028	0.0041	0.0041	0.0042	0.0028	0.0014	0.0000	0.0014	0.0042
WSC1	0.0194	0.0180	0.0139	0.0152	0.0180	0.0180	0.0180	0.0056	0.0056	0.0055	0.0055	0.0069	0.0055	0.0042	0.0028	0.0042	0.0069
WSC2	0.0194	0.0180	0.0139	0.0152	0.0180	0.0180	0.0180	0.0056	0.0056	0.0055	0.0055	0.0069	0.0055	0.0042	0.0028	0.0042	0.0069

	Rcrk1	Rcrk2	Rcrk3	Rcrk4	SGR5	SGR6	SGR7	SGR8	ShR1	ShR2	ShR3	StPat1	StPat2	StPat3	StPat4
Rcrk2	0.0125														
Rcrk3	0.0139	0.0196													
Rcrk4	0.0097	0.0140	0.0111												
SGR5	0.0671	0.0756	0.0672	0.0644											
SGR6	0.0282	0.0367	0.0295	0.0282	0.0444										
SGR7	0.0282	0.0367	0.0295	0.0282	0.0444	0.0000									
SGR8	0.0631	0.0716	0.0632	0.0604	0.0028	0.0417	0.0417								
ShR1	0.0097	0.0196	0.0112	0.0070	0.0668	0.0293	0.0293	0.0640							
ShR2	0.0111	0.0210	0.0125	0.0083	0.0670	0.0294	0.0294	0.0642	0.0028						
ShR3	0.0140	0.0239	0.0126	0.0112	0.0642	0.0266	0.0266	0.0615	0.0055	0.0055					
StPat1	0.0182	0.0266	0.0182	0.0126	0.0616	0.0295	0.0295	0.0618	0.0098	0.0097	0.0098				
StPat2	0.0167	0.0267	0.0181	0.0126	0.0672	0.0351	0.0351	0.0673	0.0097	0.0097	0.0097	0.0083			
StPat3	0.0226	0.0310	0.0198	0.0170	0.0672	0.0351	0.0351	0.0674	0.0155	0.0154	0.0126	0.0126	0.0141		
StPat4	0.0153	0.0237	0.0167	0.0111	0.0657	0.0336	0.0336	0.0658	0.0098	0.0097	0.0098	0.0042	0.0069	0.0111	
StPatME1	0.0167	0.0252	0.0153	0.0139	0.0600	0.0252	0.0252	0.0601	0.0125	0.0125	0.0069	0.0097	0.0125	0.0126	0.0097
StPatME2	0.0154	0.0238	0.0139	0.0126	0.0586	0.0238	0.0238	0.0587	0.0111	0.0111	0.0055	0.0083	0.0111	0.0112	0.0083
StPatME3	0.0154	0.0238	0.0139	0.0126	0.0586	0.0238	0.0238	0.0587	0.0111	0.0111	0.0055	0.0083	0.0111	0.0112	0.0083
StPatME4	0.0154	0.0238	0.0139	0.0126	0.0586	0.0238	0.0238	0.0587	0.0111	0.0111	0.0055	0.0083	0.0111	0.0112	0.0083
TT59_1	0.0225	0.0309	0.0236	0.0223	0.0527	0.0181	0.0181	0.0529	0.0208	0.0208	0.0181	0.0181	0.0236	0.0252	0.0196
TT59_2	0.0113	0.0196	0.0125	0.0111	0.0584	0.0237	0.0237	0.0585	0.0097	0.0097	0.0069	0.0097	0.0125	0.0140	0.0083
TT59_3	0.0113	0.0196	0.0125	0.0111	0.0584	0.0237	0.0237	0.0585	0.0097	0.0097	0.0069	0.0097	0.0125	0.0140	0.0083
TT76_1	0.0167	0.0250	0.0153	0.0139	0.0597	0.0251	0.0251	0.0599	0.0125	0.0124	0.0097	0.0125	0.0152	0.0154	0.0125
TT76_2	0.0140	0.0224	0.0139	0.0125	0.0584	0.0237	0.0237	0.0585	0.0111	0.0111	0.0083	0.0111	0.0138	0.0140	0.0111
TT76_3	0.0139	0.0223	0.0153	0.0139	0.0597	0.0251	0.0251	0.0599	0.0125	0.0124	0.0097	0.0125	0.0152	0.0154	0.0125
TT76_4	0.0153	0.0236	0.0139	0.0125	0.0583	0.0237	0.0237	0.0585	0.0111	0.0111	0.0083	0.0111	0.0138	0.0140	0.0111
WSC1	0.0181	0.0264	0.0139	0.0153	0.0613	0.0266	0.0266	0.0615	0.0126	0.0126	0.0098	0.0139	0.0166	0.0181	0.0138
WSC2	0.0181	0.0264	0.0139	0.0153	0.0613	0.0266	0.0266	0.0615	0.0126	0.0126	0.0098	0.0139	0.0166	0.0181	0.0138

	StPatME1	StPatME2	StPatME3	StPatME4	TT59_1	TT59_2	TT59_3	TT76_1	TT76_2	TT76_3	TT76_4	WSC1
StPatME2	0.0014											
StPatME3	0.0014	0.0000										
StPatME4	0.0014	0.0000	0.0000									
TT59_1	0.0139	0.0125	0.0125	0.0125								
TT59_2	0.0028	0.0014	0.0014	0.0014	0.0111							
TT59_3	0.0028	0.0014	0.0014	0.0014	0.0111	0.0000						
TT76_1	0.0055	0.0041	0.0041	0.0041	0.0138	0.0028	0.0028					
TT76_2	0.0041	0.0028	0.0028	0.0028	0.0125	0.0014	0.0014	0.0014				
TT76_3	0.0055	0.0041	0.0041	0.0041	0.0125	0.0014	0.0014	0.0028	0.0000			
TT76_4	0.0041	0.0028	0.0028	0.0028	0.0125	0.0014	0.0014	0.0014	0.0000	0.0014		
WSC1	0.0069	0.0055	0.0055	0.0055	0.0152	0.0042	0.0042	0.0042	0.0028	0.0042	0.0028	
WSC2	0.0069	0.0055	0.0055	0.0055	0.0152	0.0042	0.0042	0.0042	0.0028	0.0042	0.0028	0.0000